

Distinguishing shared ancestral polymorphism from recent introgression in genes with recombination

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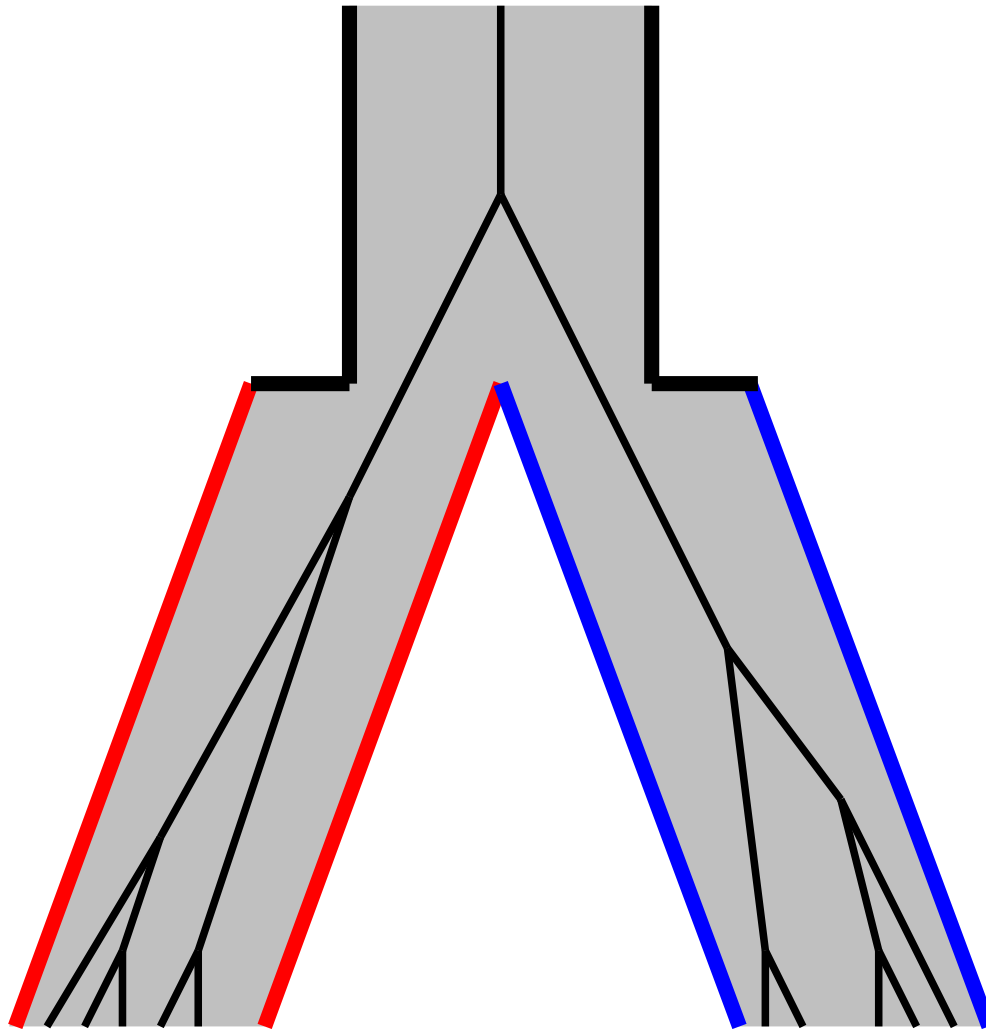
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Distinguishing shared **ancestral polymorphism** from recent **introgression**

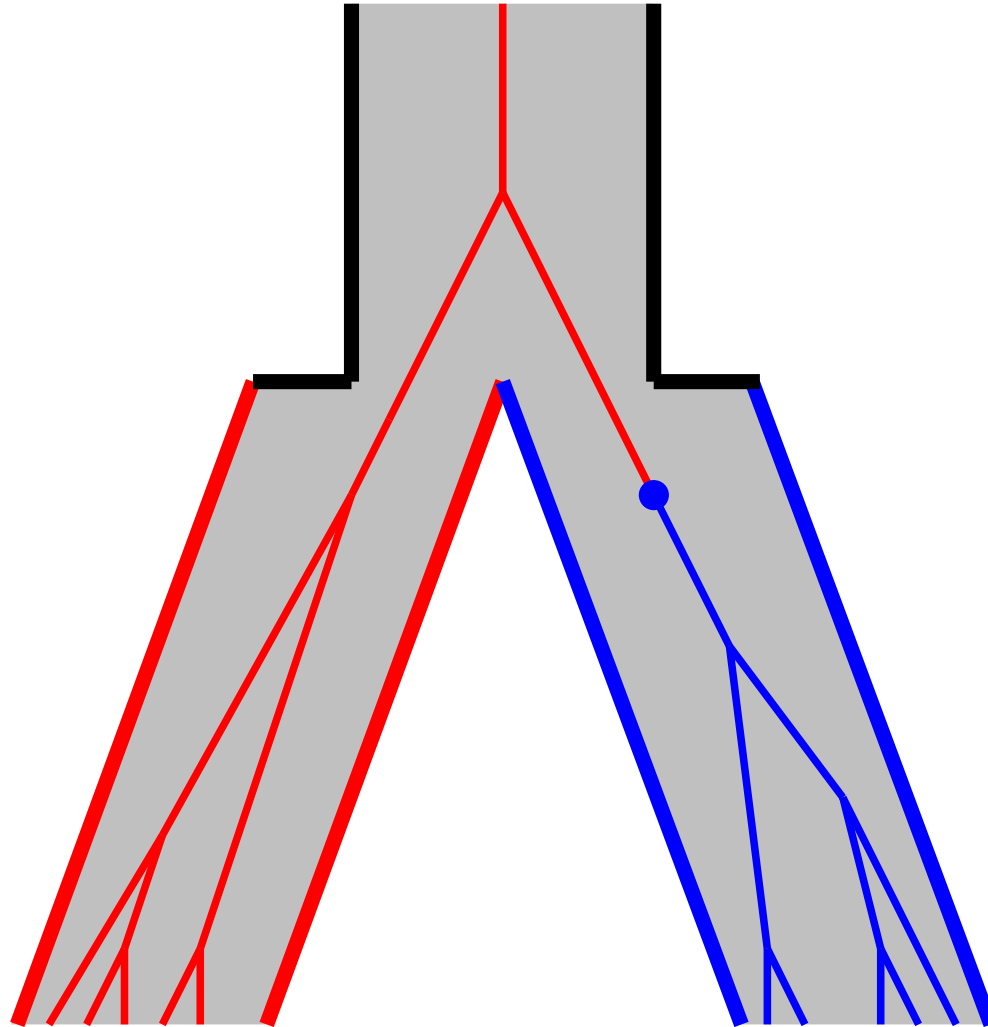
Miguel Navascués & Frantz Depaulis
CNRS UMR 7625 Écologie et Évolution (ENS/UPMC)



