Distinguishing modes of convergent adaptation

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Convergent adaptation

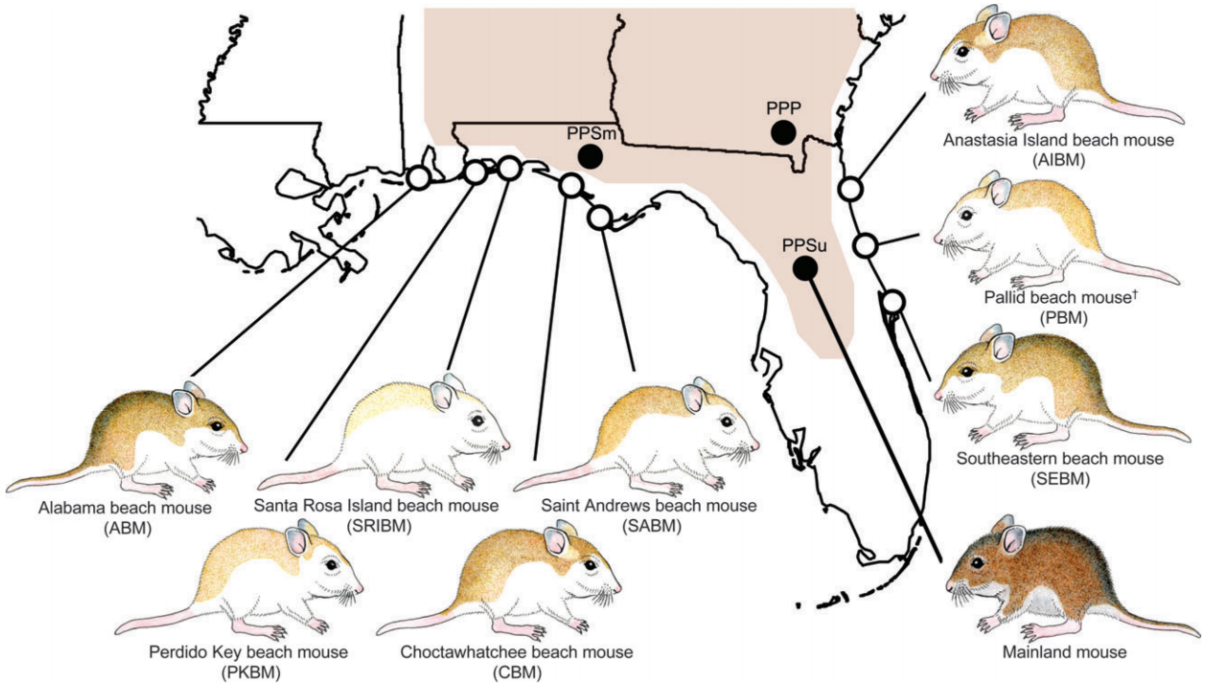
Adaptation across similar environments

Many levels of convergent adaptation:

Phenotypic level across species

http://webecoist.momtastic.com/2012/09/10/arctic-animals-37-photos-of-snow-white-wildlife/

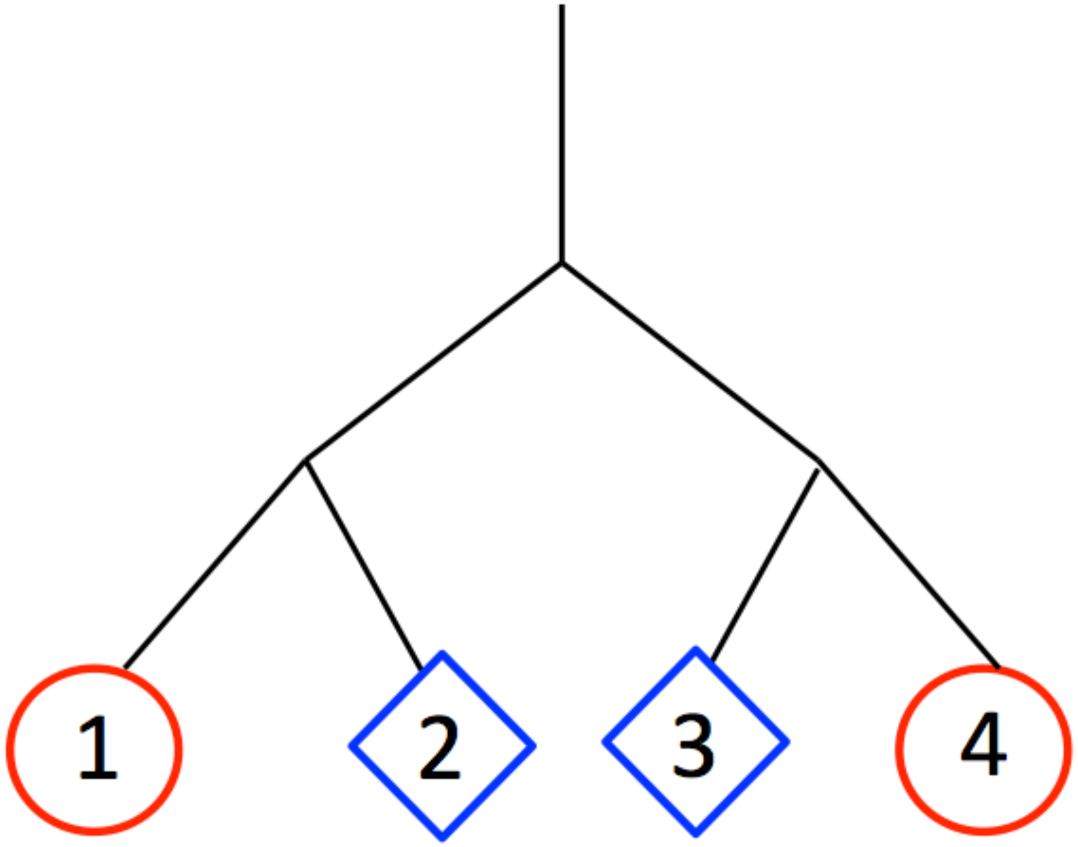
Phenotypic level within species



Steiner et al., *MBE* (2009)

Modes of genotypic convergent adaptation

Multiple populations respond to similar environmental pressure using same genes



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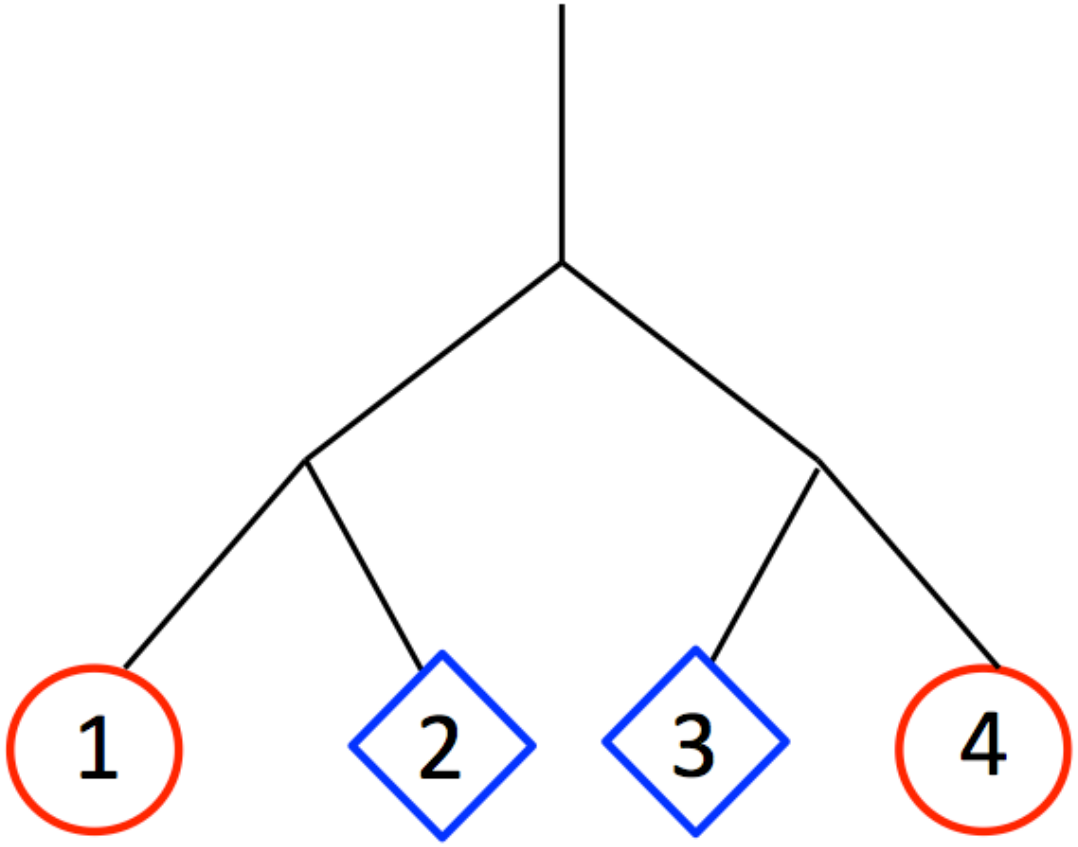

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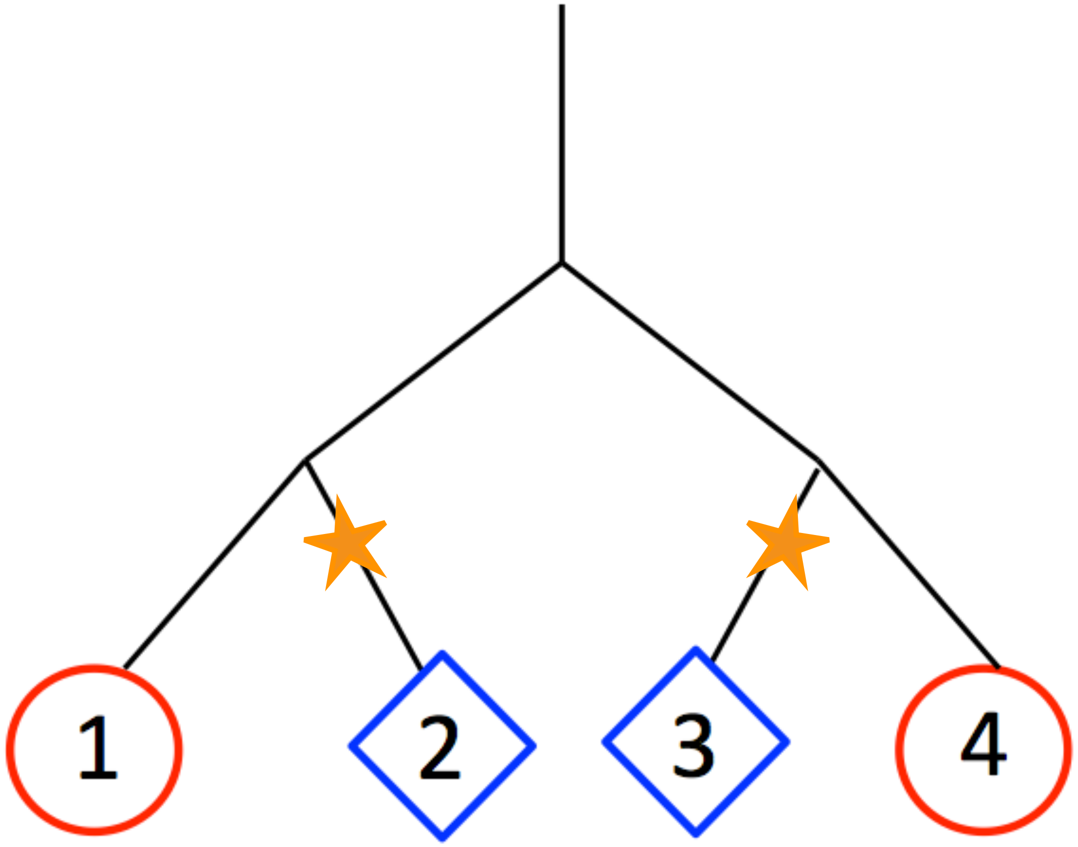
1. Independent mutations in isolated populations



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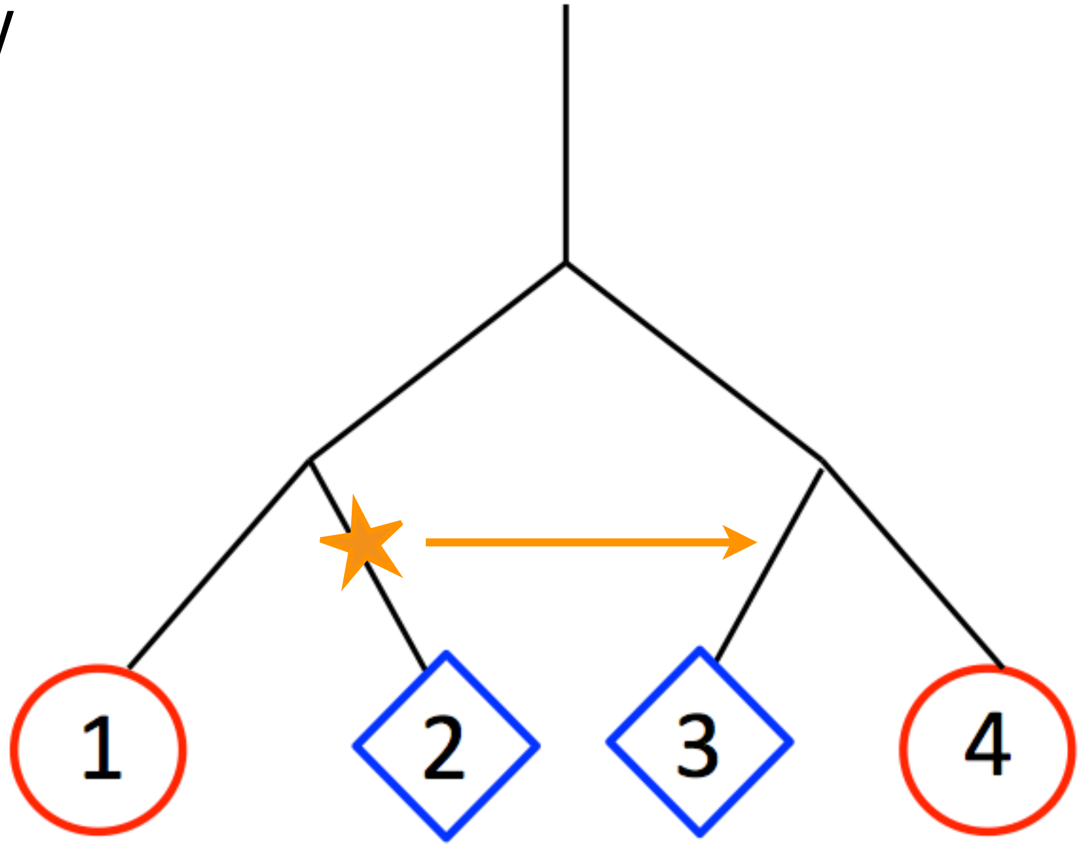
1. Independent mutations in isolated populations
2. Single origin with gene flow

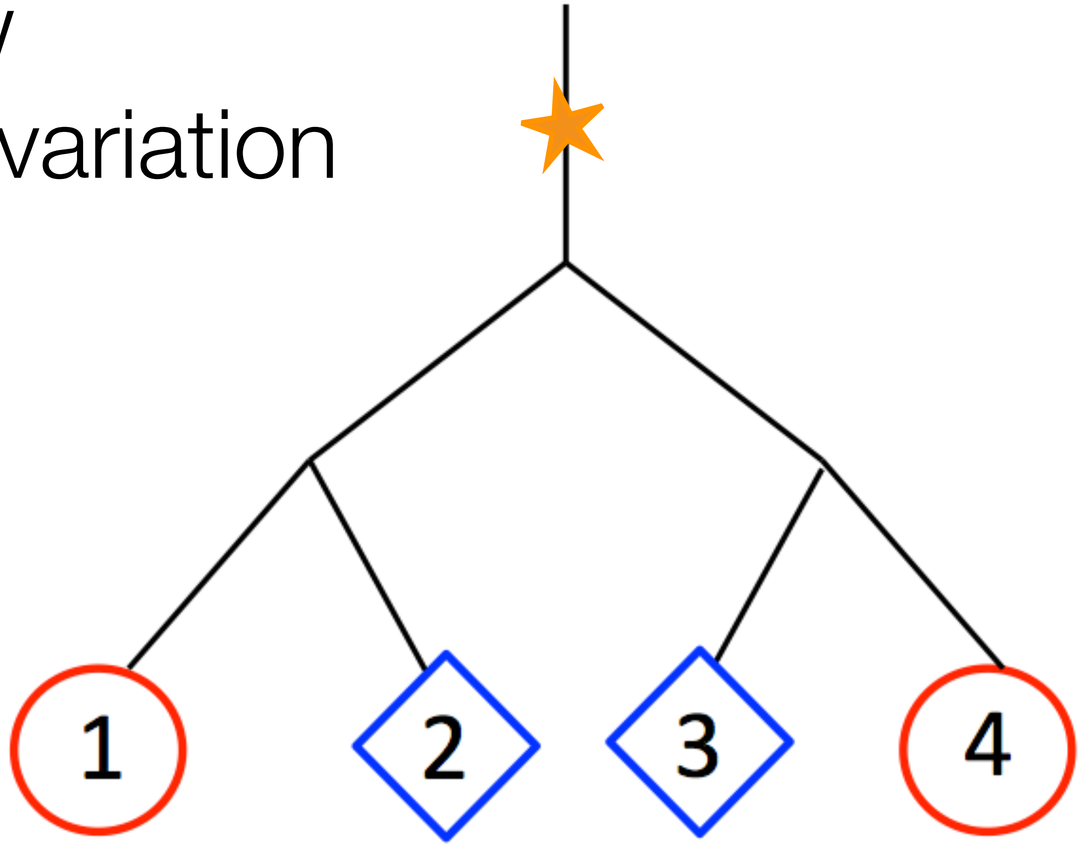


Modes of genotypic convergent adaptation

Multiple populations respond to similar environmental pressure using same genes

What is the basis of this adaptation?