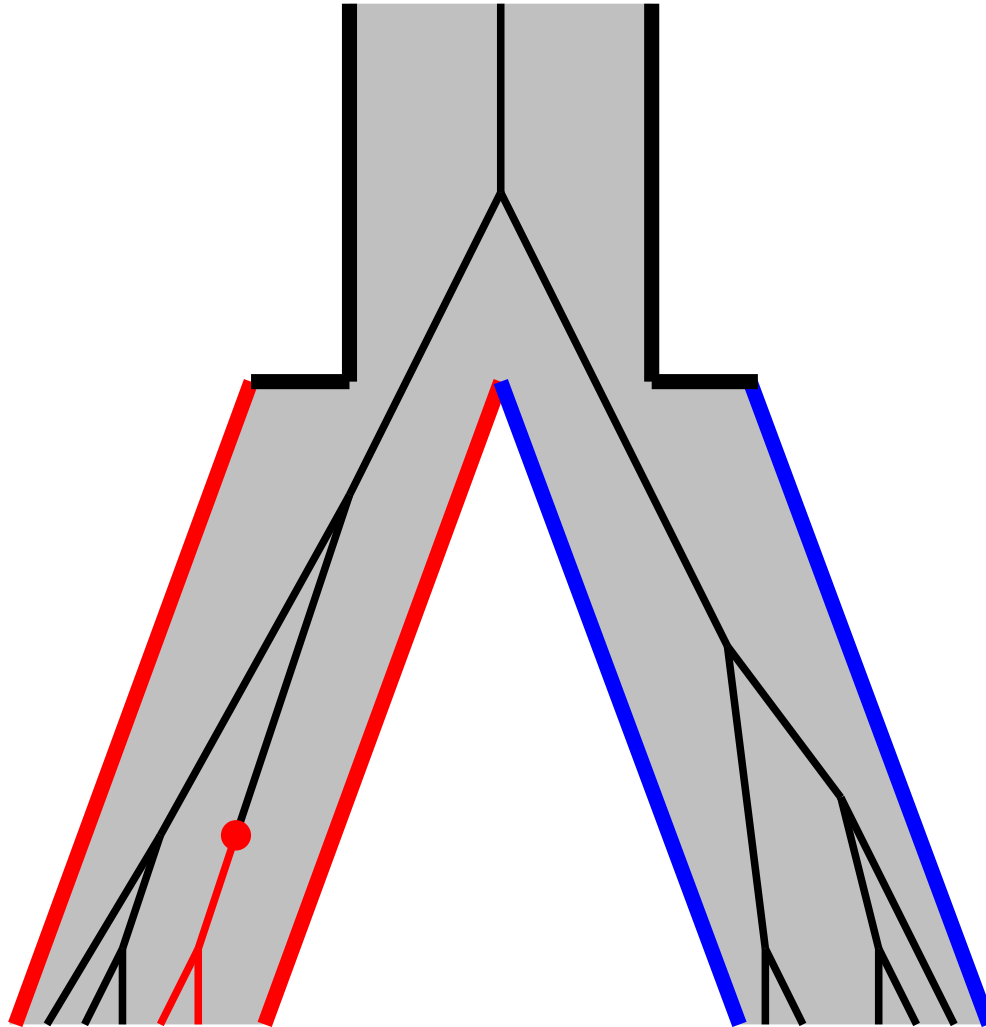
Polymorphisms between two species



Fixed polymorphism

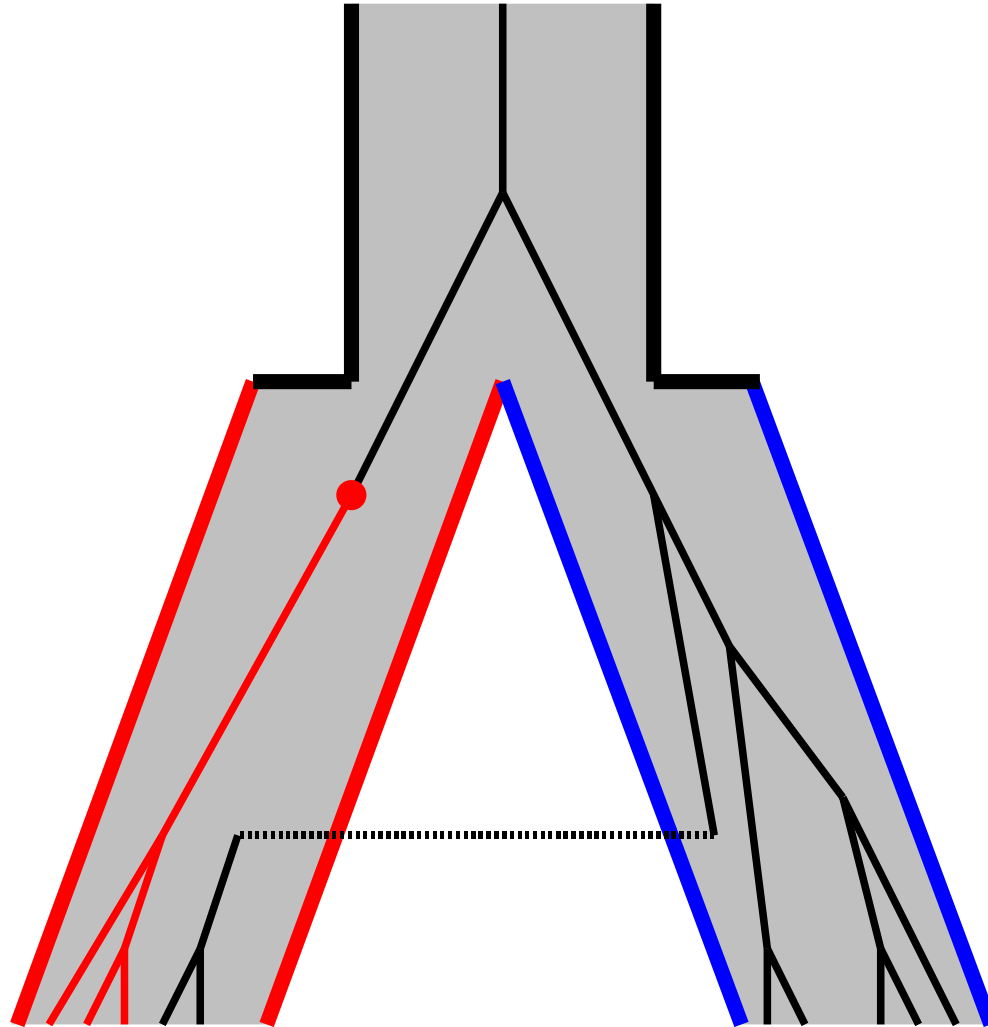


Exclusive polymorphism



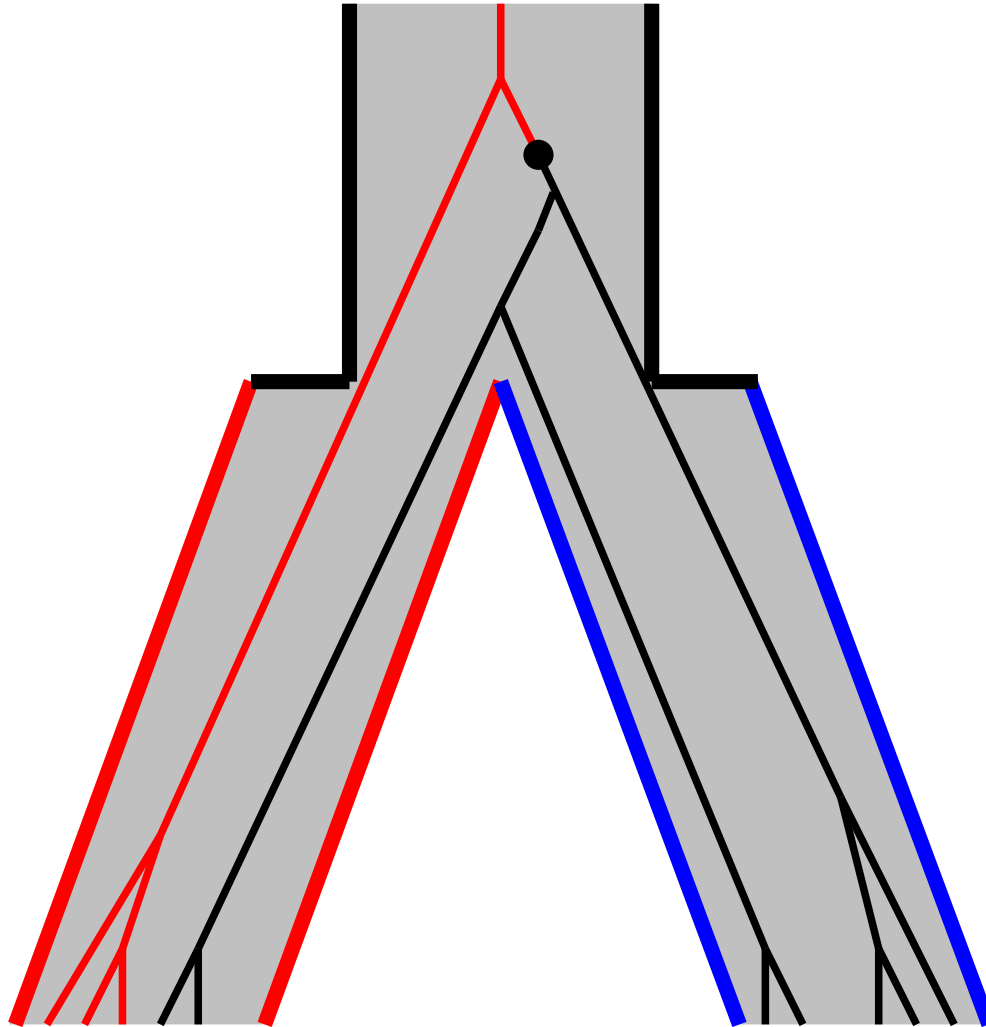
Exclusive polymorphism

Introgression



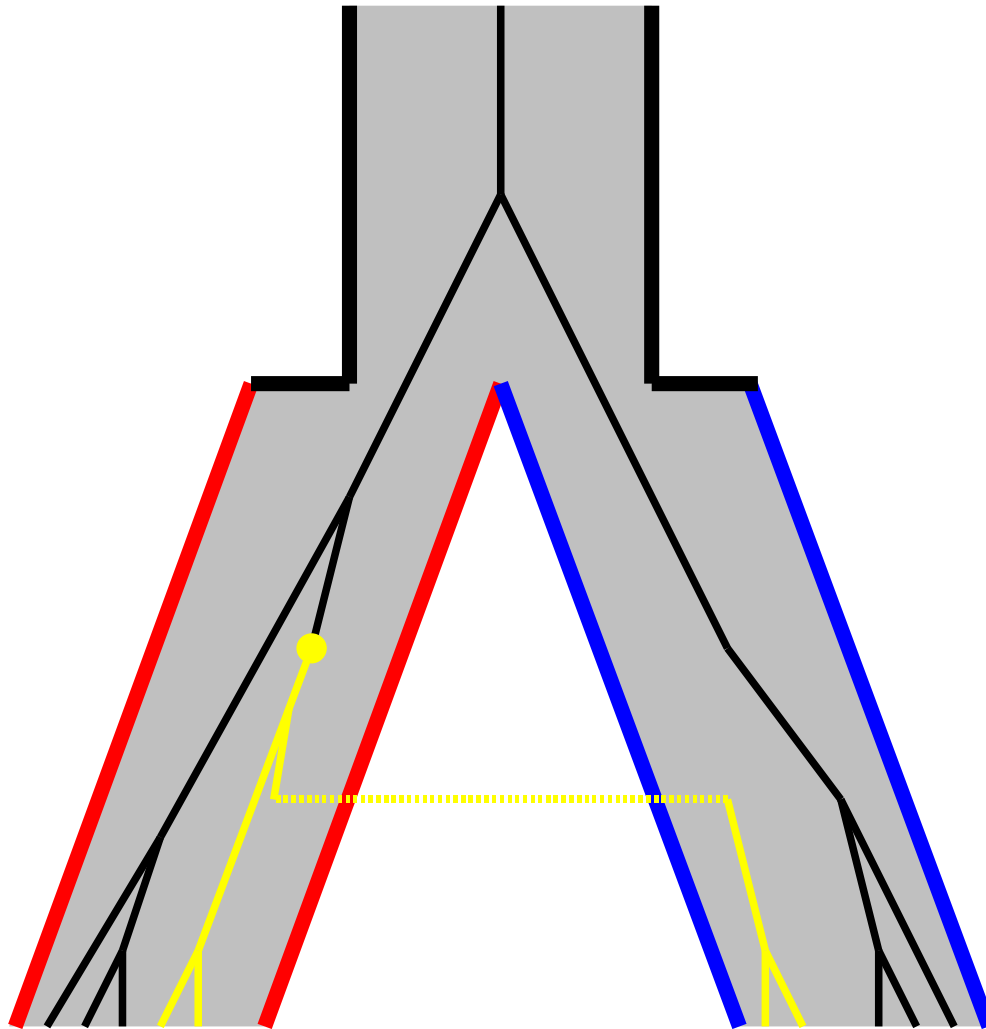
Exclusive polymorphism

Ancestral



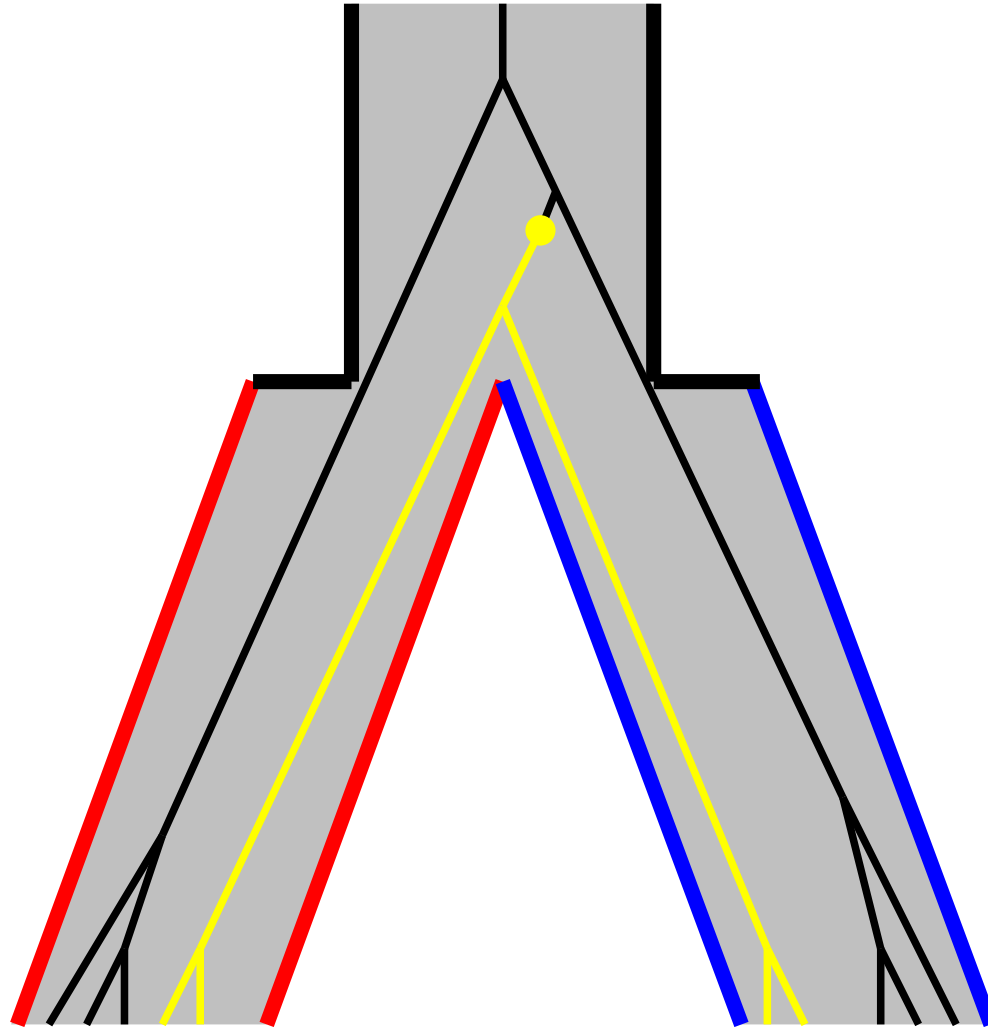
Shared polymorphism

Introgression



Shared polymorphism

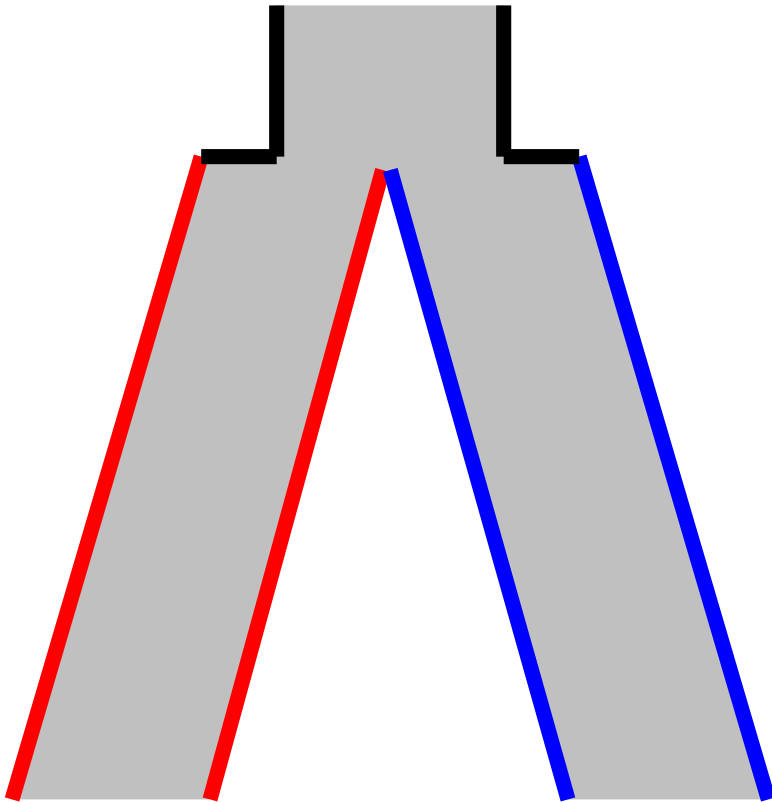
Ancestral



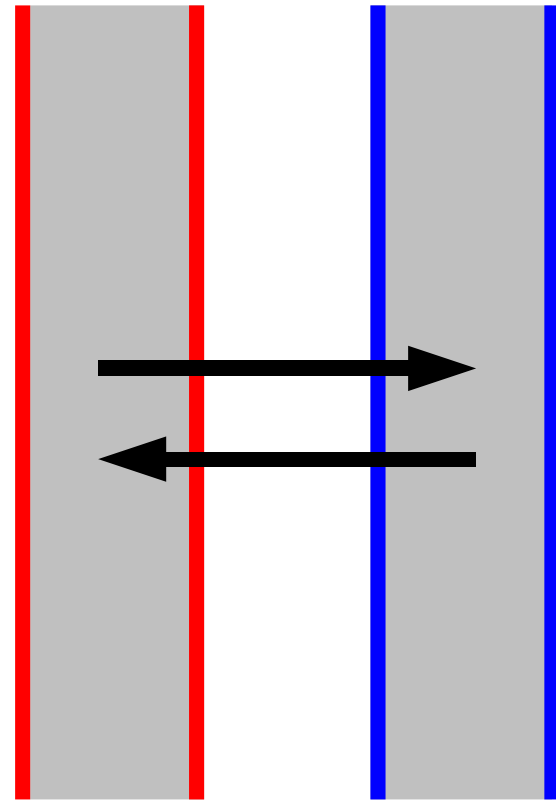
Interpretation of F_{ST}

Isolation vs. Migration

$$F_{ST} \approx 1 - e^{-t/2N}$$

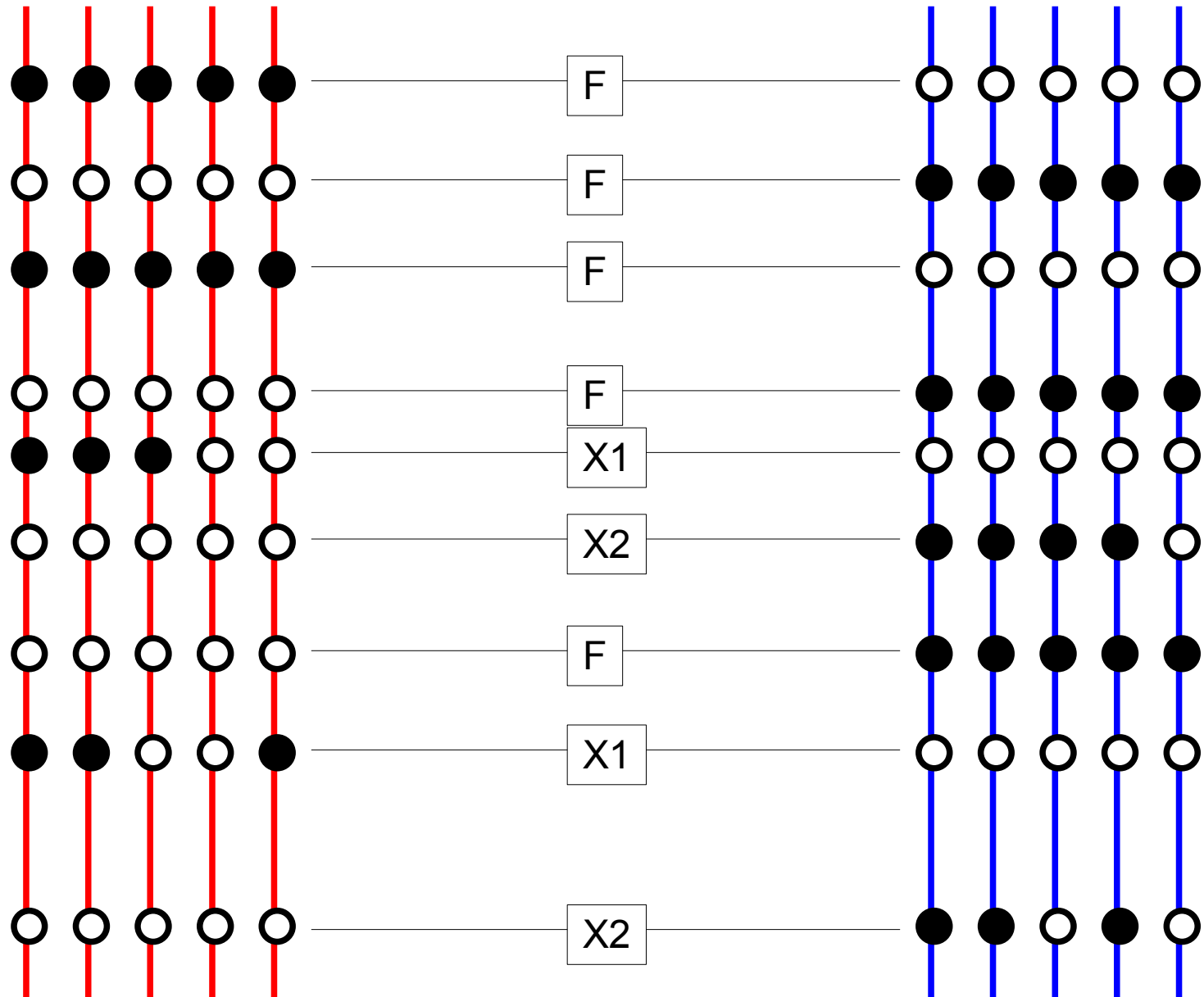


$$F_{ST} \approx \frac{1}{1 + 4Nm}$$



POPULATION 1

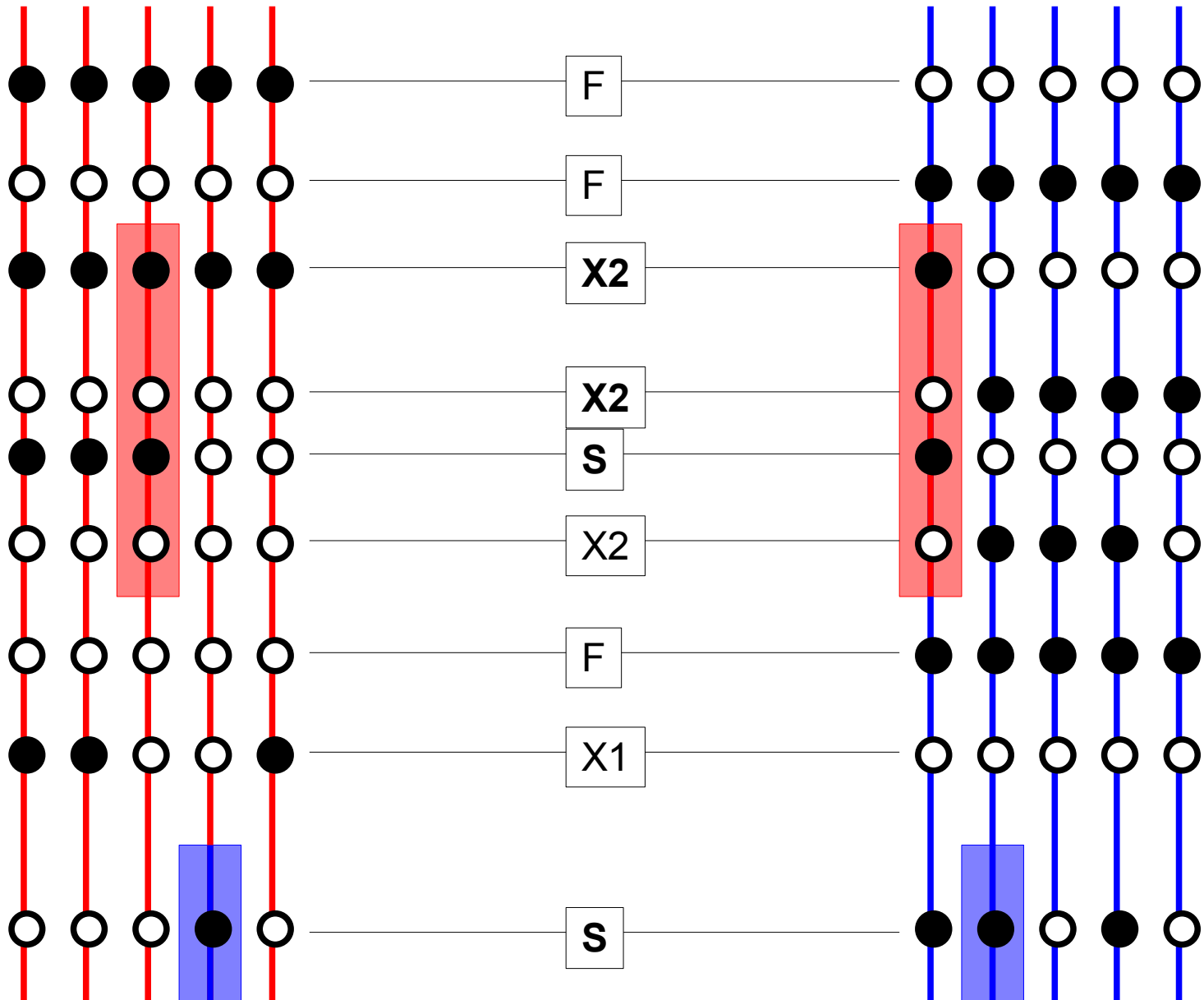