1. Independent mutations in isolated populations
2. Single origin with gene flow
3. Shared ancestral standing variation

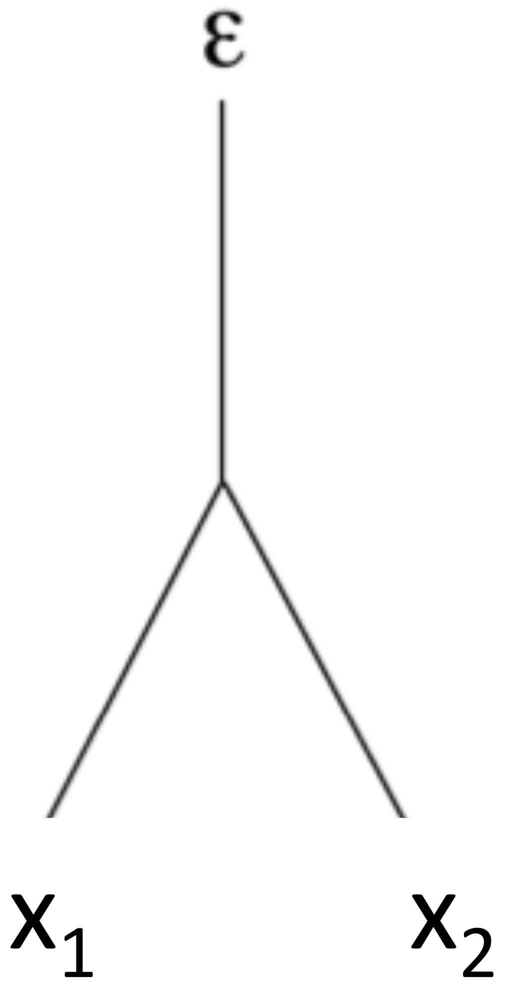


How can we distinguish modes of convergent adaptation using population genomic data?

1. Model allele frequencies around selected site
    - Null model
    - Variance within populations experiencing selection
    - Covariance between selected populations

2. Composite-likelihood approach to distinguish between these models

Effect of drift on population allele frequencies



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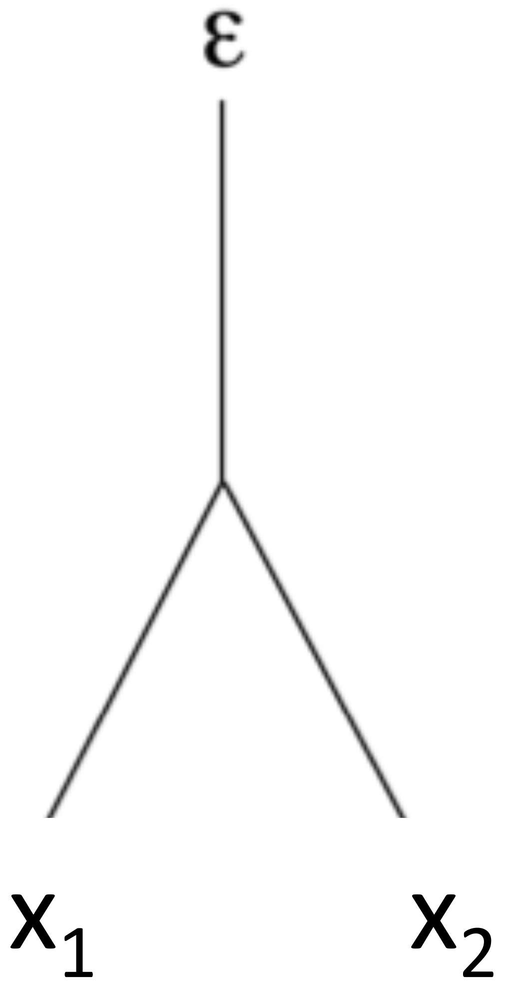

$$\mathbb{E}[\Delta x_1] = \mathbb{E}[\Delta x_2] = 0$$

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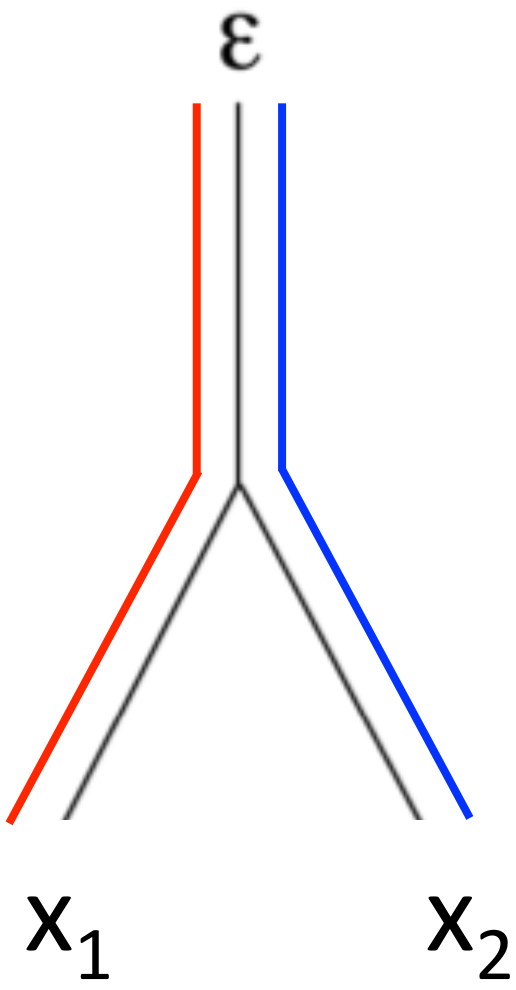

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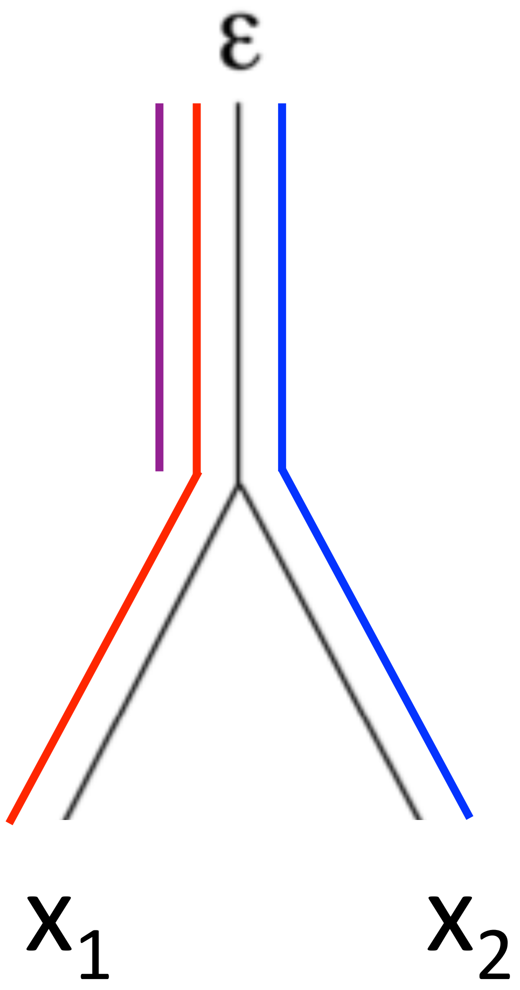

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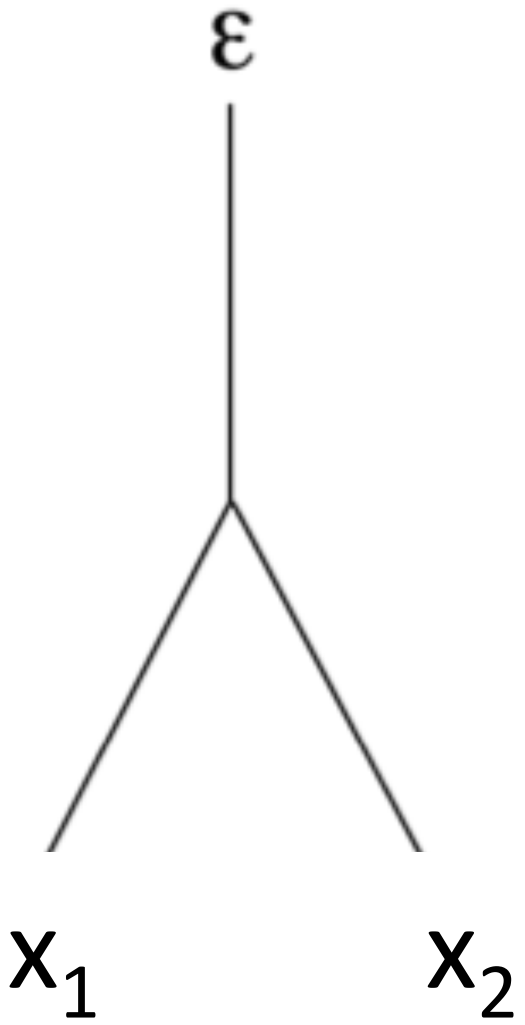
$$\mathrm{Cov}[\Delta x_1] = \epsilon(1-\epsilon) f_{12}$$

Coancestry coefficients

$$f_{ii} = \frac{\mathrm{Var}[x_i]}{\epsilon(1-\epsilon)}$$



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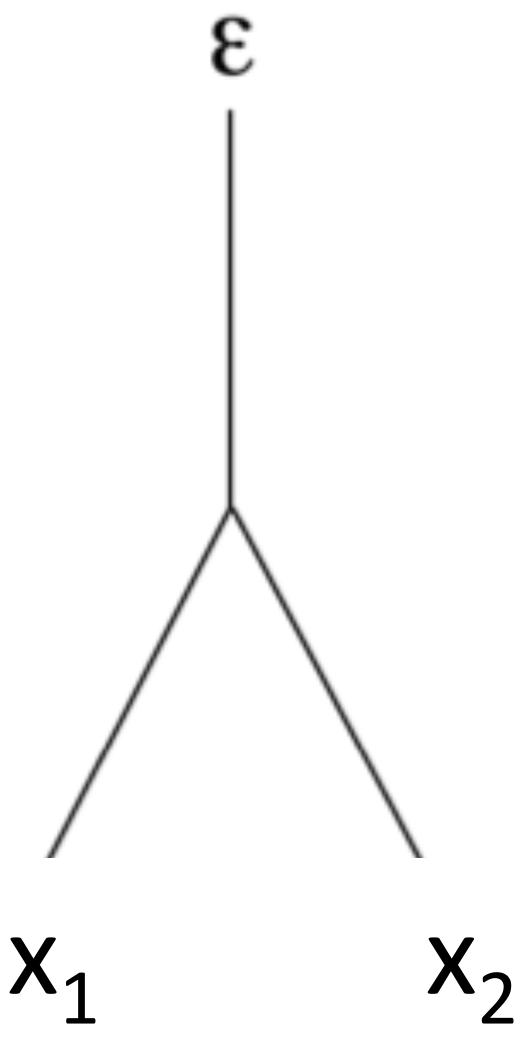
Probability a pair of lineages coalesce before reaching the ancestral population



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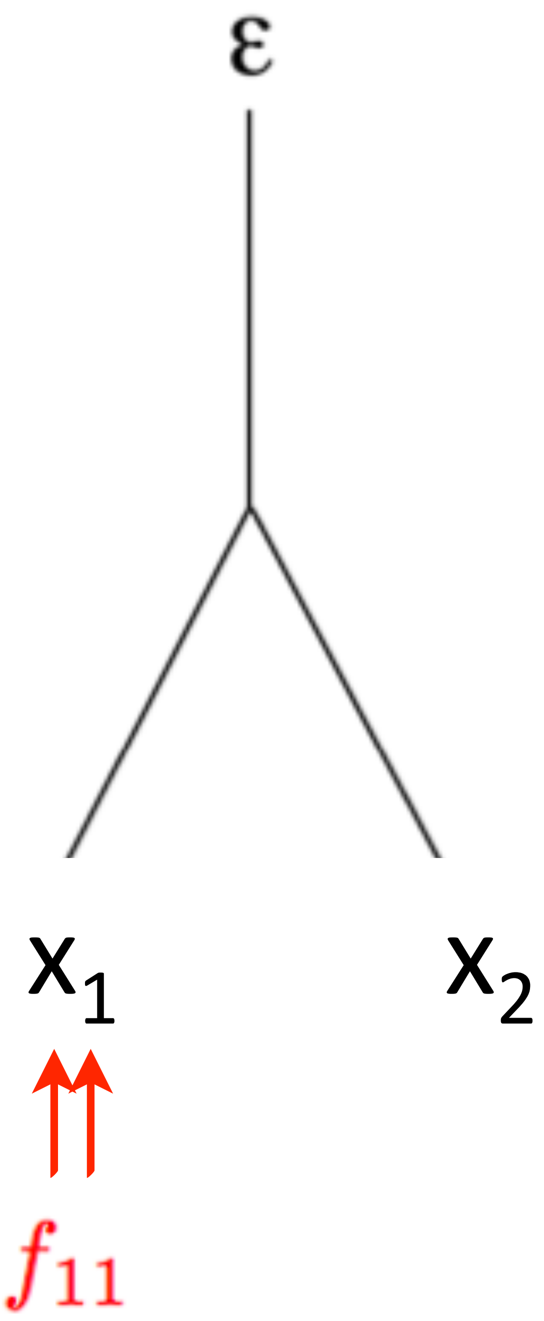

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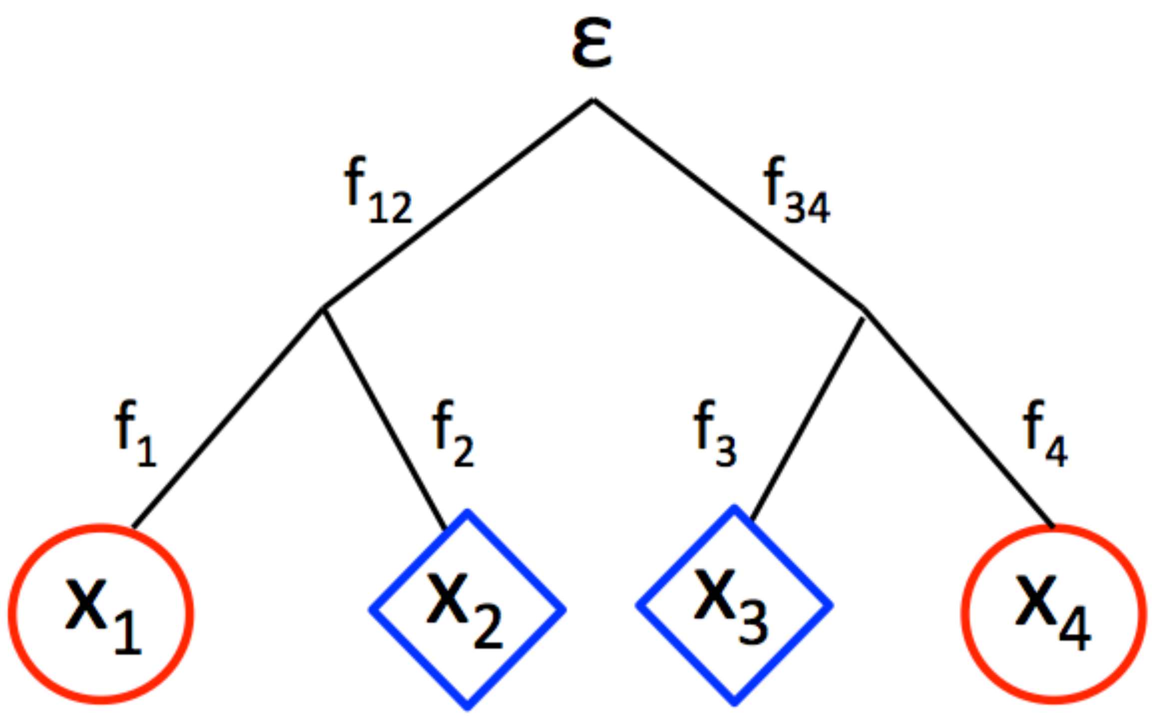
Four population model



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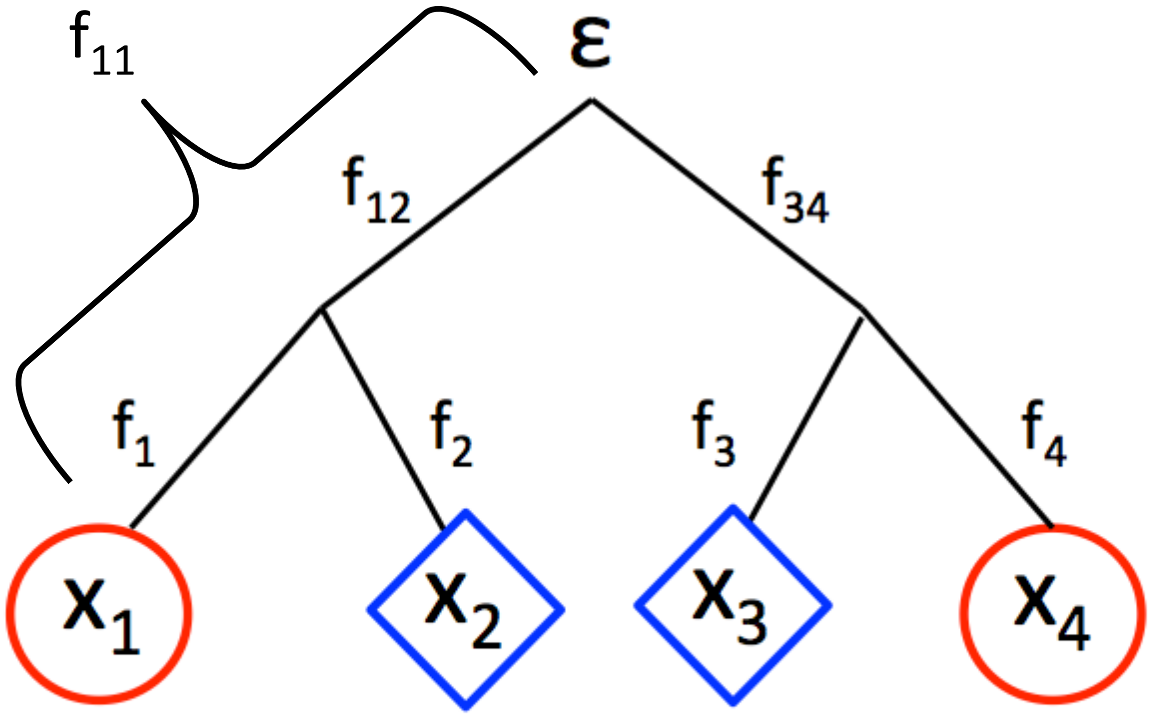

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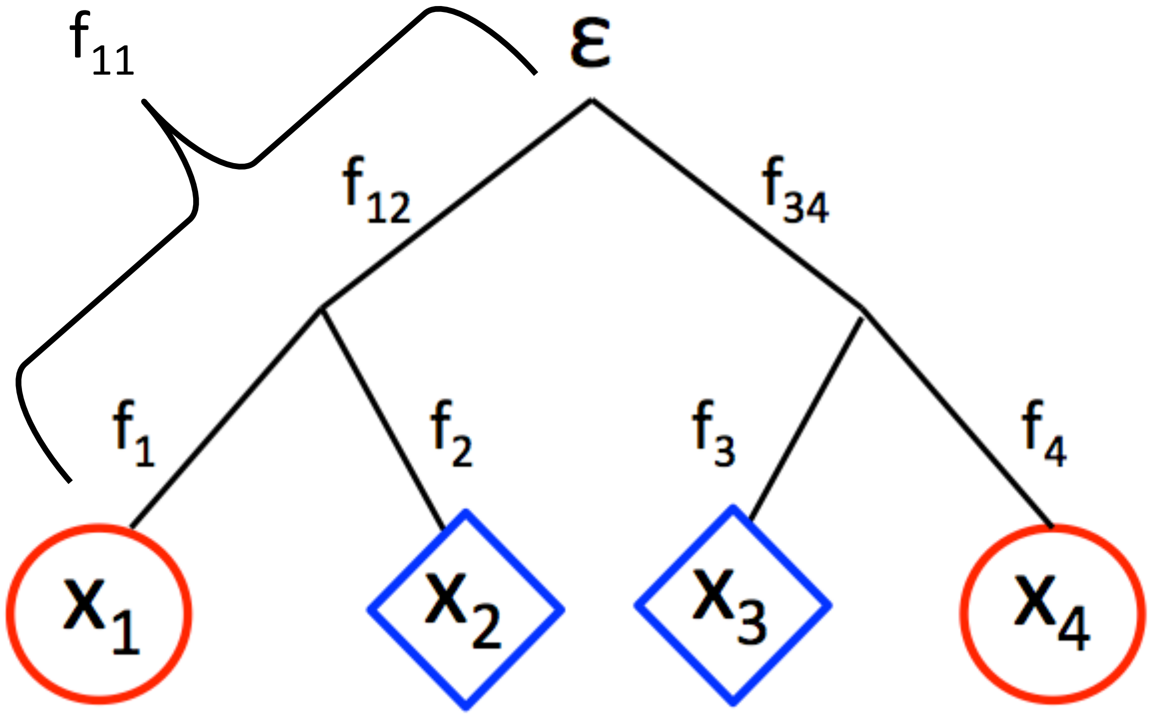

$$\mathbf{F} = \begin{bmatrix} f_{11} & f_{12} & 0 & 0 \\ f_{12} & f_{22} & 0 & 0 \\ 0 & 0 & f_{33} & f_{34} \\ 0 & 0 & f_{34} & f_{44} \end{bmatrix}$$

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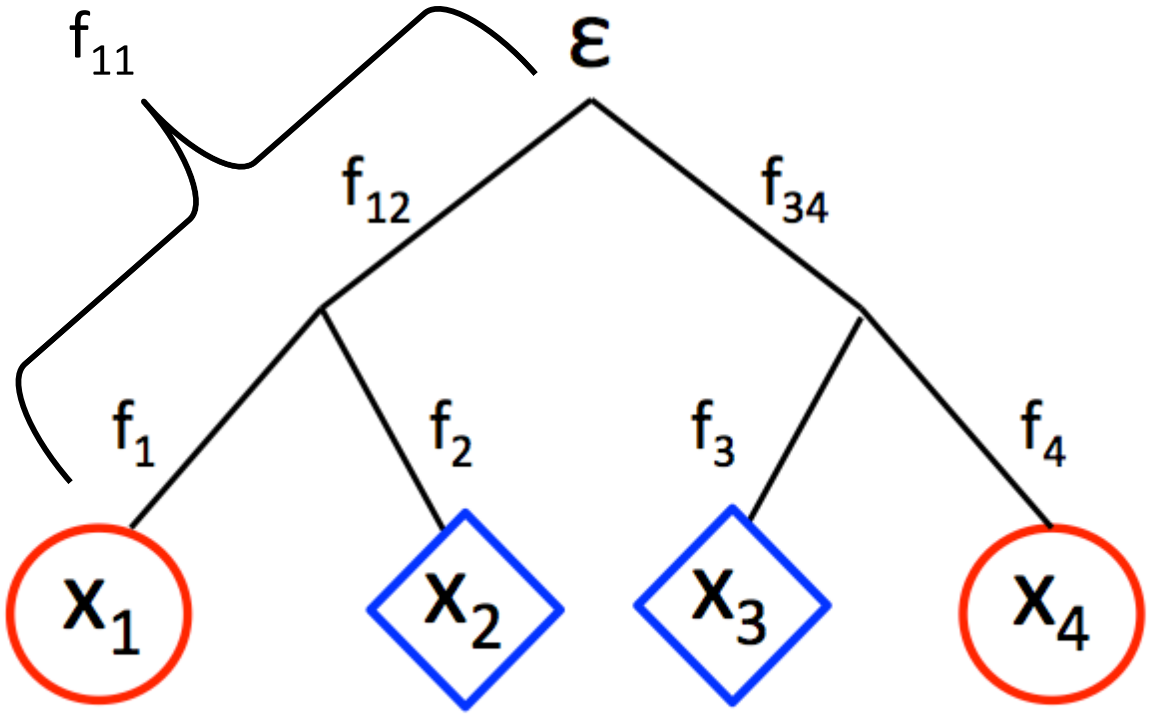

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We can model population allele frequencies as multivariate normal

$$\vec{x} \sim \mathcal{N}(\epsilon\vec{1},\, \epsilon(1-\epsilon)\mathbf{F})$$

Cavalli-Sforza et al., 1964; Nicholson et al., 2002;
Weir and Hill, 2002; Coop et al., 2010; Samanta et al., 2009

Effect of hitchhiking

Selection impacts linked neutral allele frequencies

$$\mathbb{E}[\Delta x_1] = 0$$

$$\mathrm{Var}[\Delta x_1] = \epsilon(1 - \epsilon)y^2$$

JH Gillespie, *Genetics* (2000)

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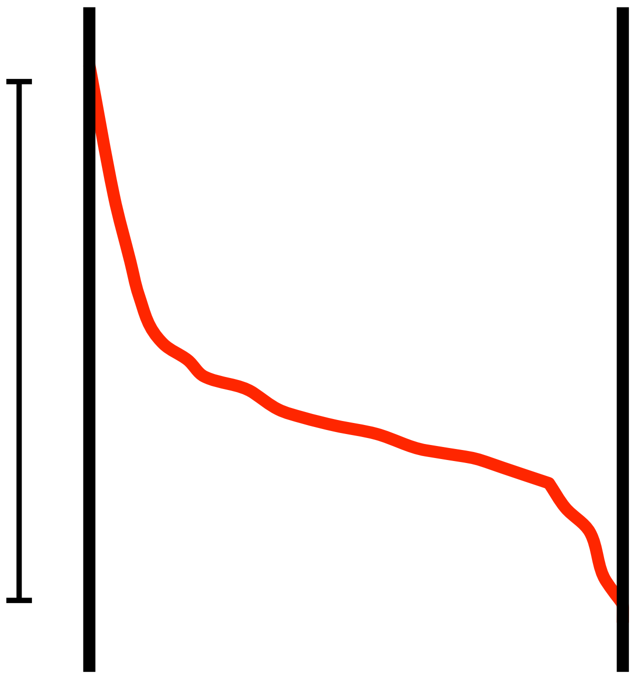
Probability a pair of lineages coalesce during the selective sweep

JH Gillespie, *Genetics* (2000)

Selective sweeps increase probability of coalescing

y^2 = probability two lineages coalesce during the sweep = probability neither recombine off of the beneficial background

$$t_s \approx \frac{2log(2N_e)}{s}$$



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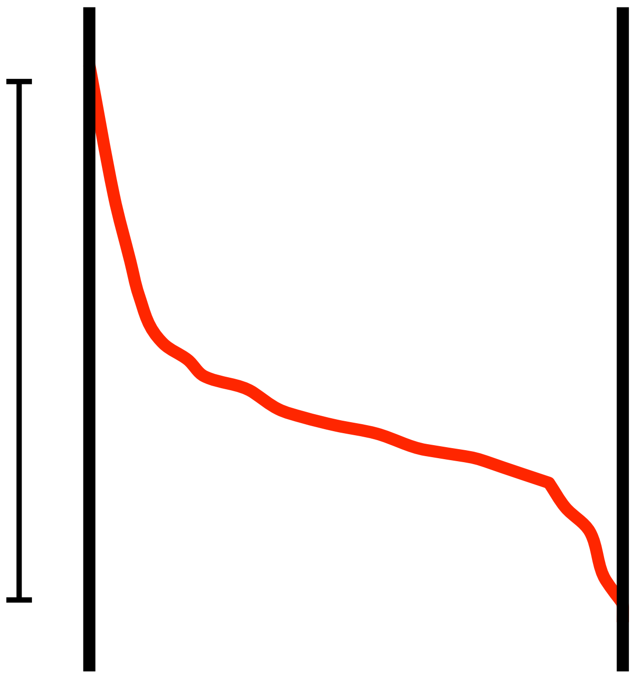

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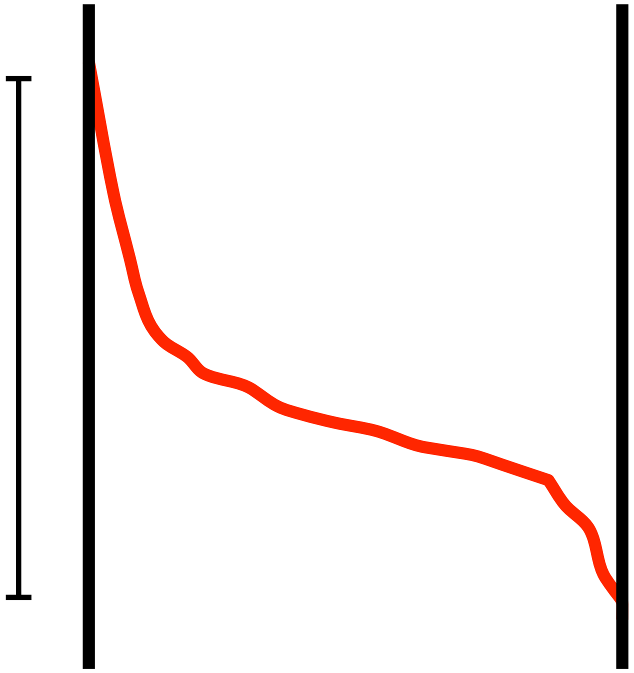

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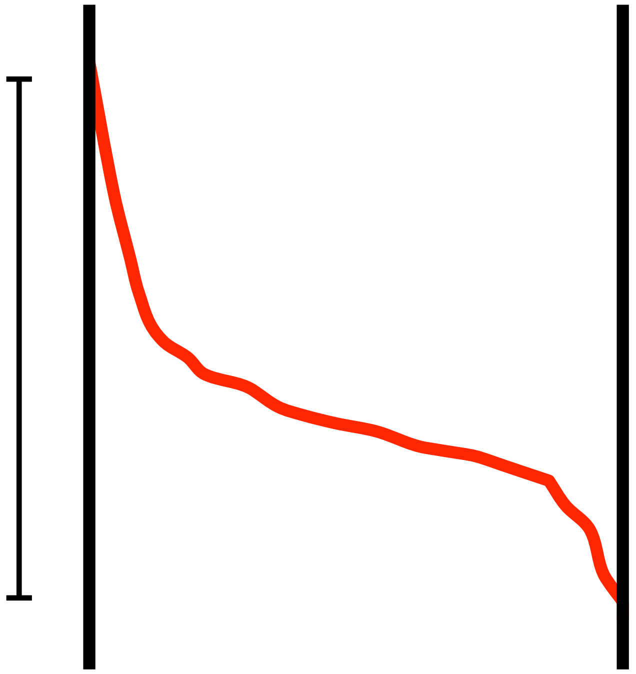

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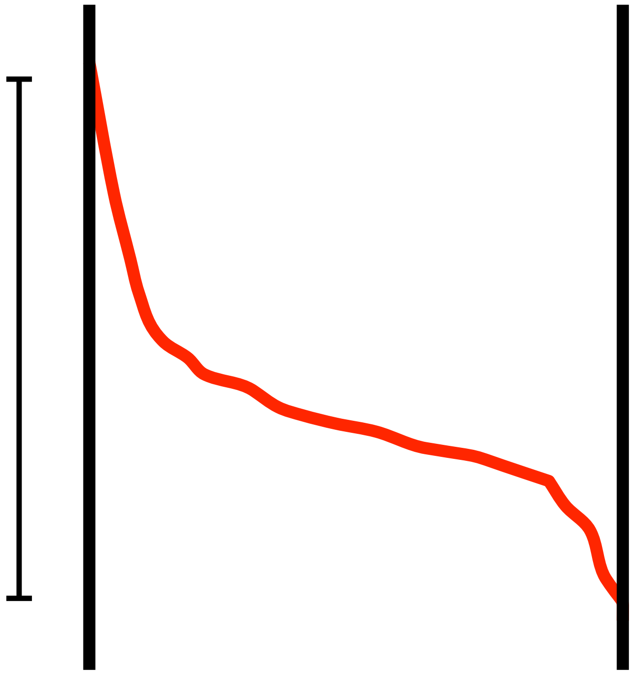

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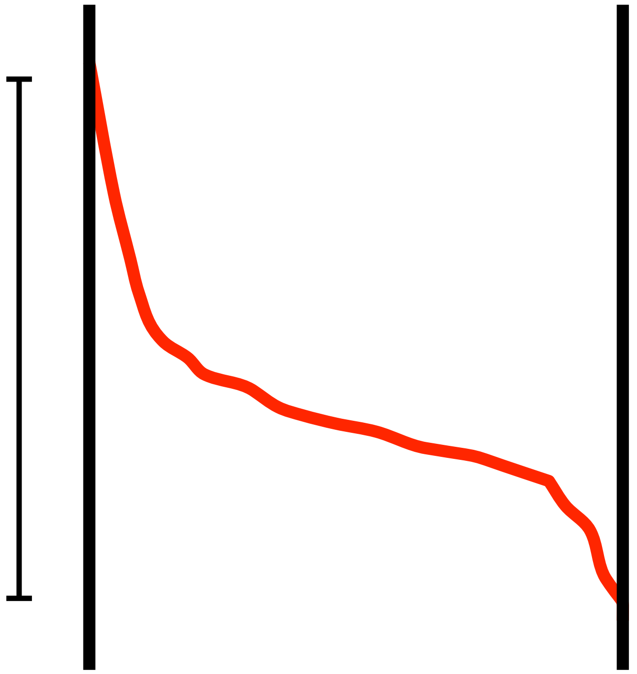

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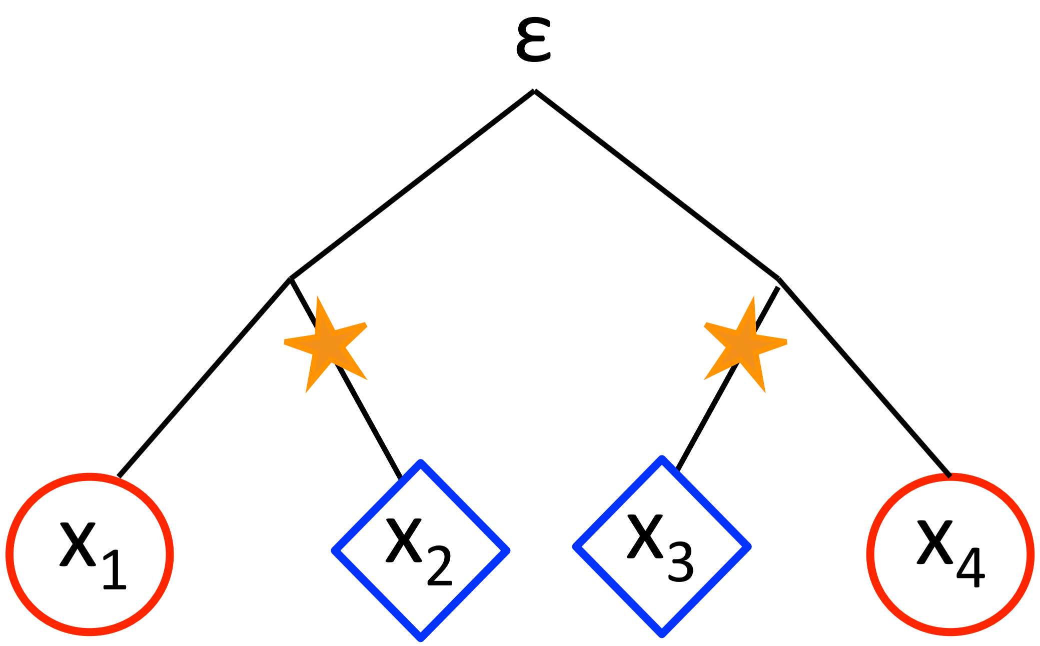