POPULATION 2



● derived state ○ ancestral state

POPULATION 1

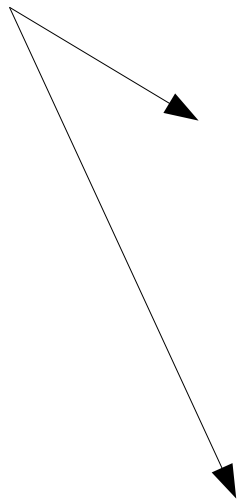
POPULATION 2



● derived state ○ ancestral state

Statistics: number of runs

$n^+ = 8, n^- = 7$



****--*-* ** *-*---**
1 2 3 4 5 6 7 8

NR=8

random

*******--**
1 2

NR=2

clustered

Statistics: length of runs

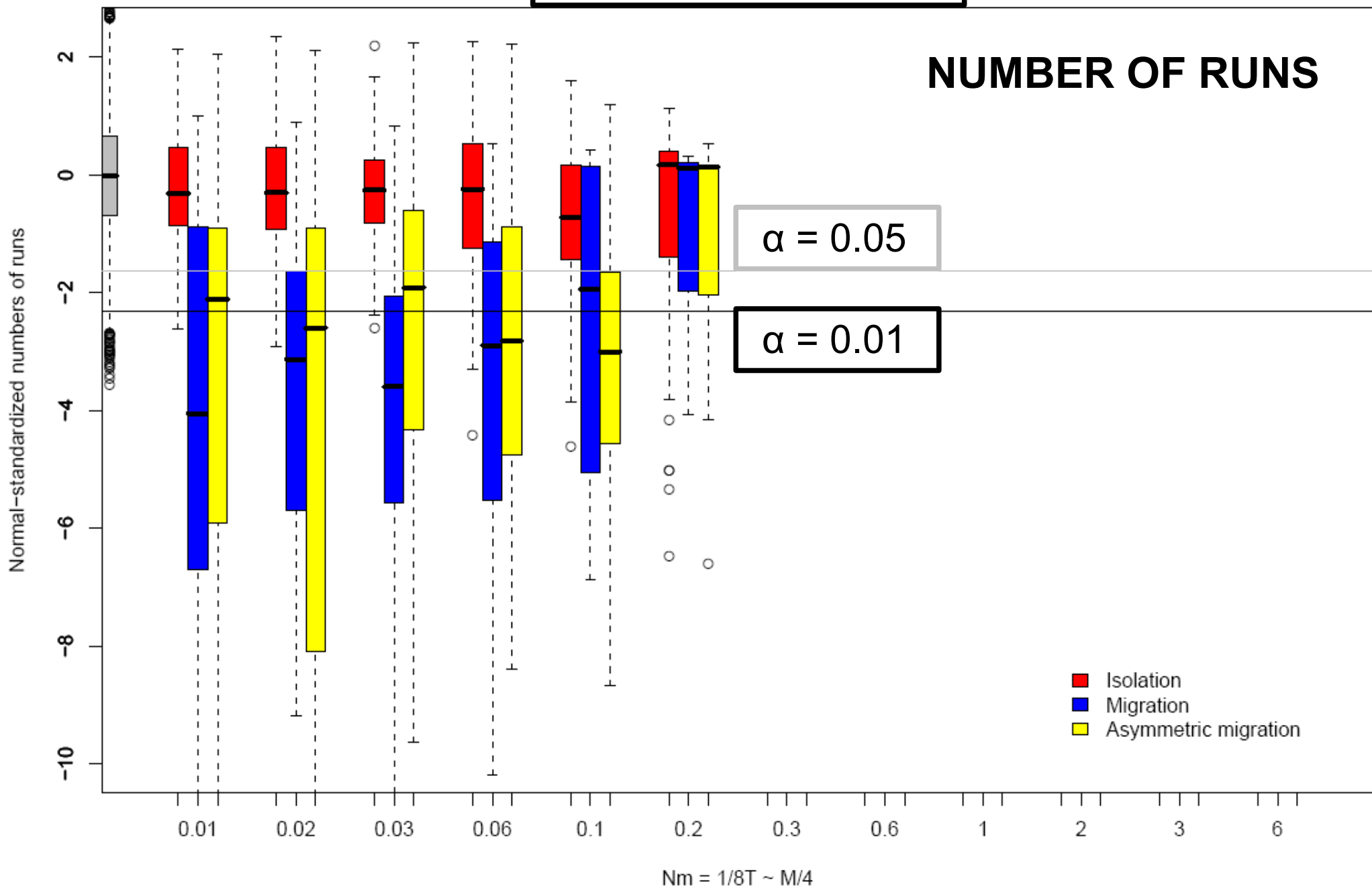
$$n^+ = 7, n^- = 8$$