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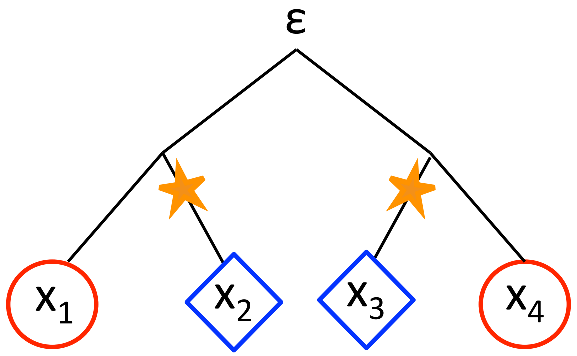
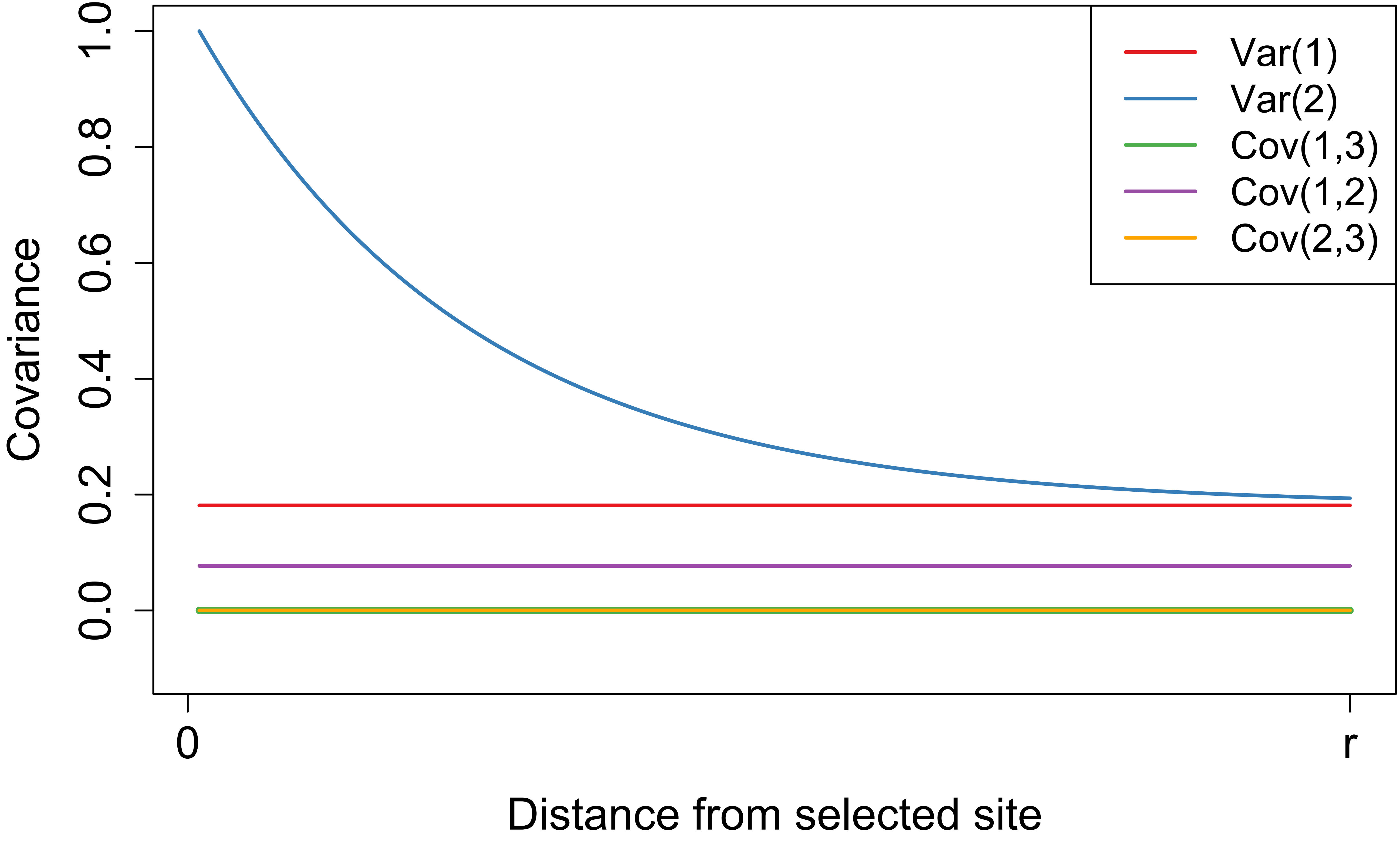
Independent mutation model variances and covariances





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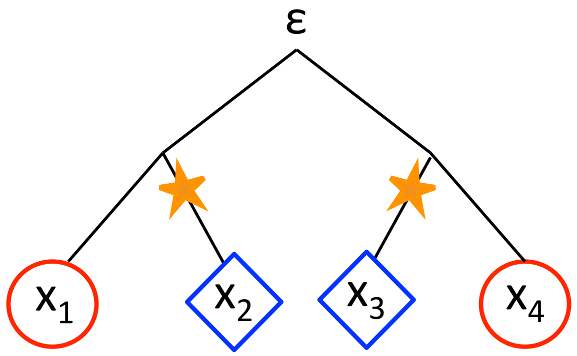
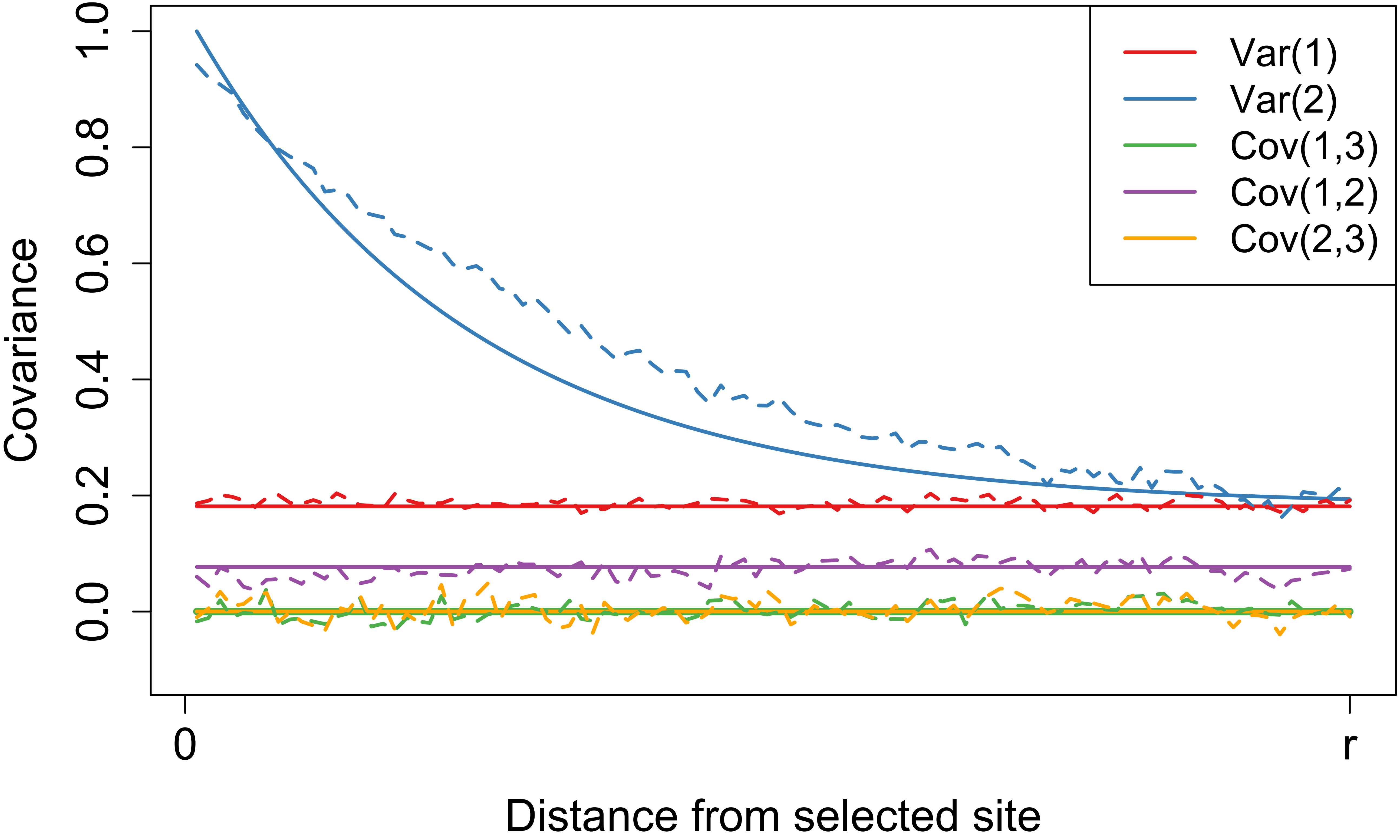
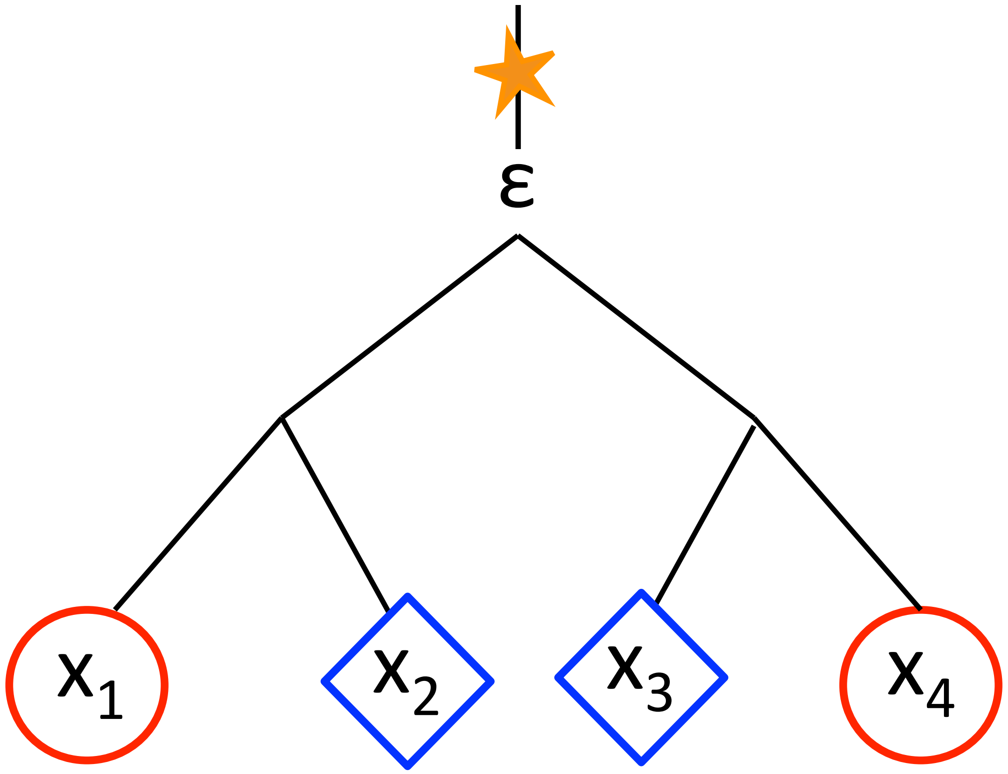




2. Shared ancestral standing variation



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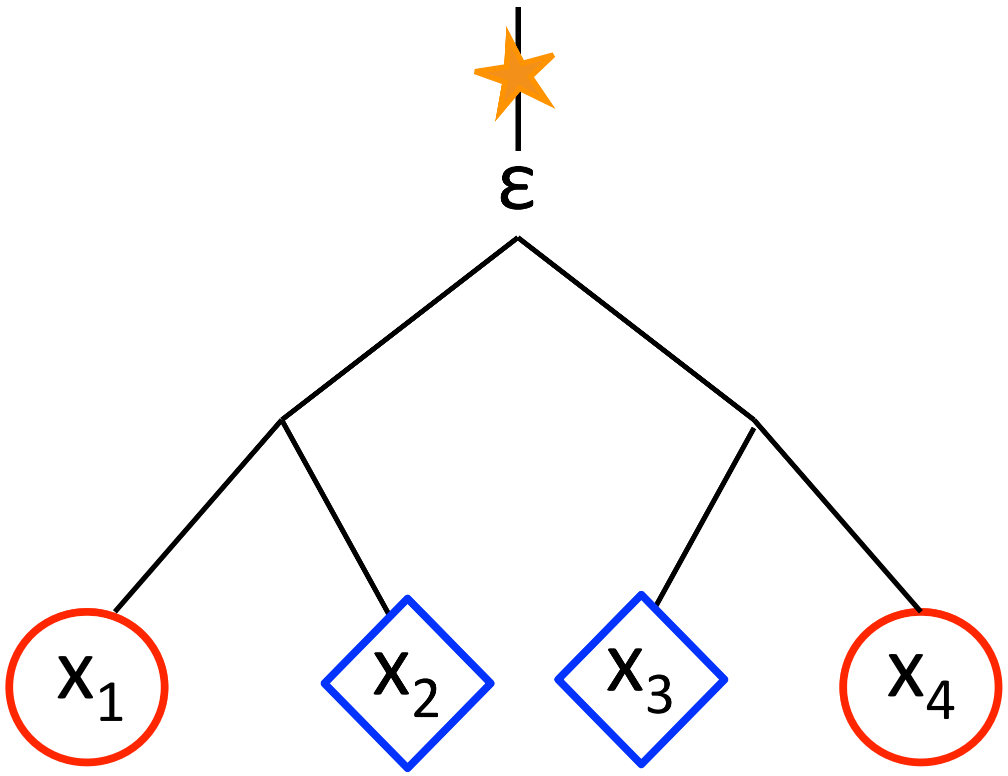

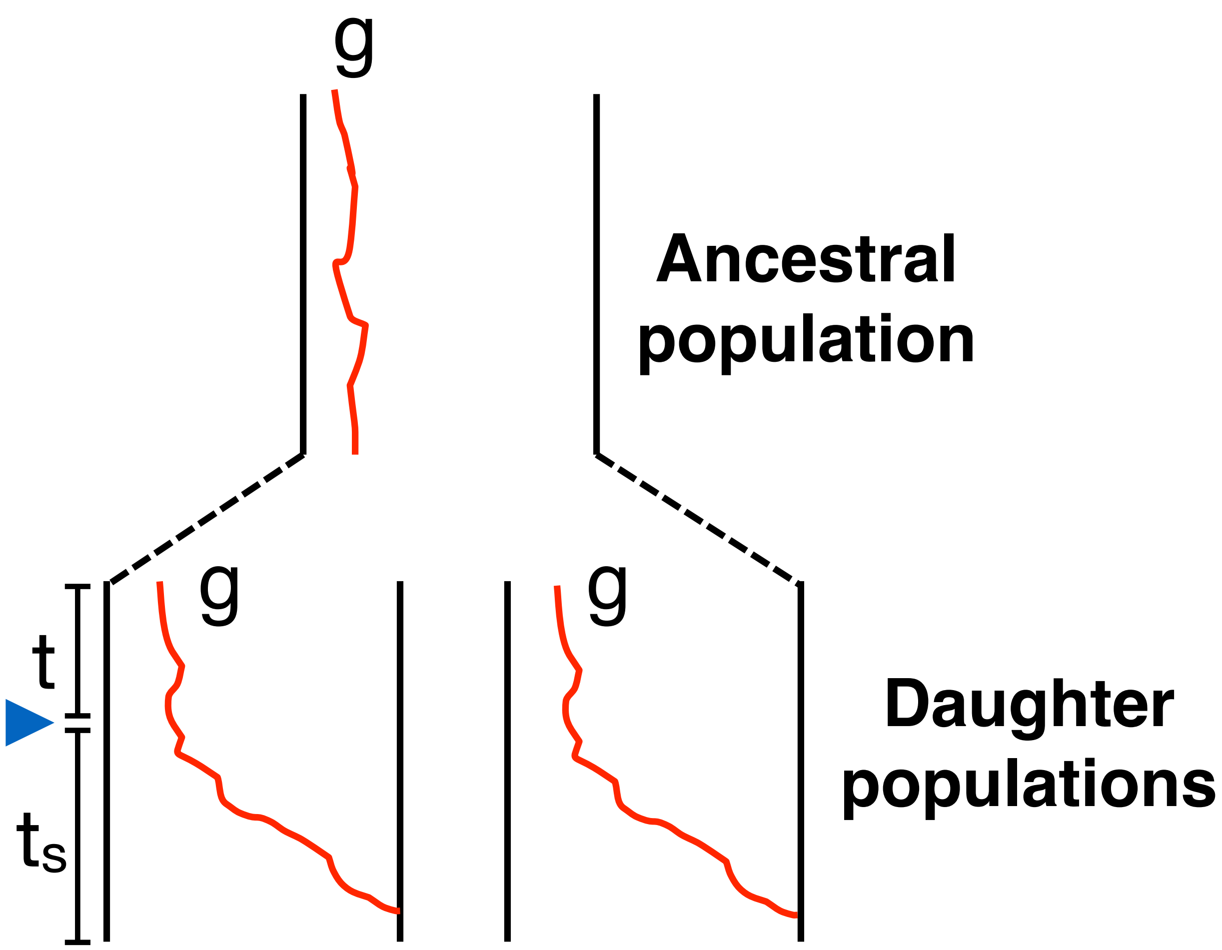

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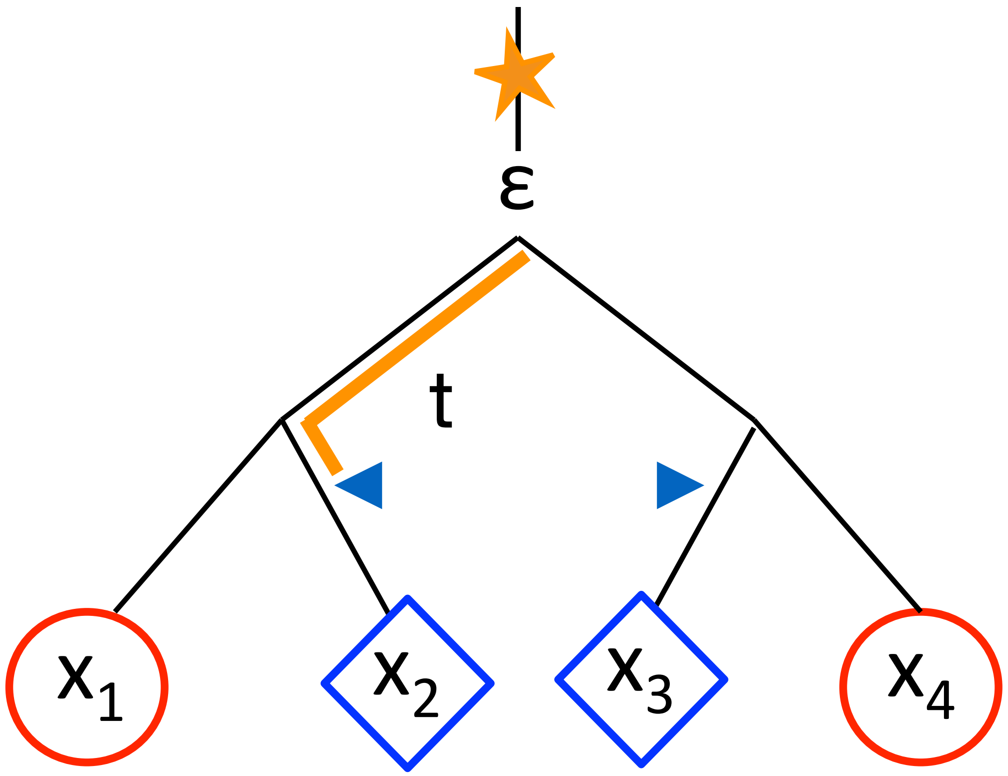

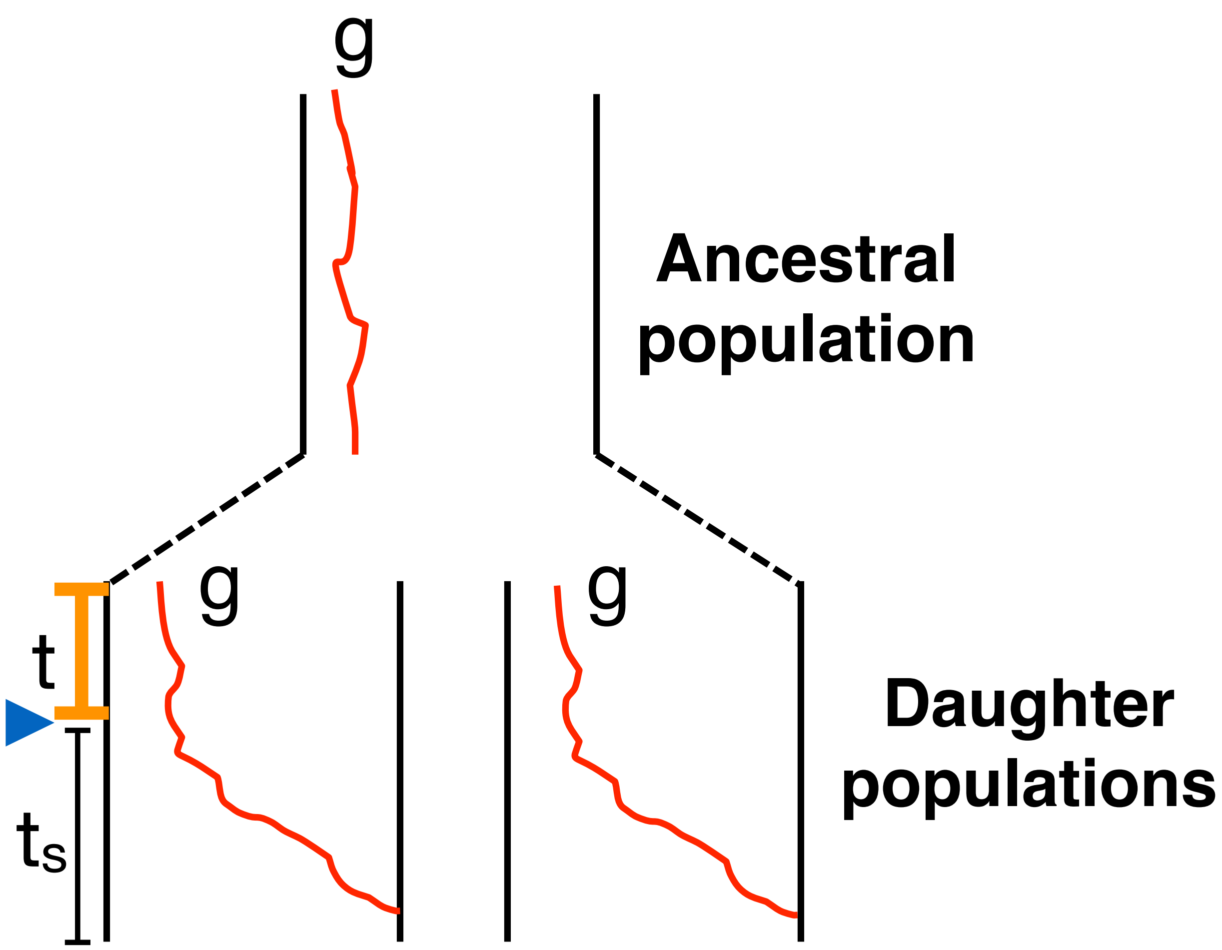

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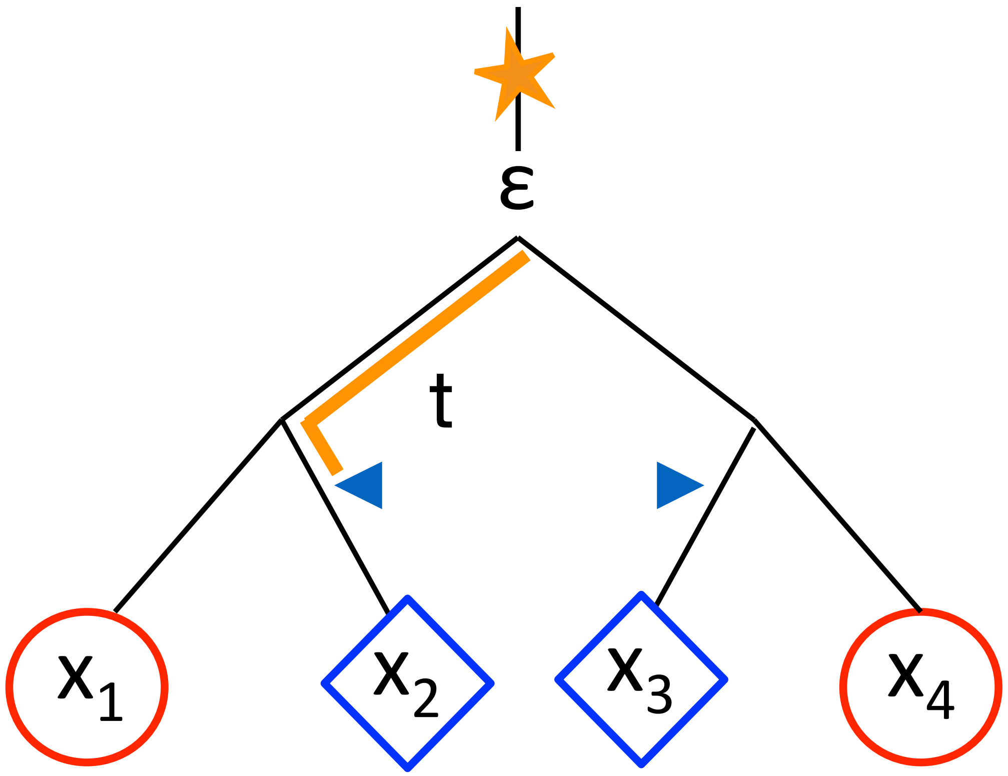

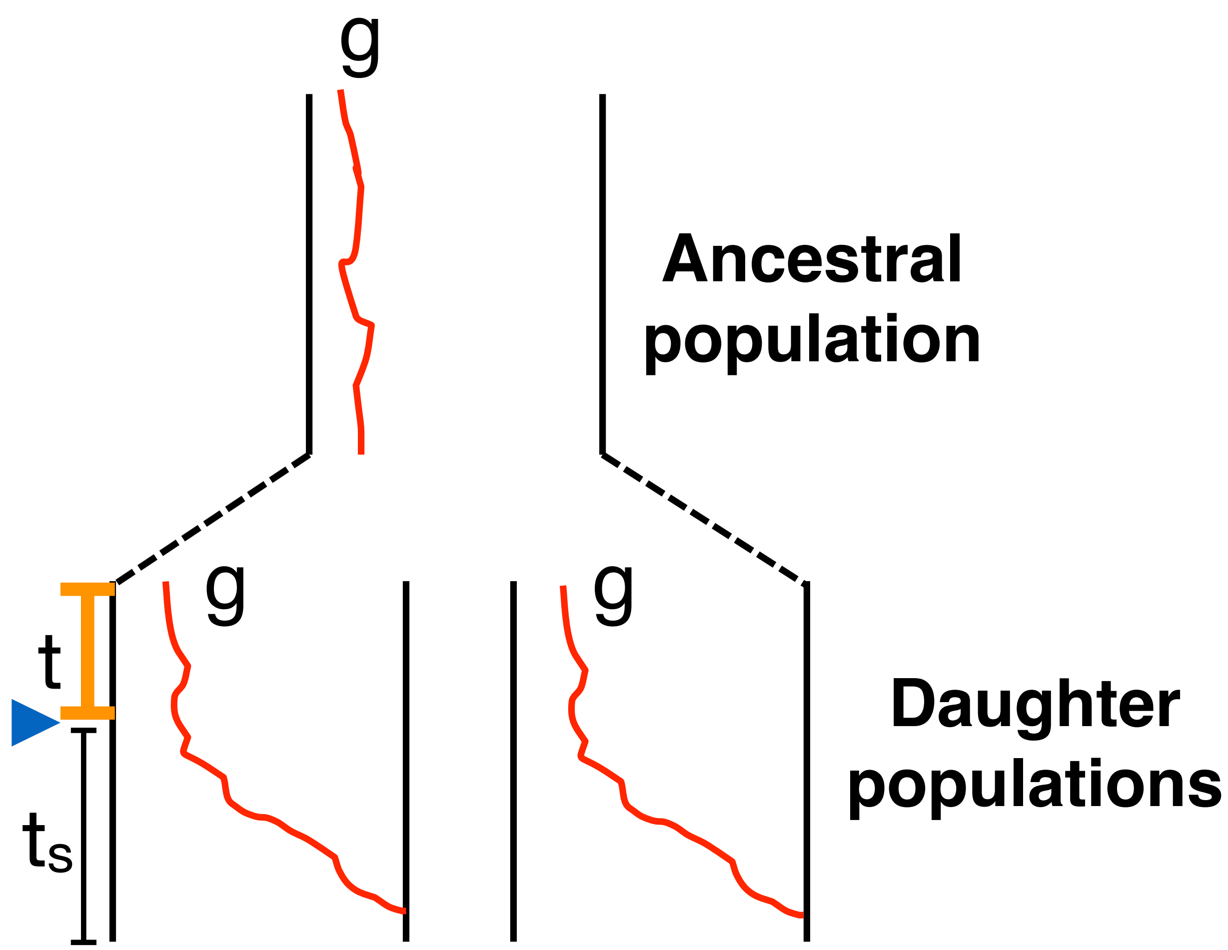

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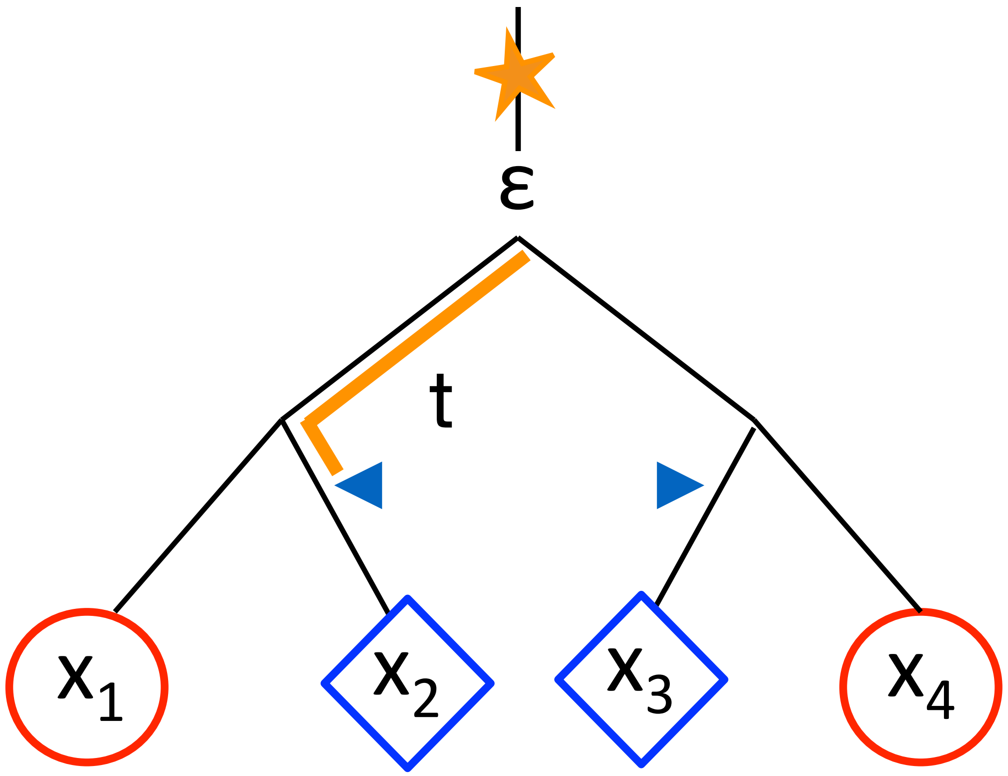

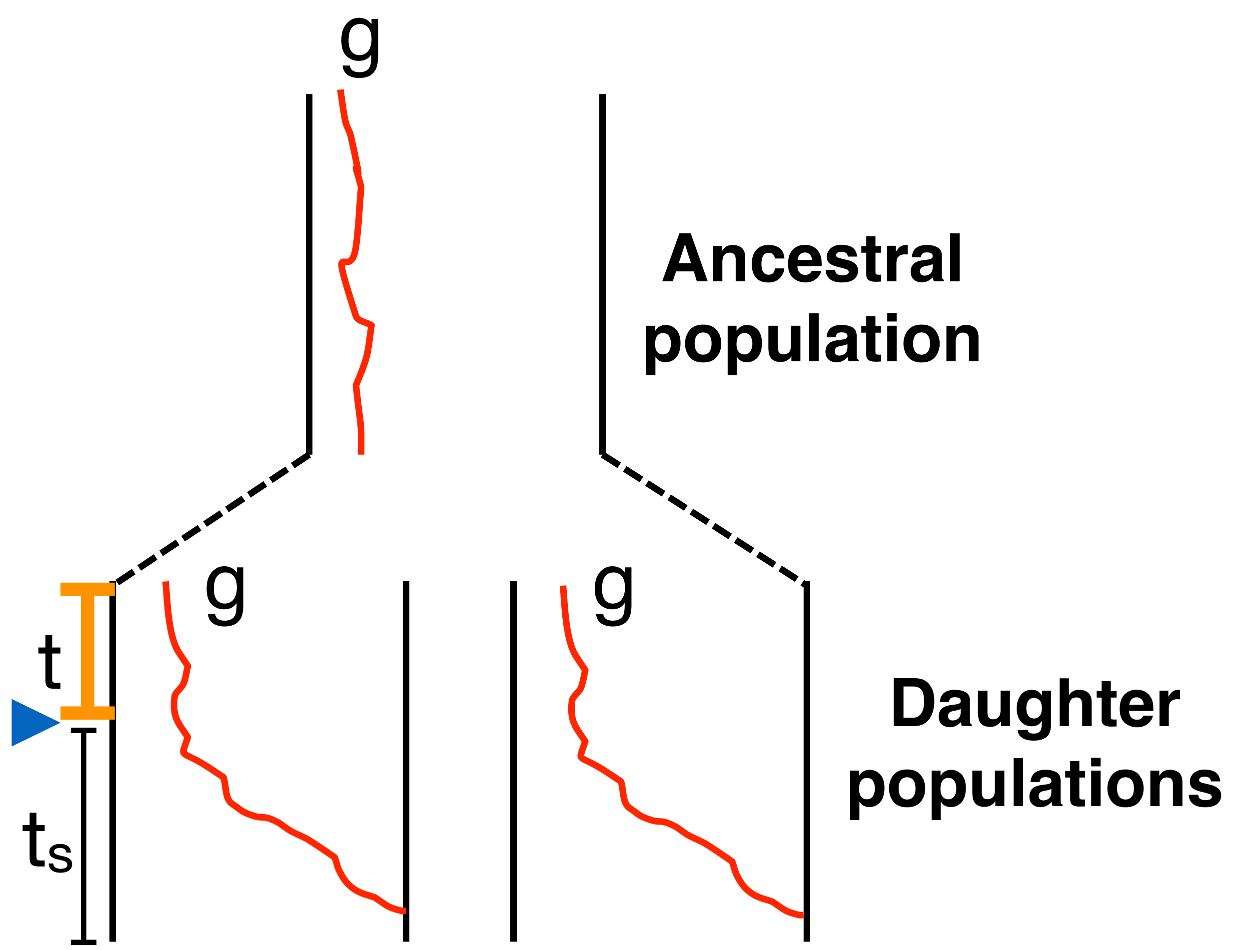

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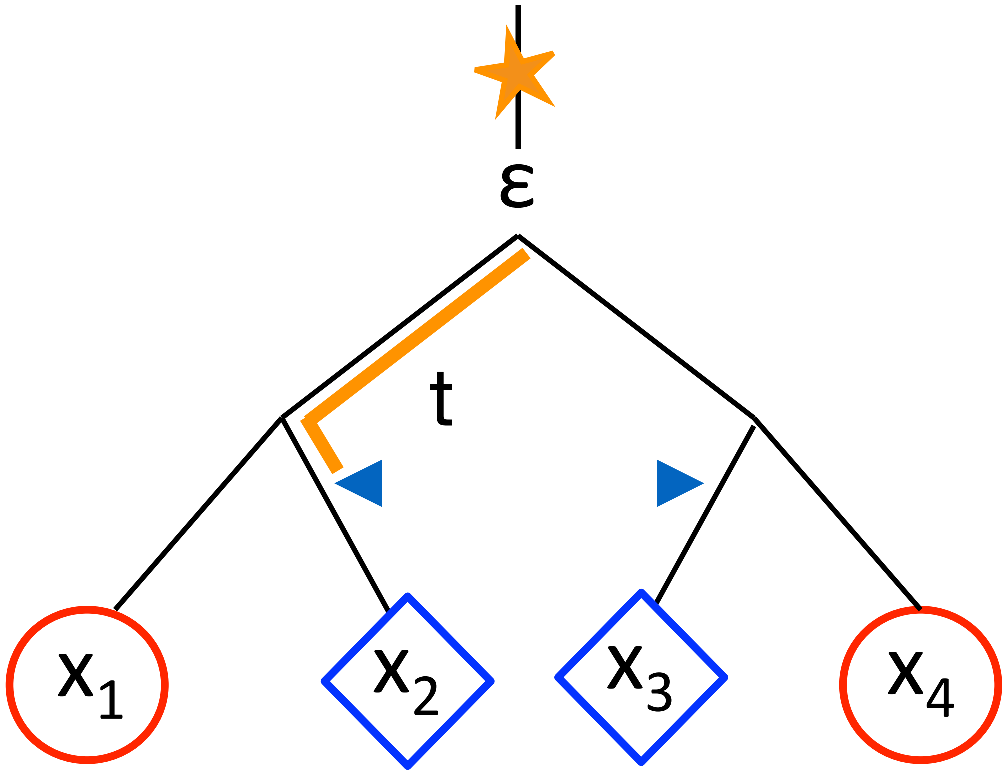