$$\begin{array}{l} \text{"-----"} \\ - * - ** - - - * - - ** - * \end{array} + 7 \text{ random cuts } (*) = \text{Lengths } (-): 1, 1, 0, 3, 2, 0, 1, 0$$

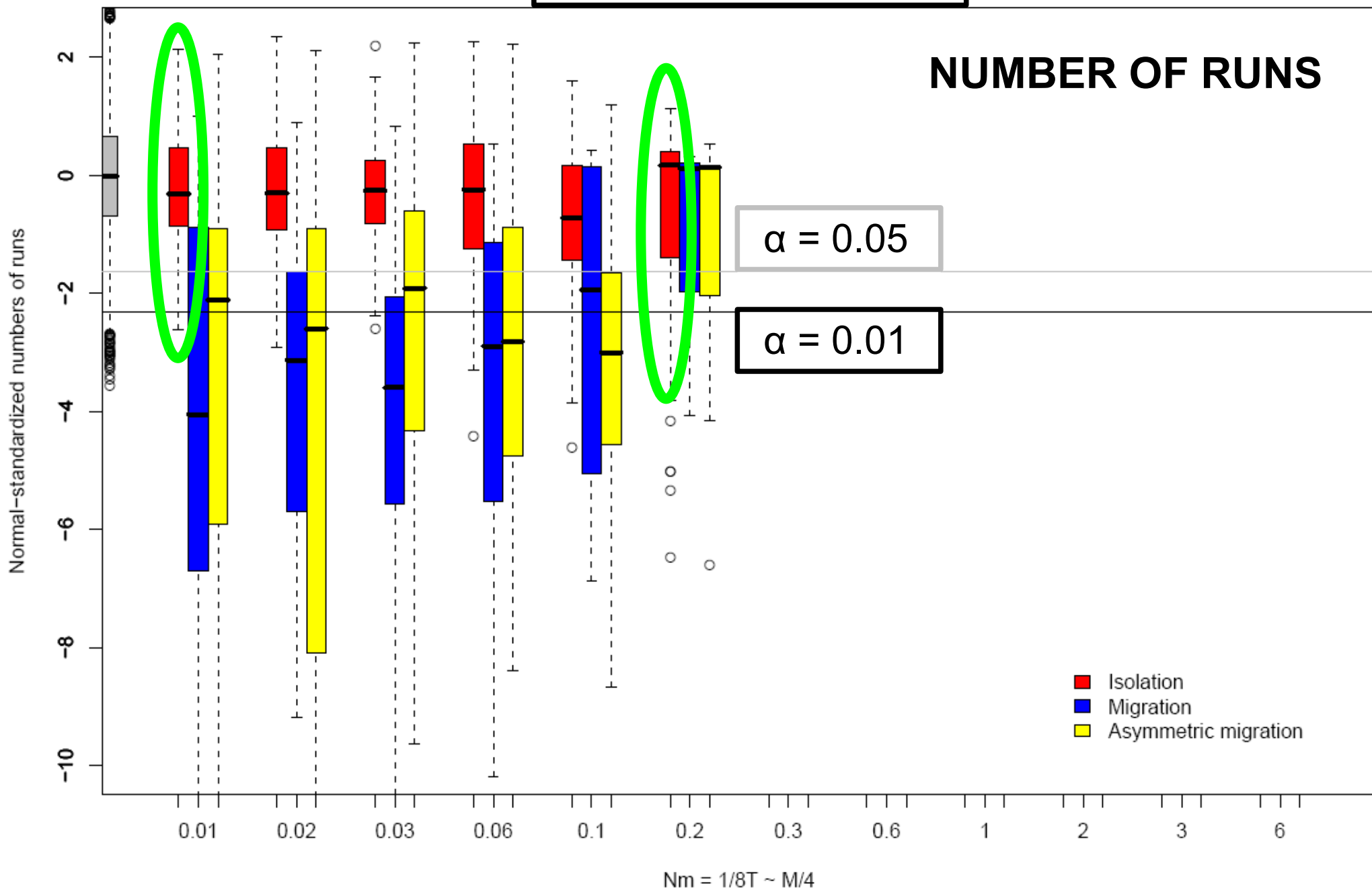
$$\begin{array}{l} \text{"-----"} \\ - - - - - * * * * * - - - - \end{array} + 7 \text{ clustered cuts } (*) = \text{Lengths } (-): 5, 0, 0, 0, 0, 0, 0, 3$$

F(*) vs. S+X(-)