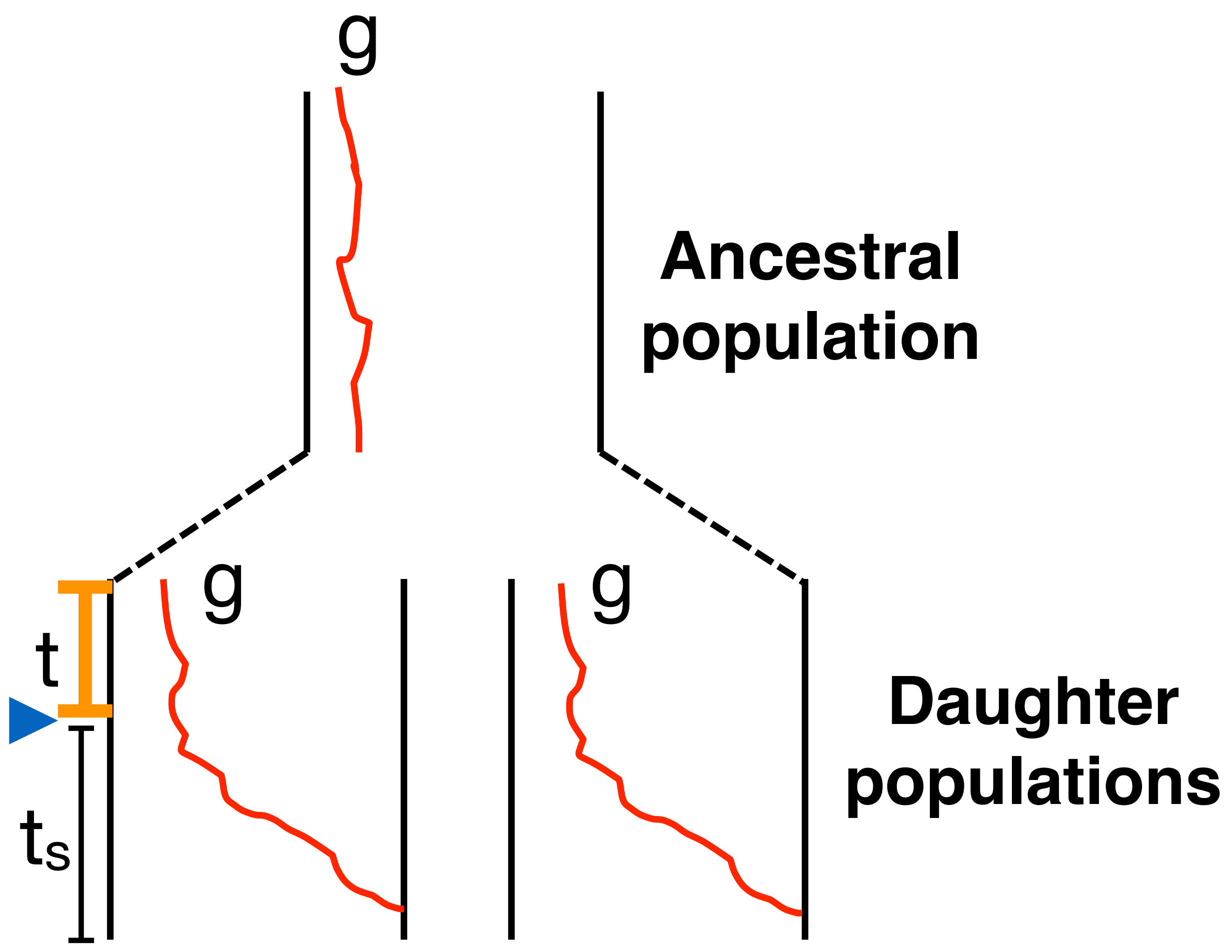

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Berg and Coop 2015
Poster 130B

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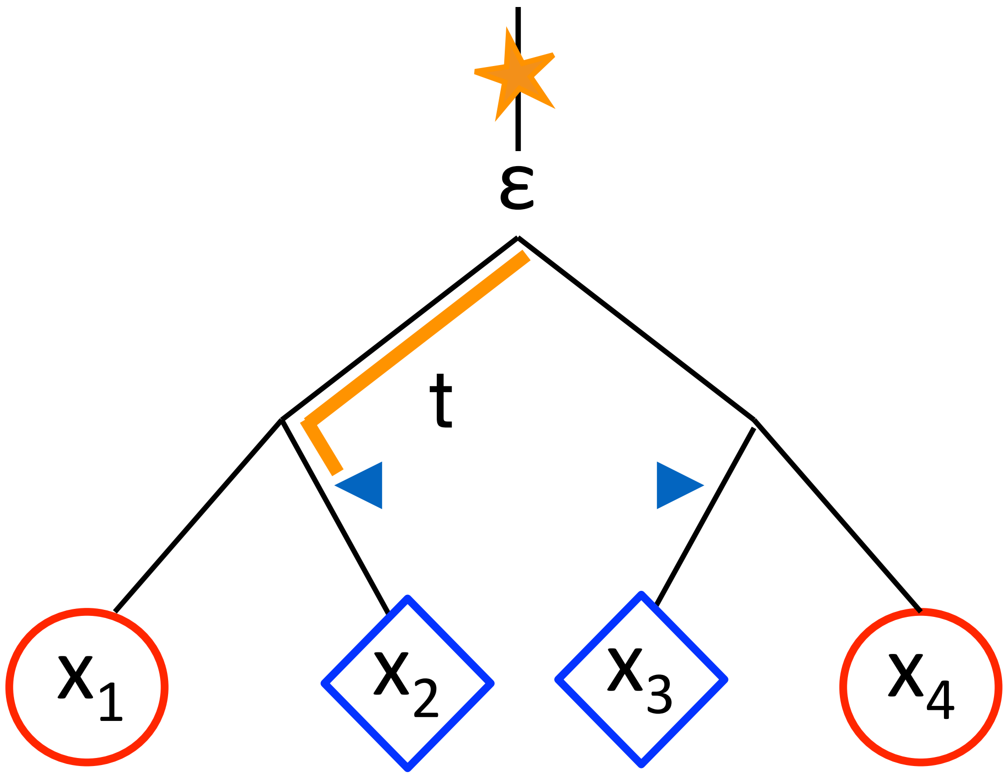

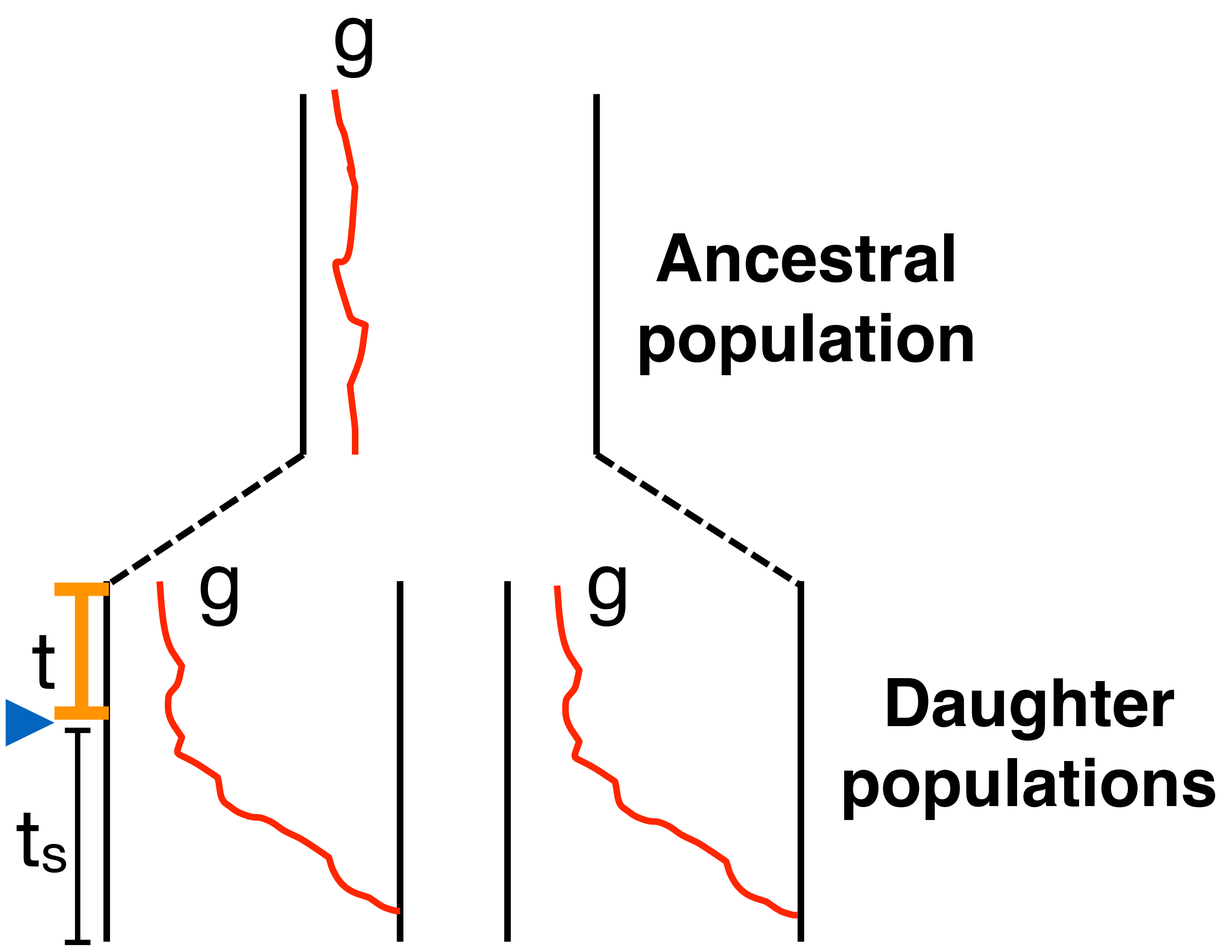

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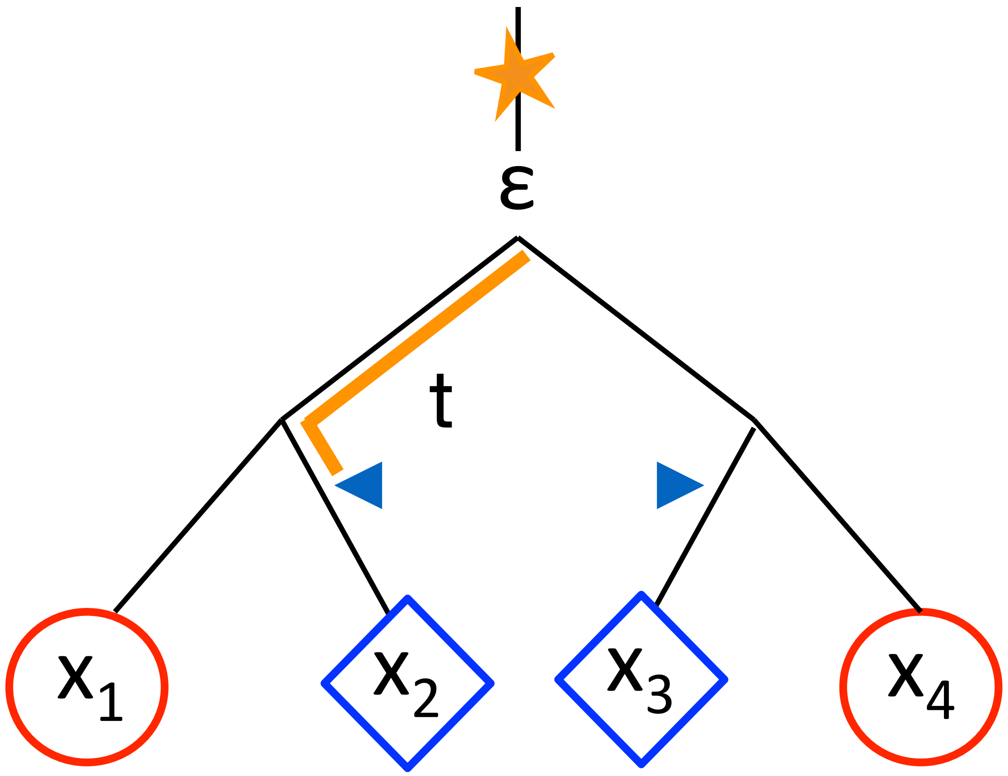

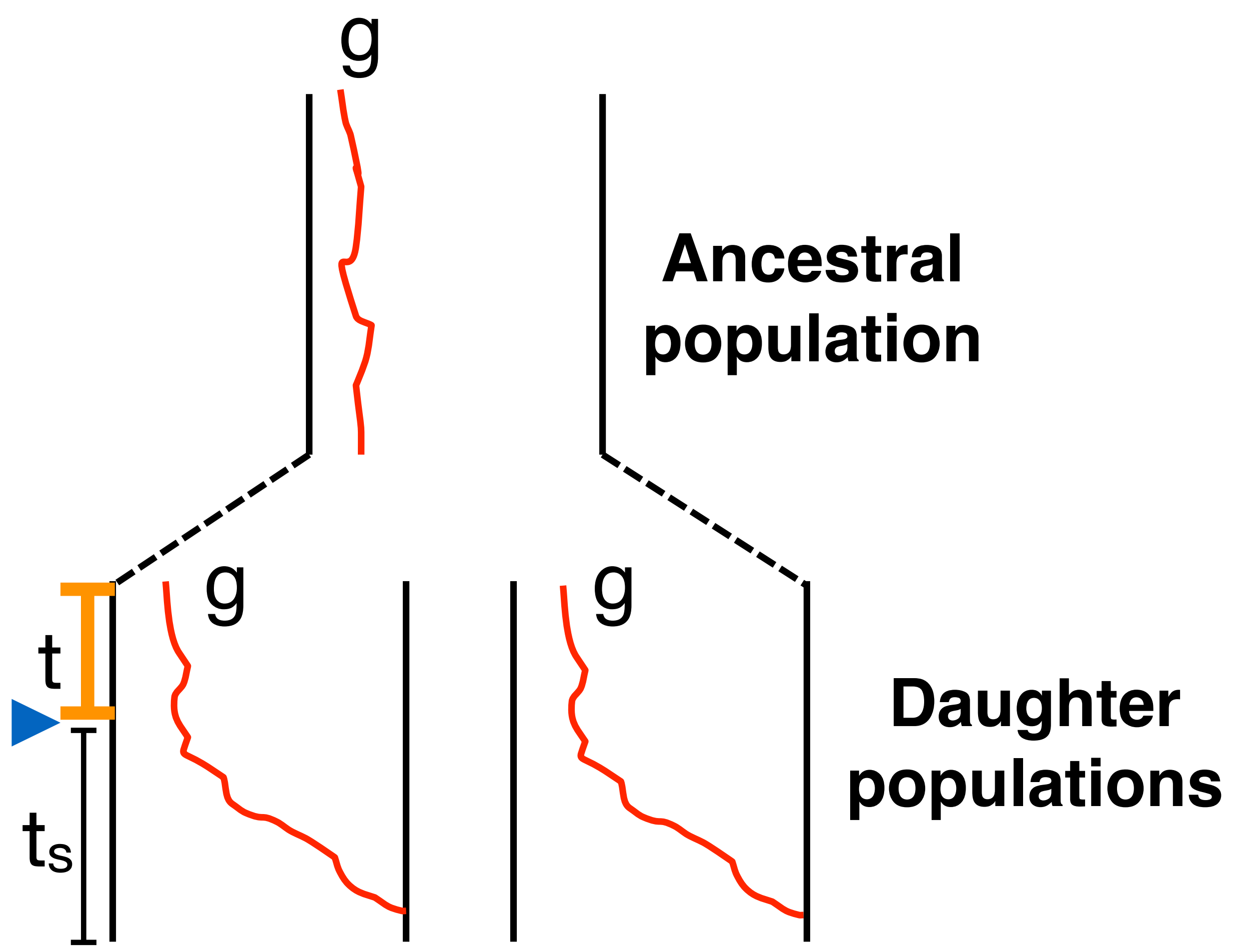

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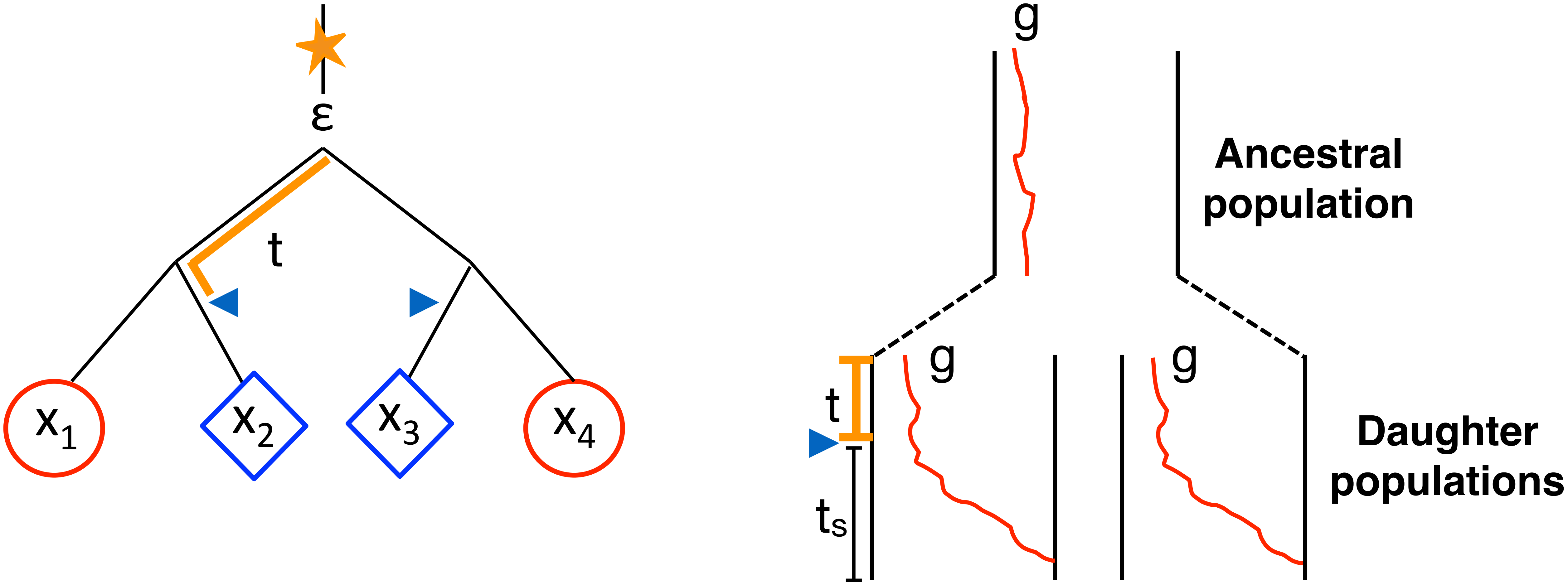