NUMBER OF RUNS

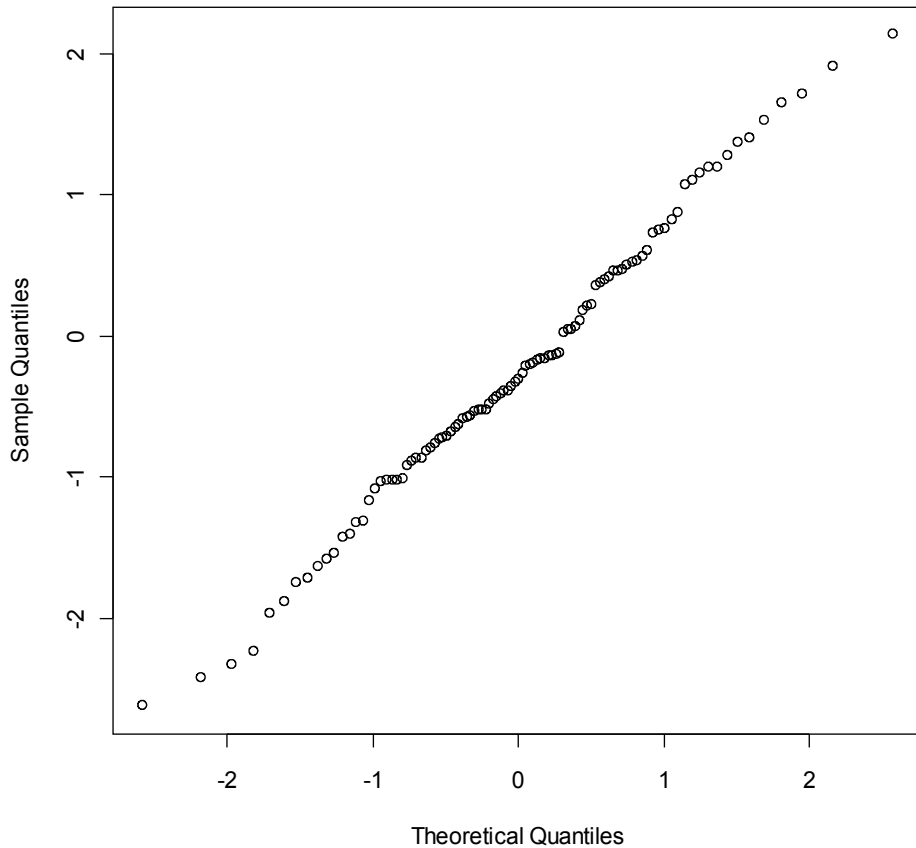


F(*) vs. S+X(-)



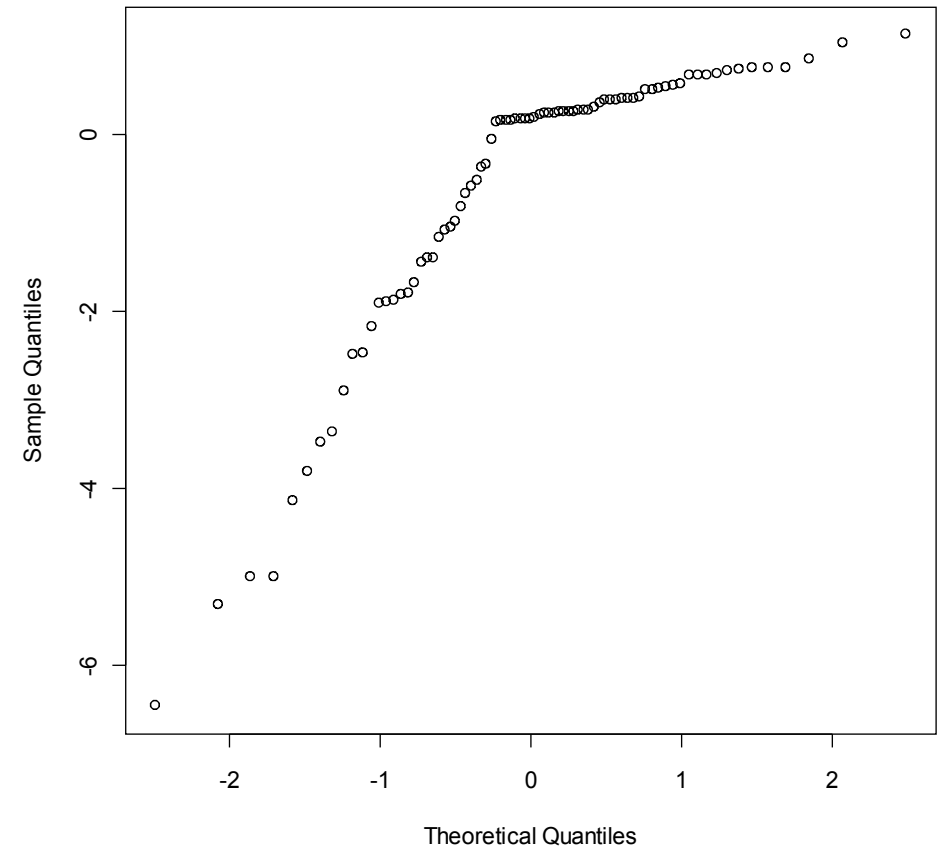
Isolation as null hypothesis

Normal Q-Q Plot



Isolation: $T=12.5$

Normal Q-Q Plot

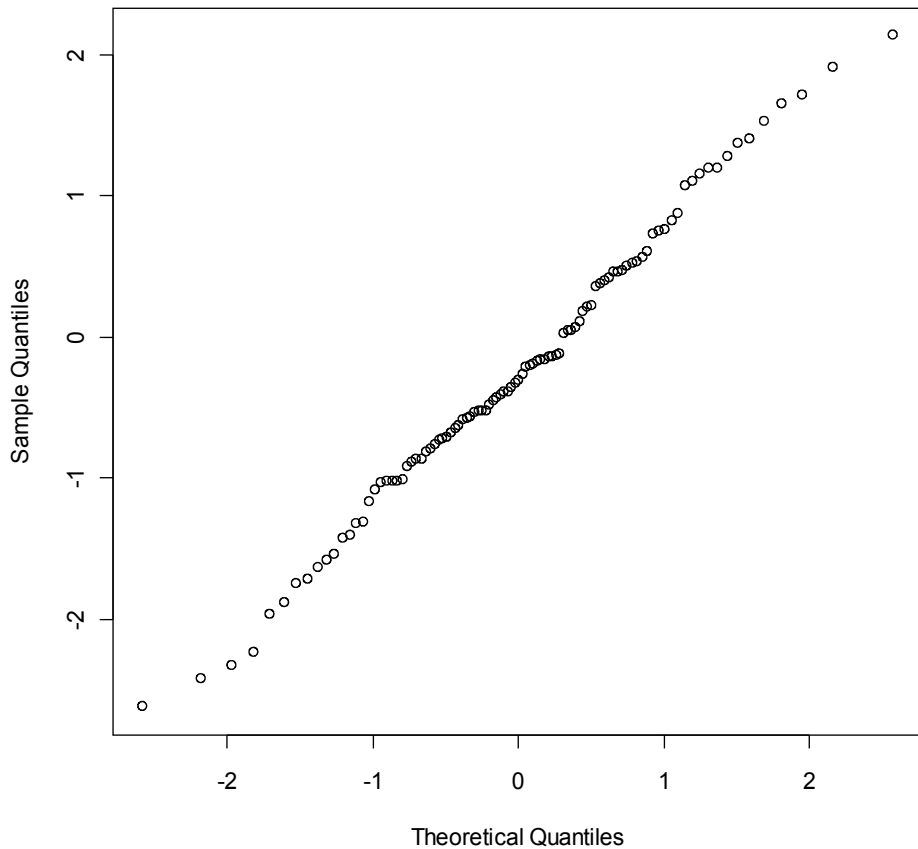


Isolation: $T=0.625$

(T: time scaled to population size)

Test with several loci

Normal Q-Q Plot



Kolmogorov–Smirnov test (on 10 loci)

Isolation: 1/10

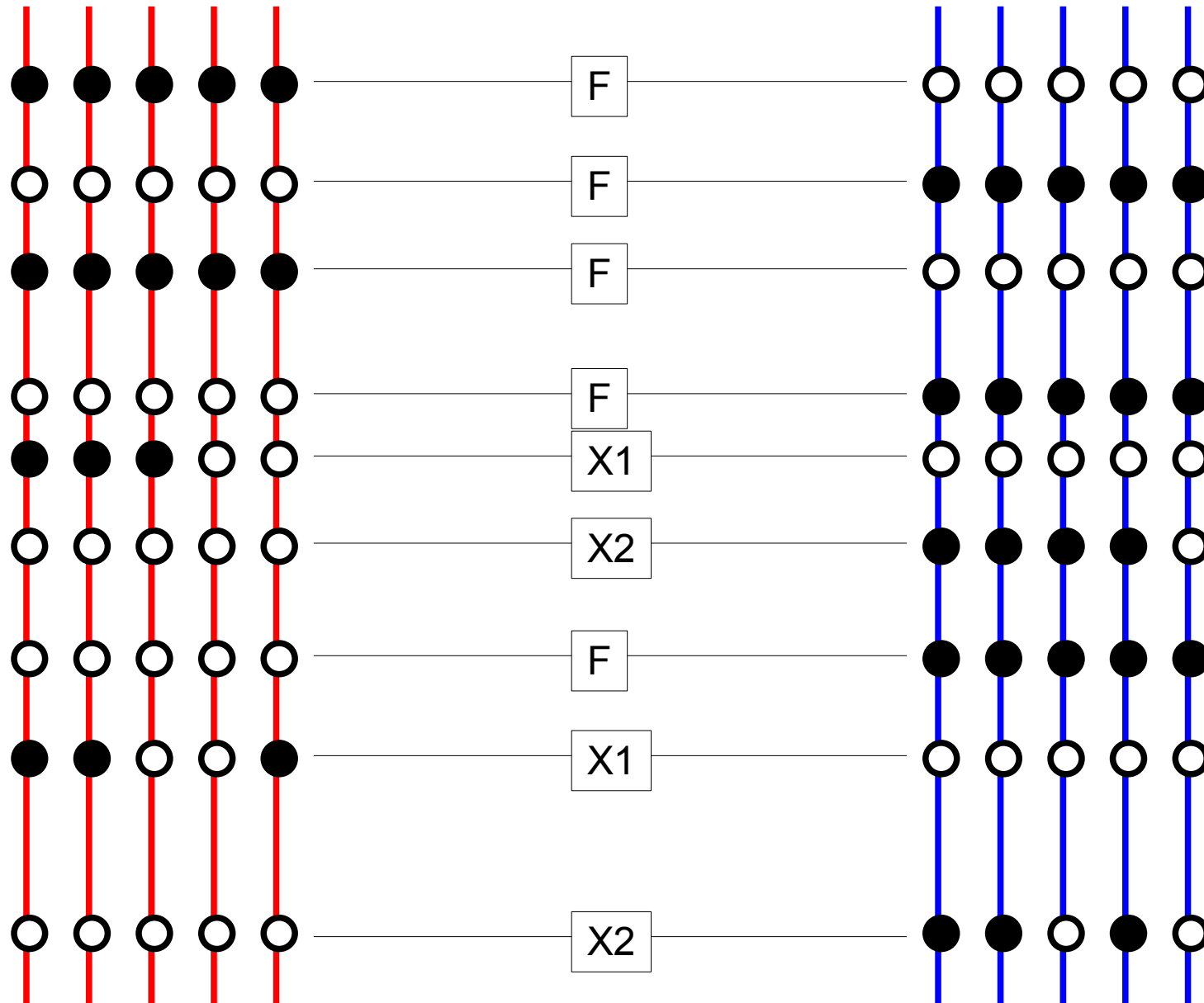
Migration: 9/10

Asymmetric mig.: 10/10

Asymmetric migration

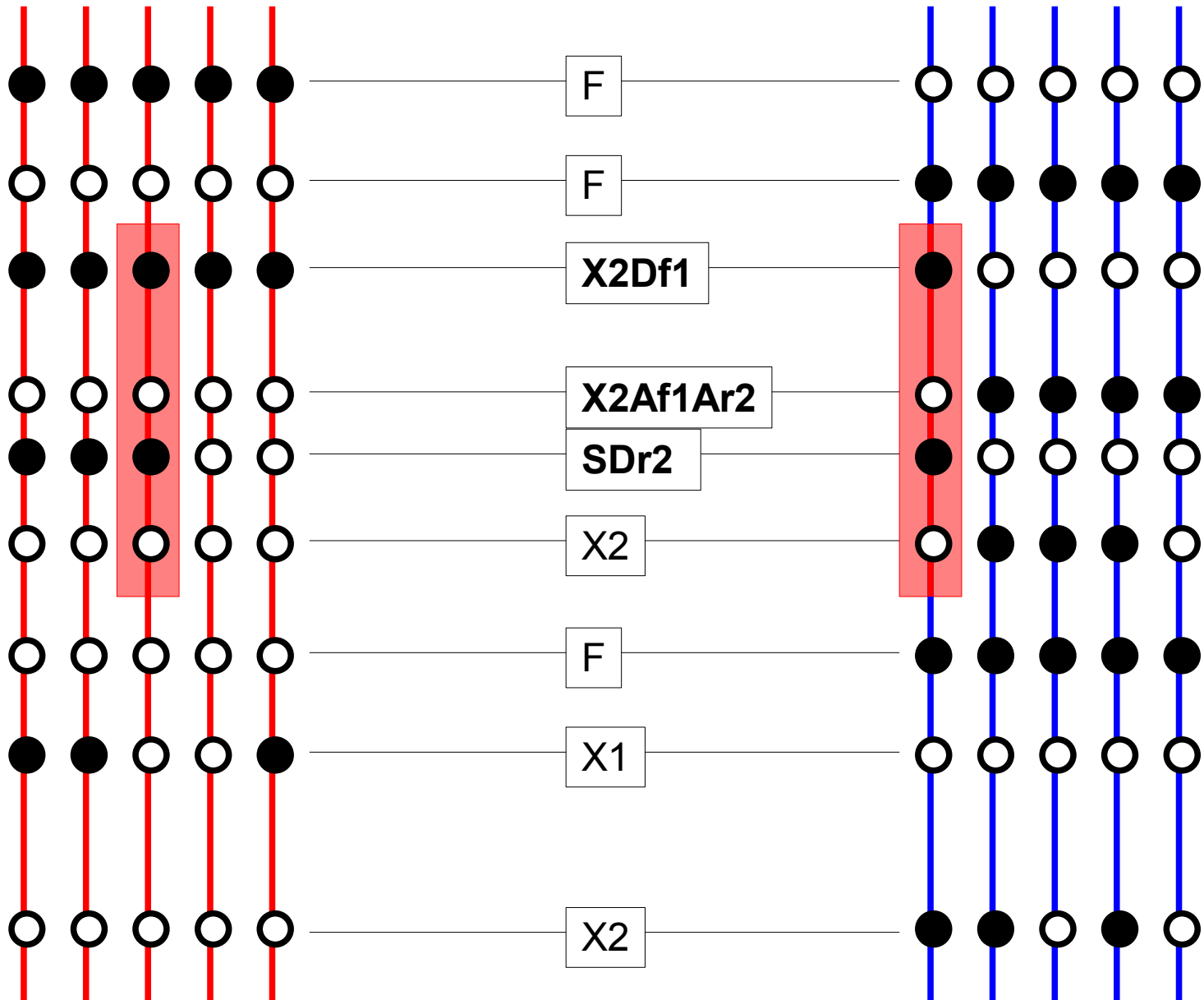
POPULATION 1

POPULATION 2



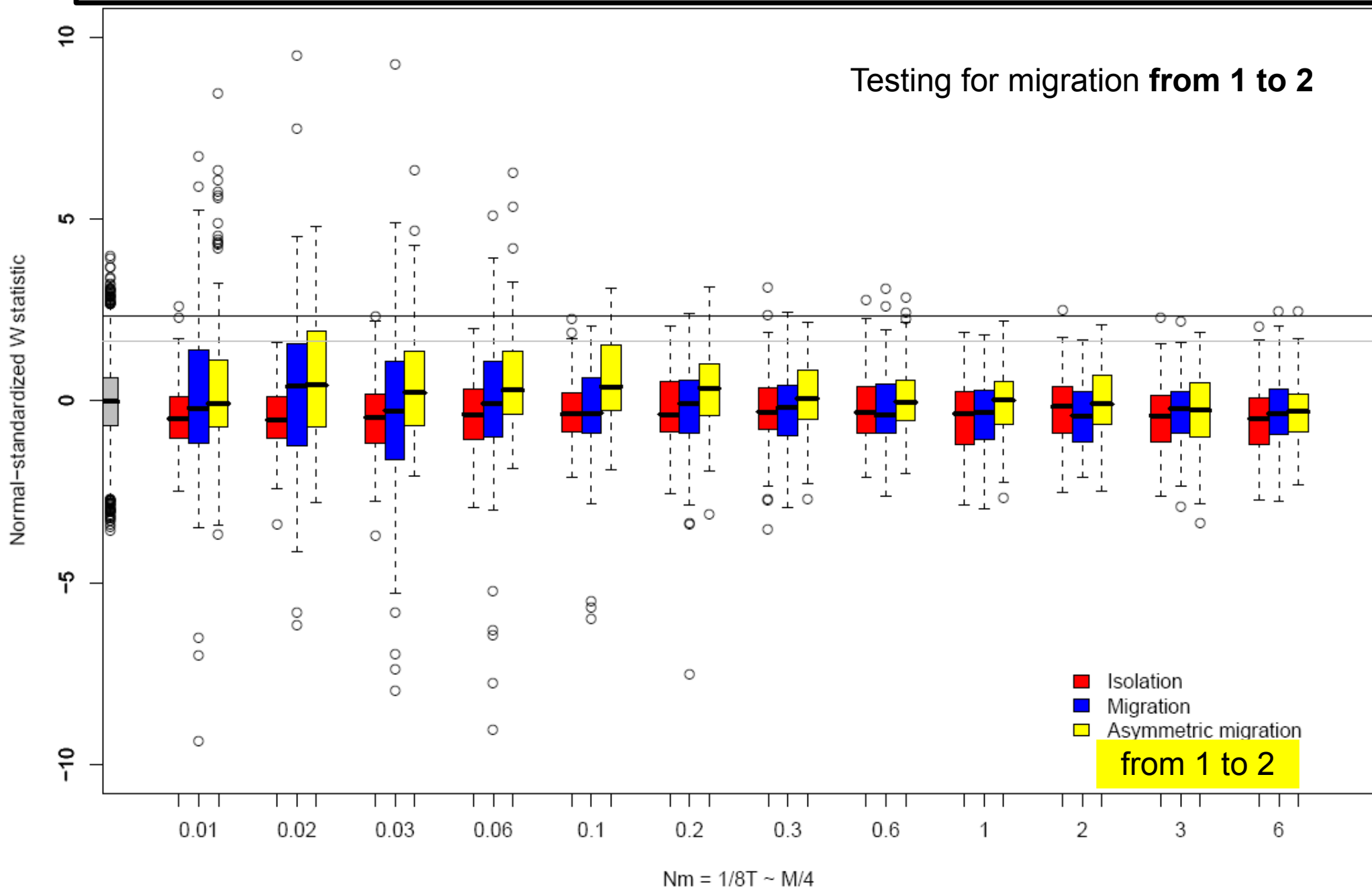
POPULATION 1

POPULATION 2