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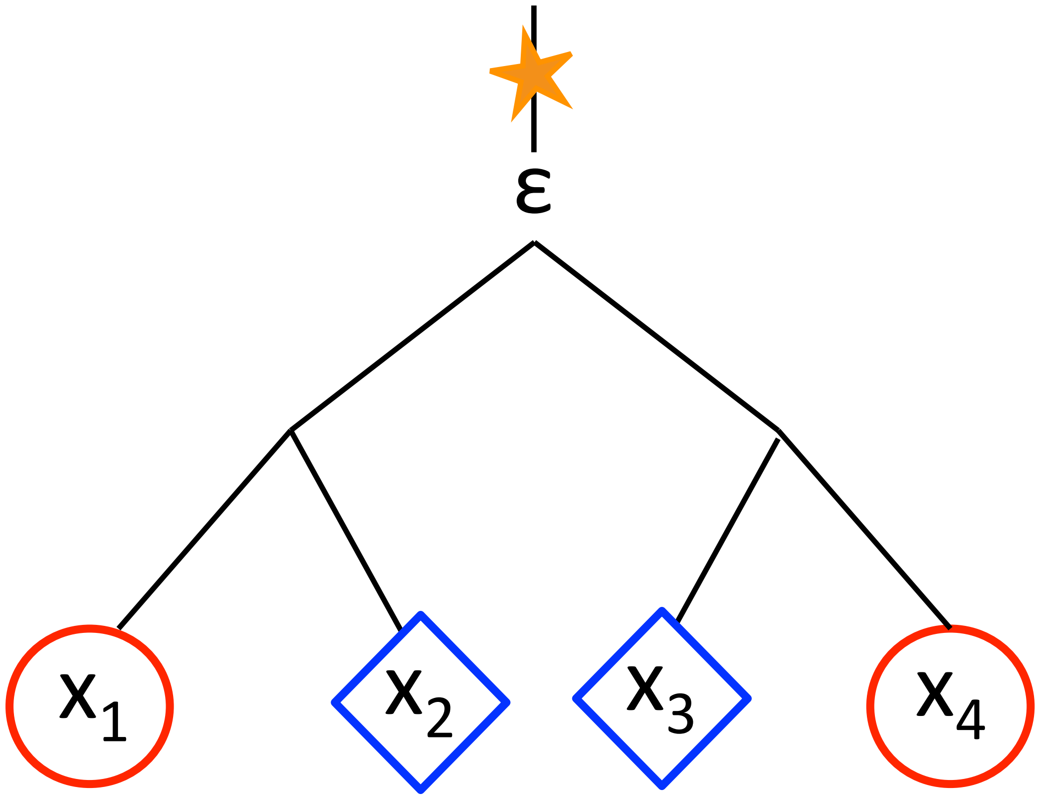

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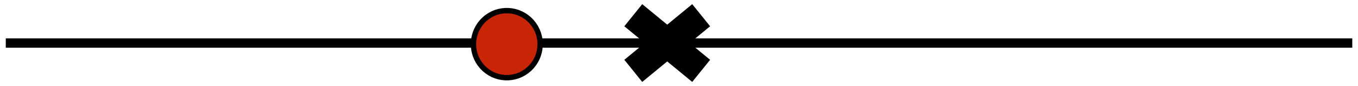
Inference method

Given location of selected site and model, can calculate probability of observed neutral allele frequencies a given distance from selected site.

$$P(D_l \mid r_l, \mathbf{F}, \Theta_M, M) \approx \mathcal{N}(D_l \mid \epsilon_l,\ \mathbf{F} + \Omega_M(r_l, \mathbf{F}, \Theta_M))$$



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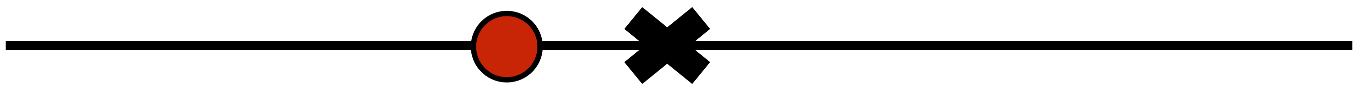

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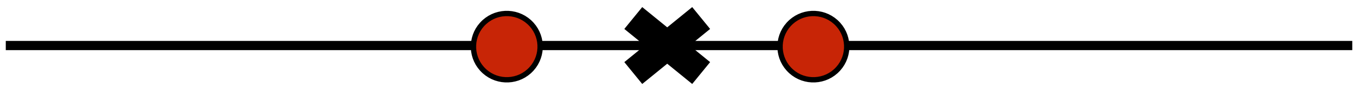

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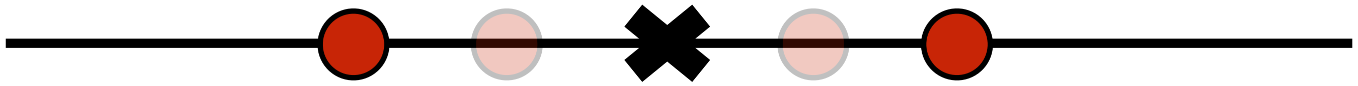
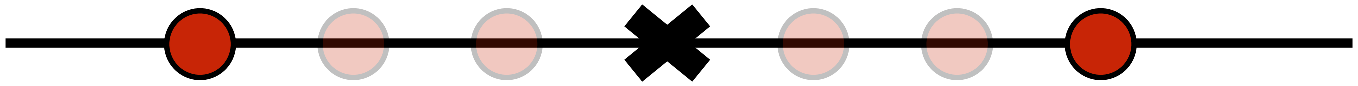


Inference method

Given location of selected site and model, can calculate probability of observed neutral allele frequencies a given distance from selected site.

$$P(D_l \mid r_l, \mathbf{F}, \Theta_M, M) \approx \mathcal{N}(D_l \mid \epsilon_l,\, \mathbf{F} + \Omega_M(r_l, \mathbf{F}, \Theta_M))$$



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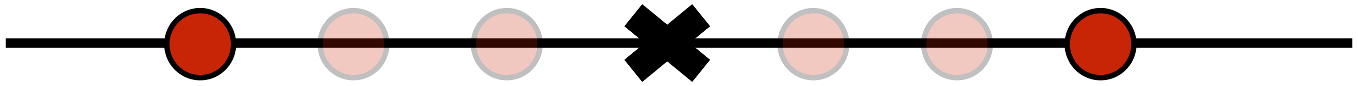


$$\mathcal{L}(\Theta_M, M; D) = (\prod_{i=1}^{L_{left}} P(D_i \mid r_i, \mathbf{F}, \Theta_M, M))(\prod_{j=1}^{L_{right}} P(D_j \mid r_j, \mathbf{F}, \Theta_M, M))$$

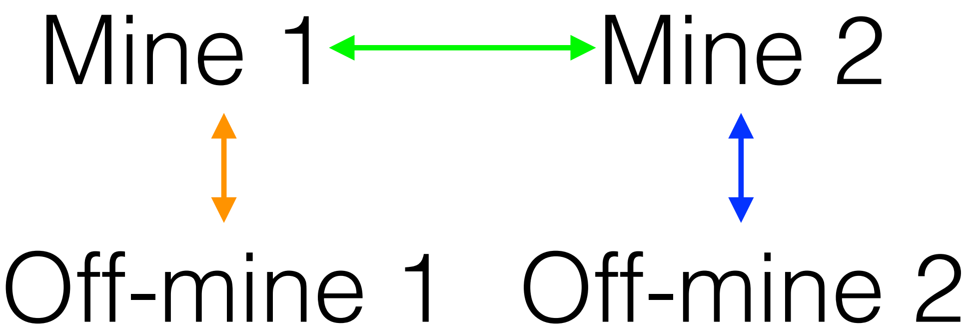
Kim and Stephan, 2002; Nielsen et al., 2005; Chen et al., 2010; Racimo, 2015

Application to data:

Mimulus guttatus adaptation to copper on mine tailings in California

John Willis

Kevin Wright



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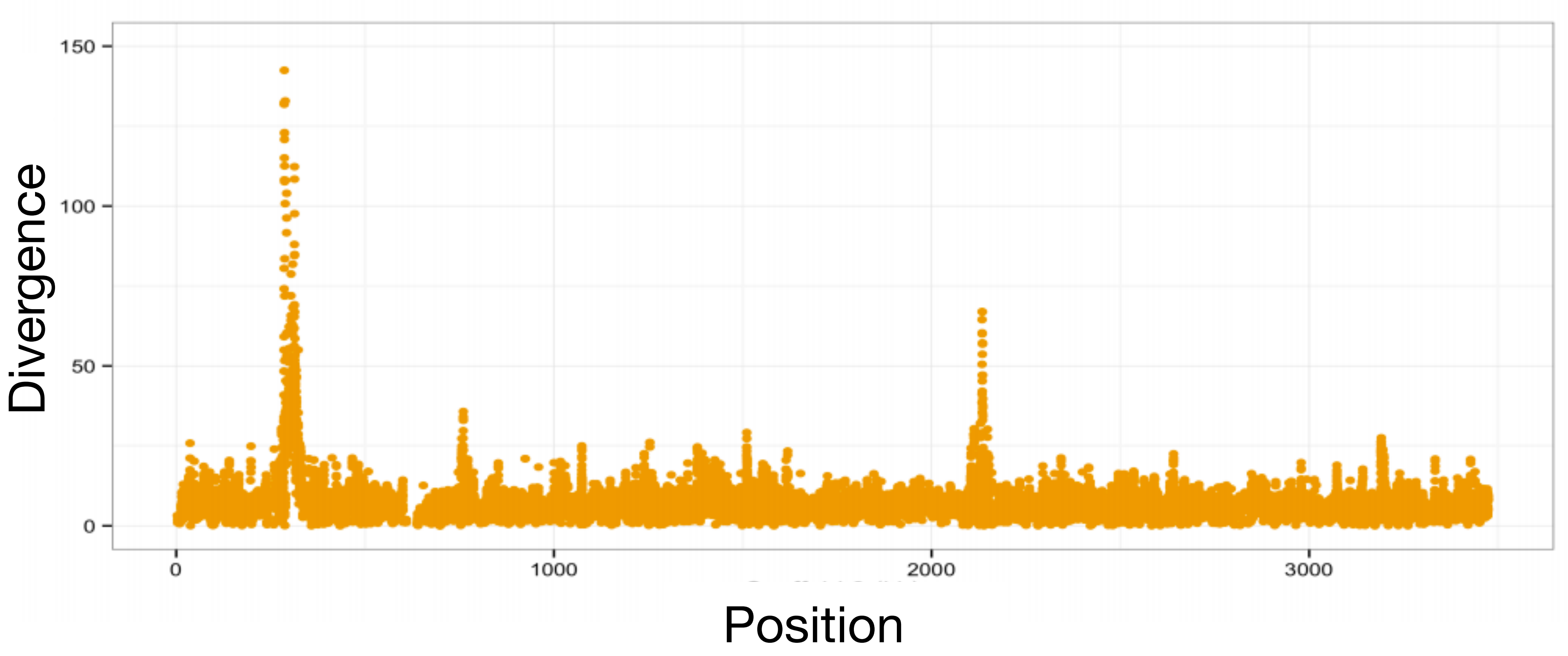

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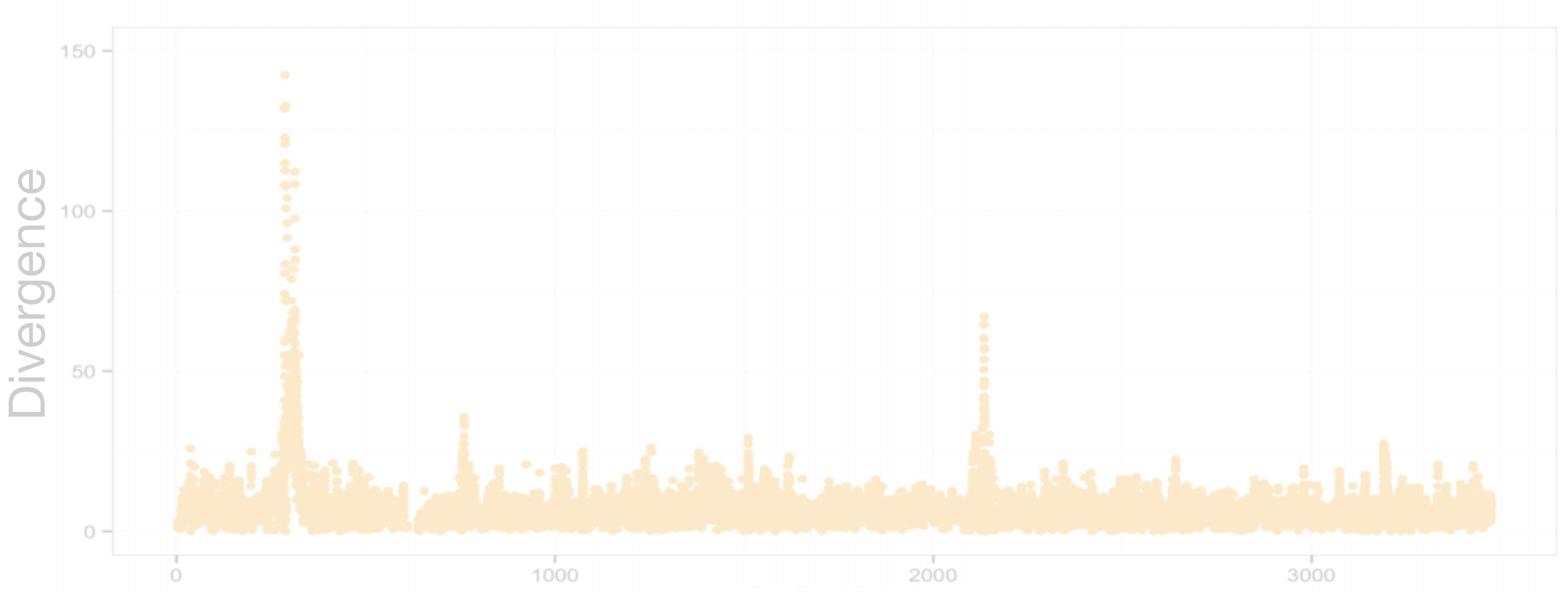
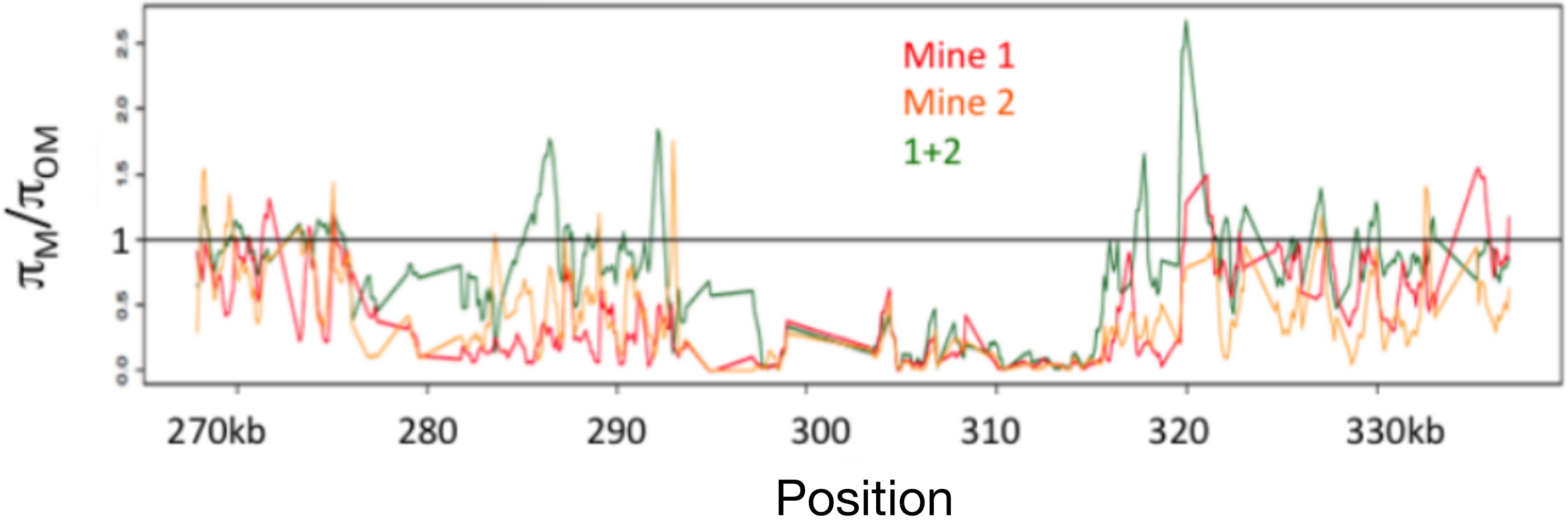
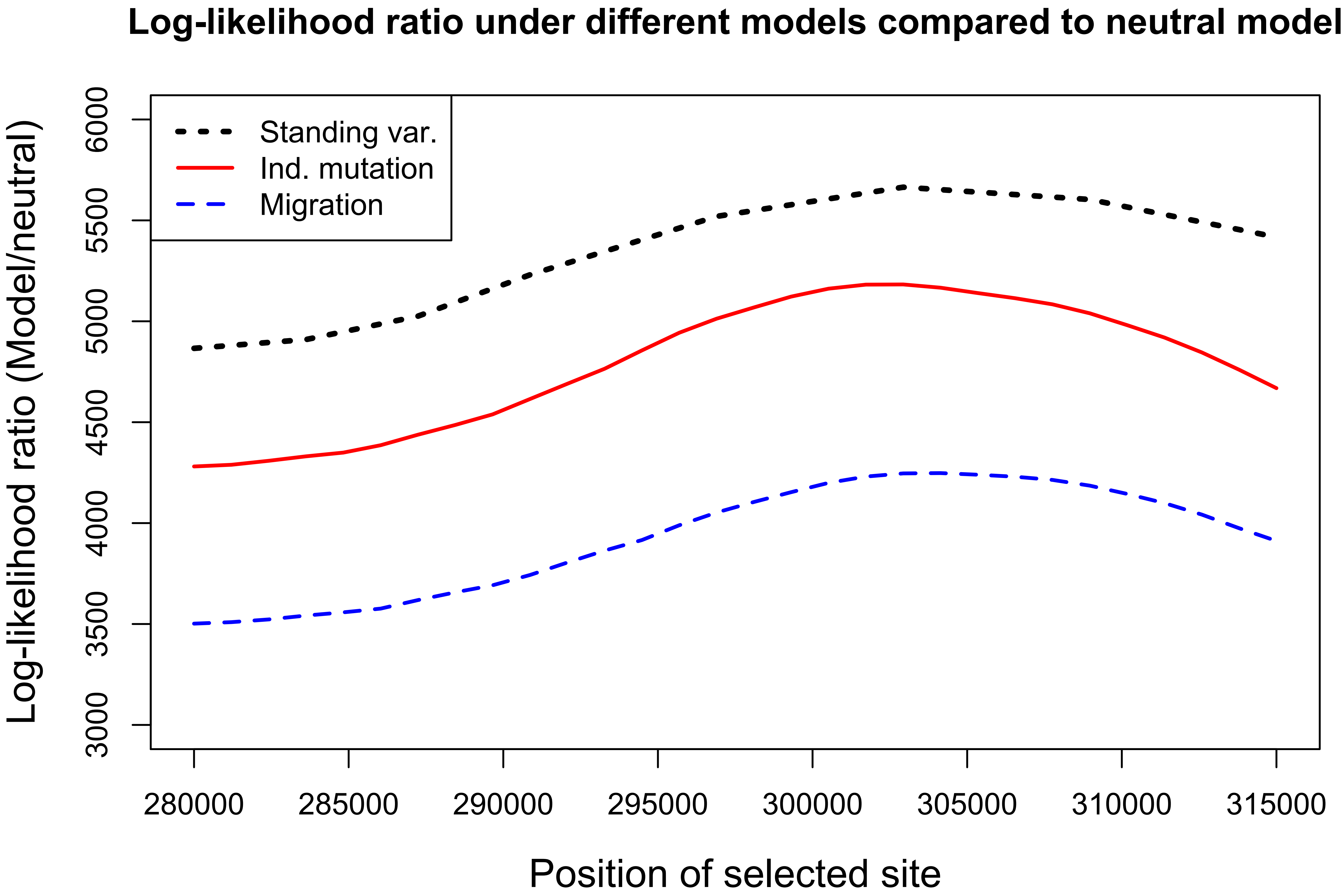
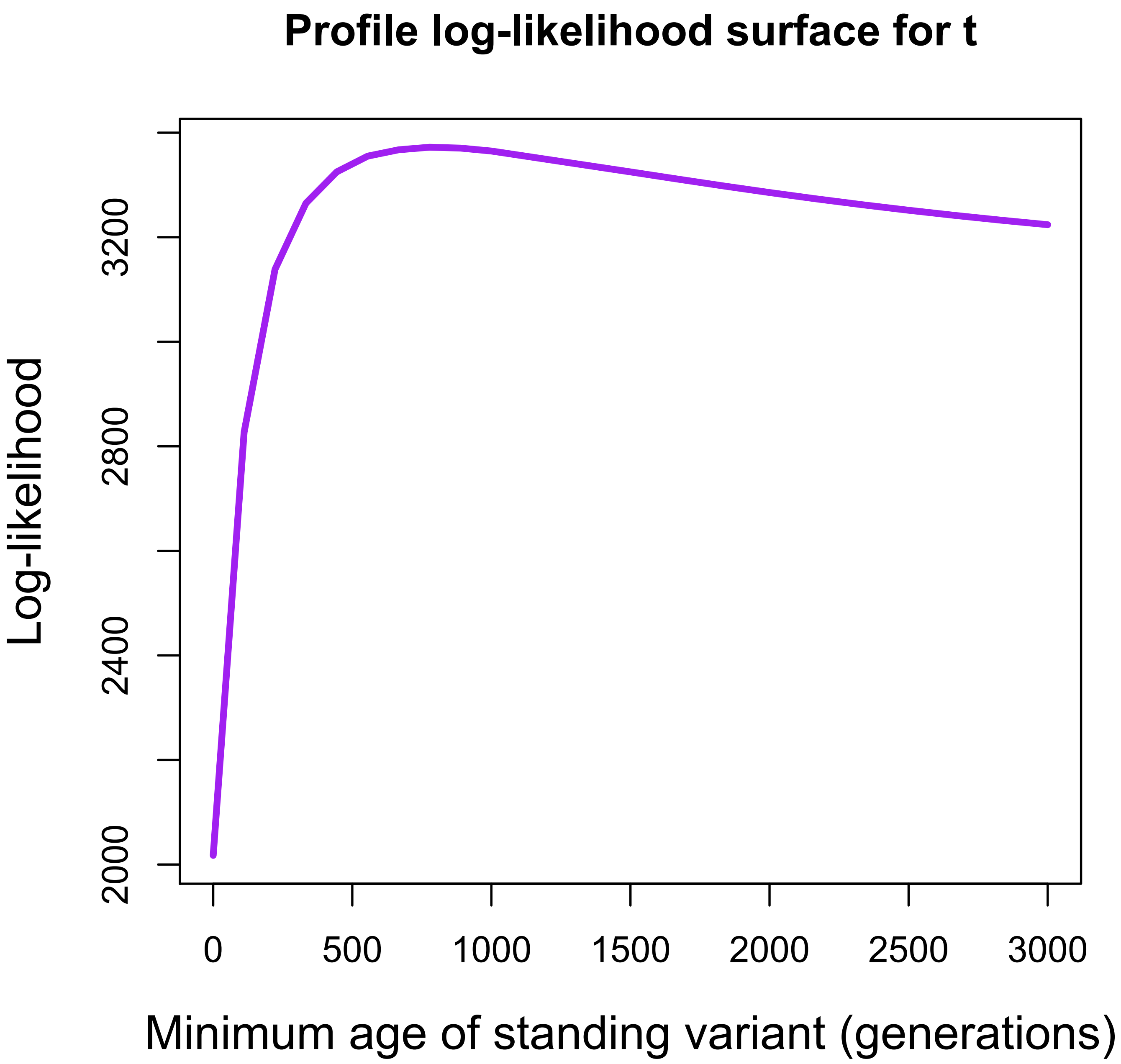


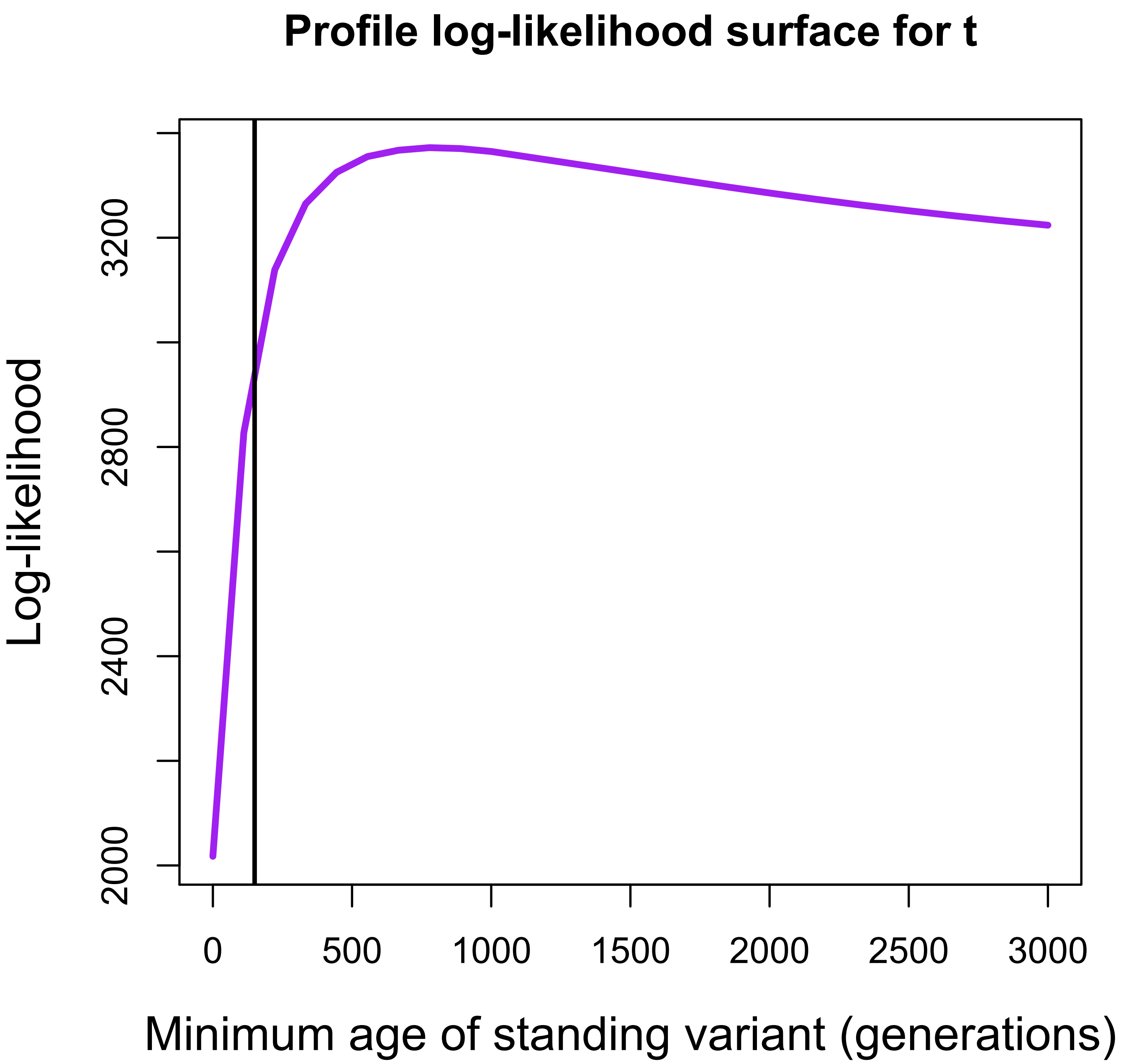



Log-likelihood ratio under different models compared to neutral model
Standing var.
Ind. mutation
Migration
Log-likelihood ratio (Model/neutral)
3000
3500
4000
4500
5000
5500
6000
280000
285000
290000
295000
300000
305000
310000
315000
Position of selected site

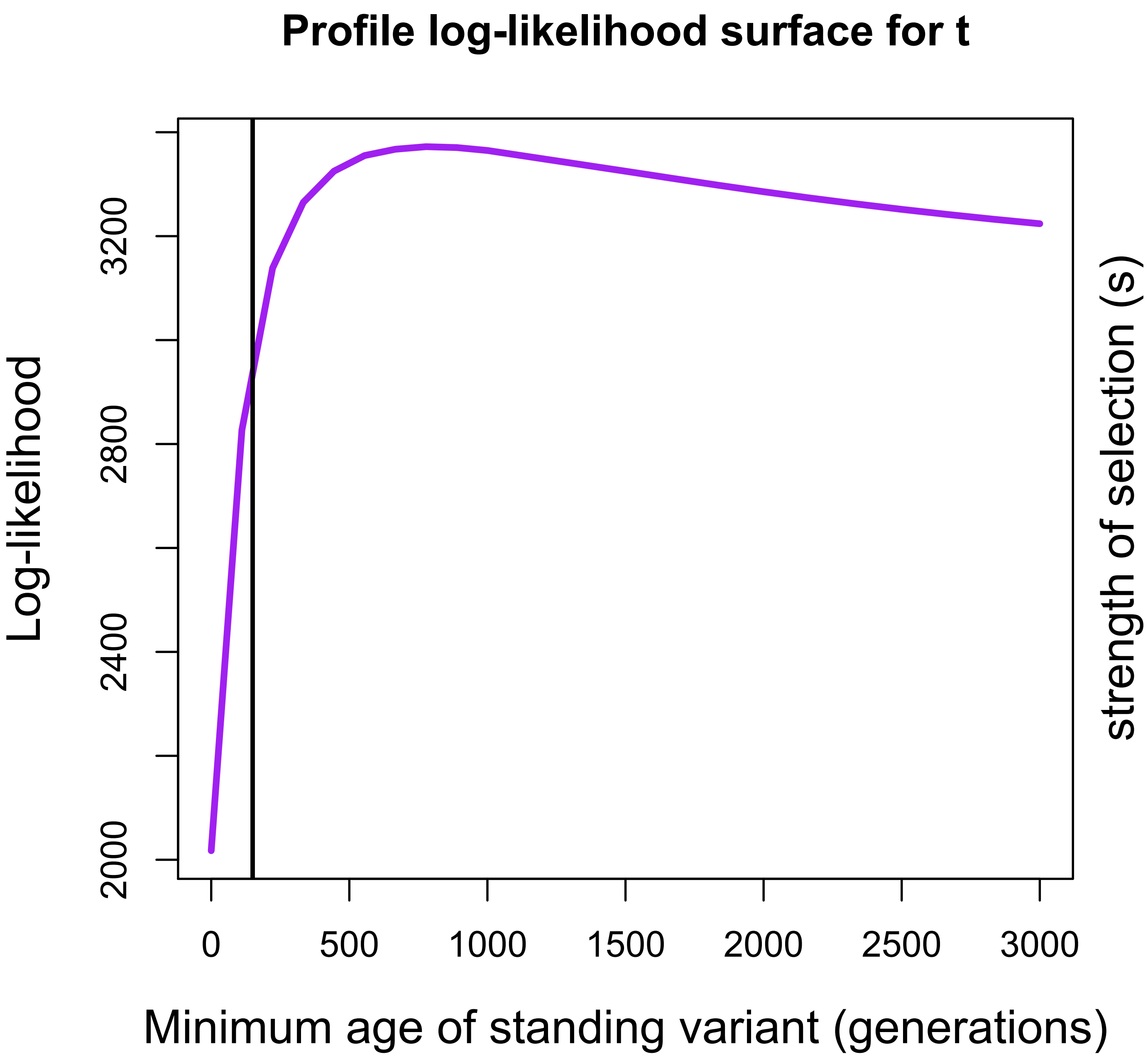
Under standing variation at most likely selected site



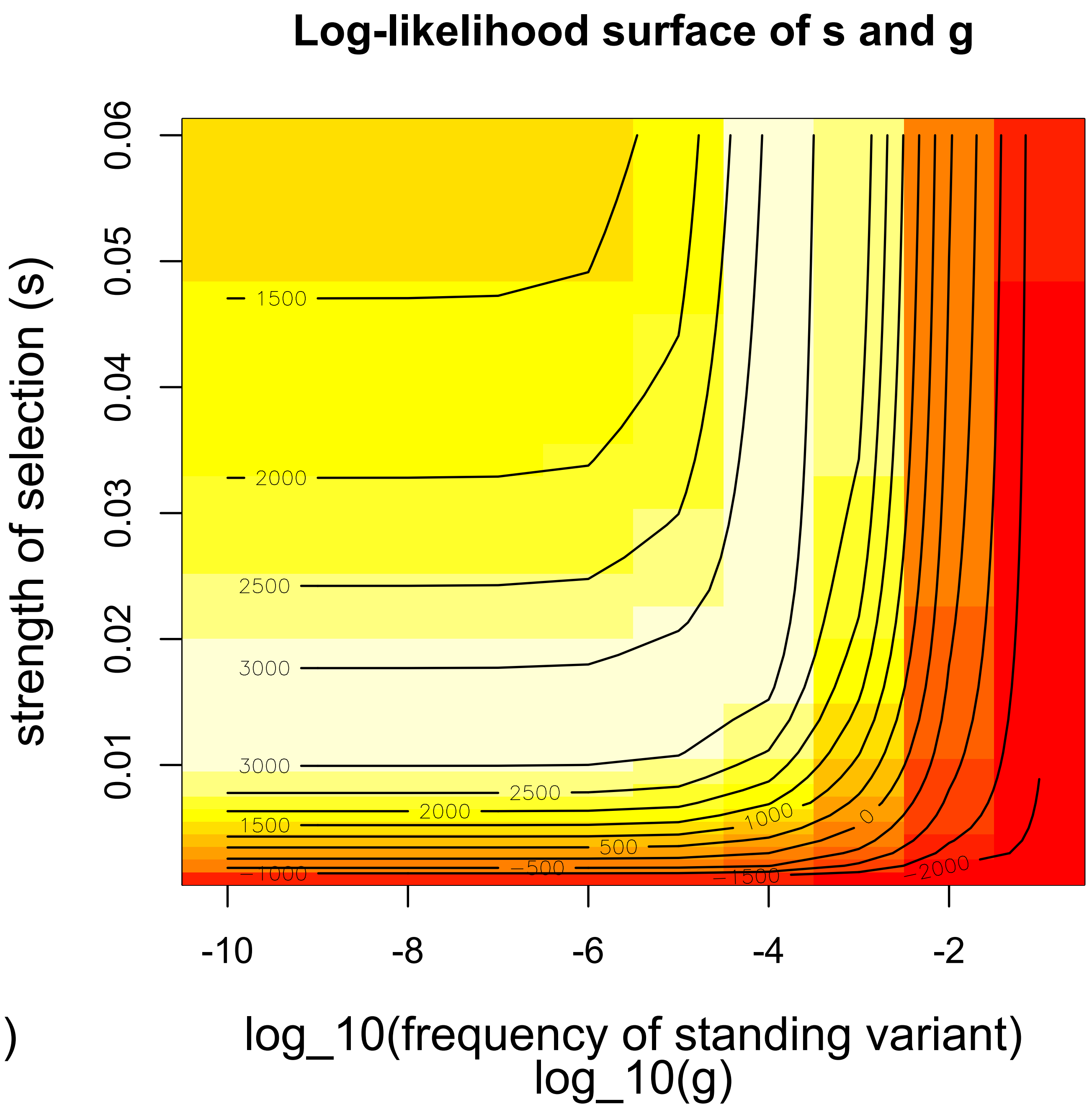
Under standing variation at most likely selected site



Under standing variation at most likely selected site



Profile log-likelihood surface for t



Log-likelihood surface of s and g

Conclusions

1. Can define models for modes of convergent adaptation for multiple populations with arbitrary relationships

2. Applied inference method to Mimulus guttatus copper tolerance data
    - Can apply to a wide range of other datasets

Thank you!

The Coop Lab

Jeremy Berg, Gideon Bradburd, Graham Coop, Alisa Sedghifar, Chenling Xu,
Ivan Juric, Simon Aeschbacher, Vince Buffalo

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GENETIC DIVERSITY IN TOP "SWEEP REGION".