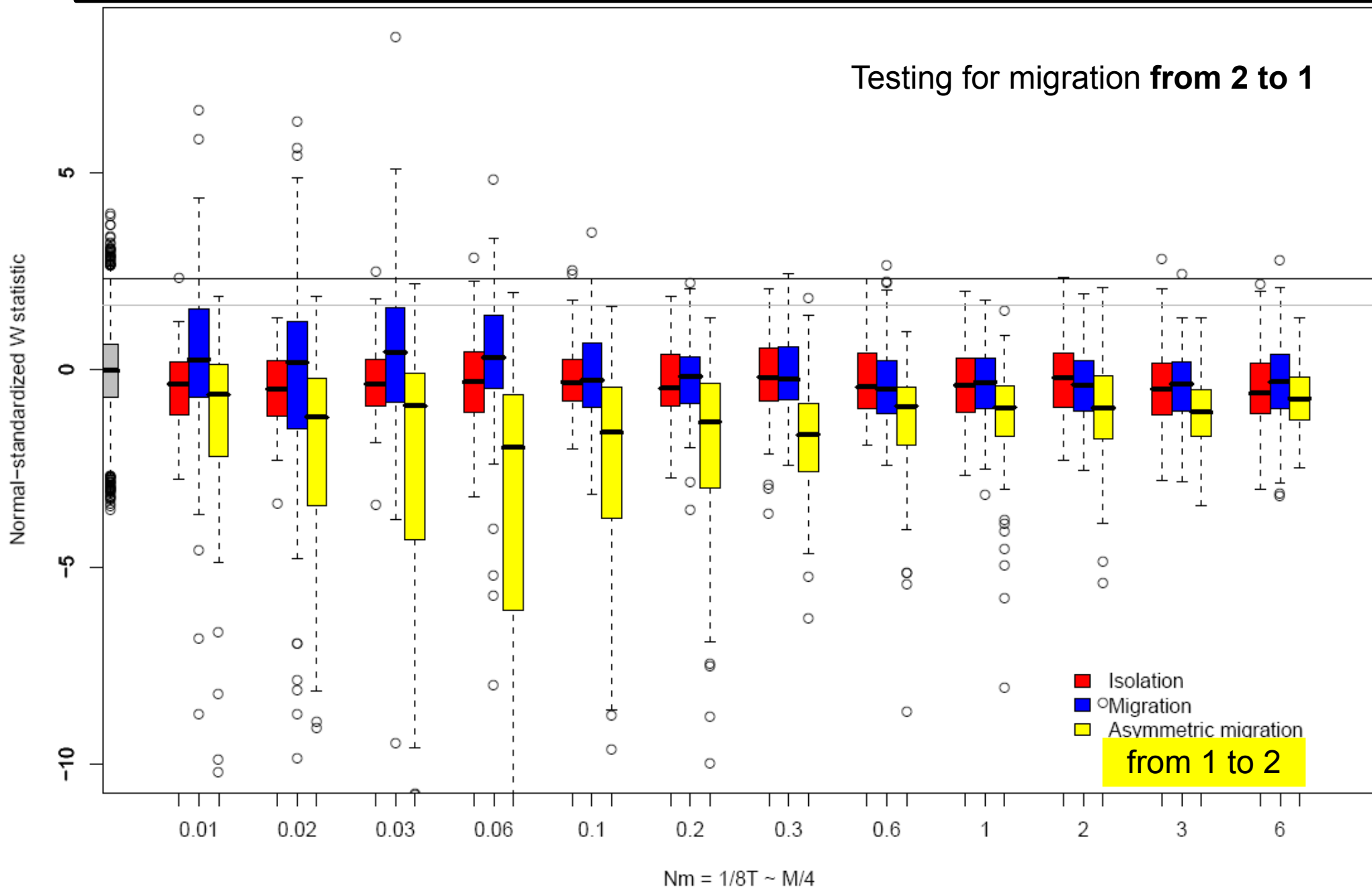
● Derived state ○ Ancestral state

SDr2+X2Df1+X2Af1Ar2 vs. SDr1+X1Df2+X1Af2Ar2



SDr1+X1Df2+X1Af2Ar1 vs. SDr2+X2Df1+X2Af1Ar1

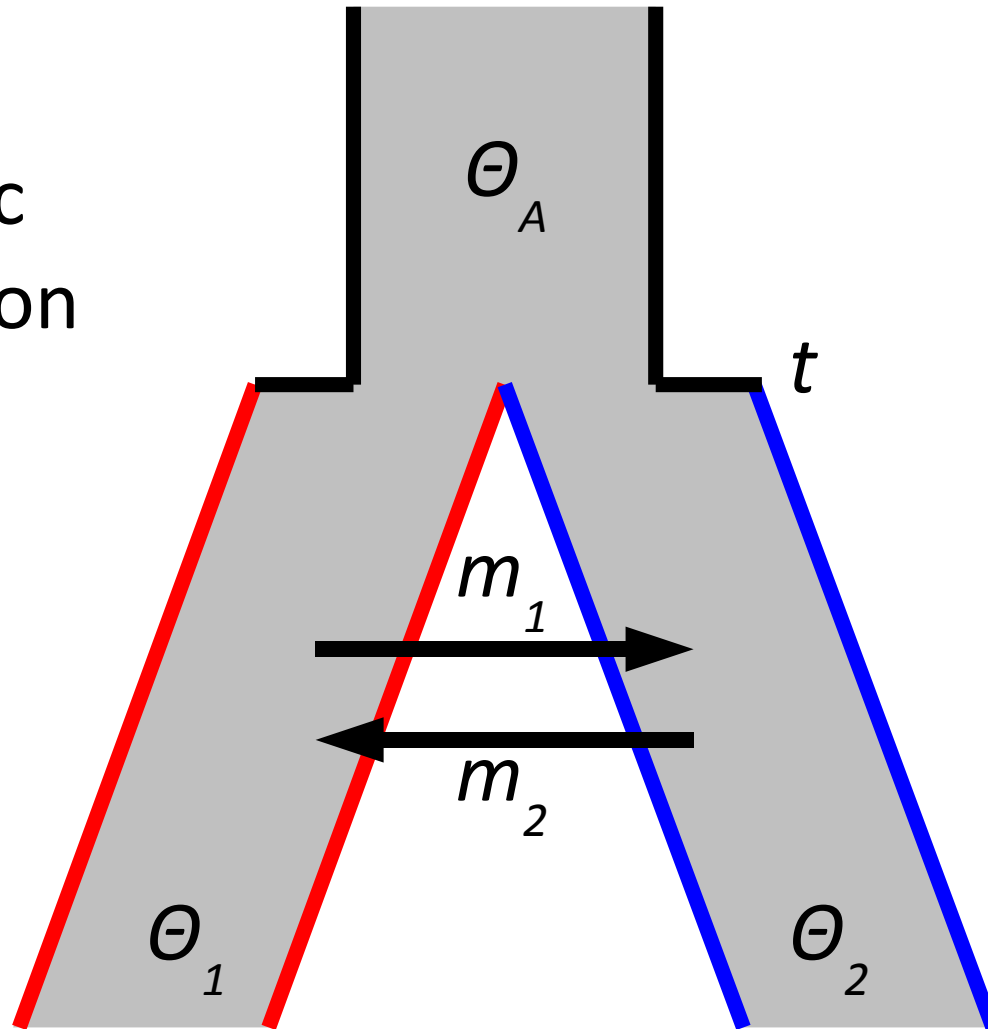
Testing for migration from 2 to 1



Likelihood Coalescent MCMC

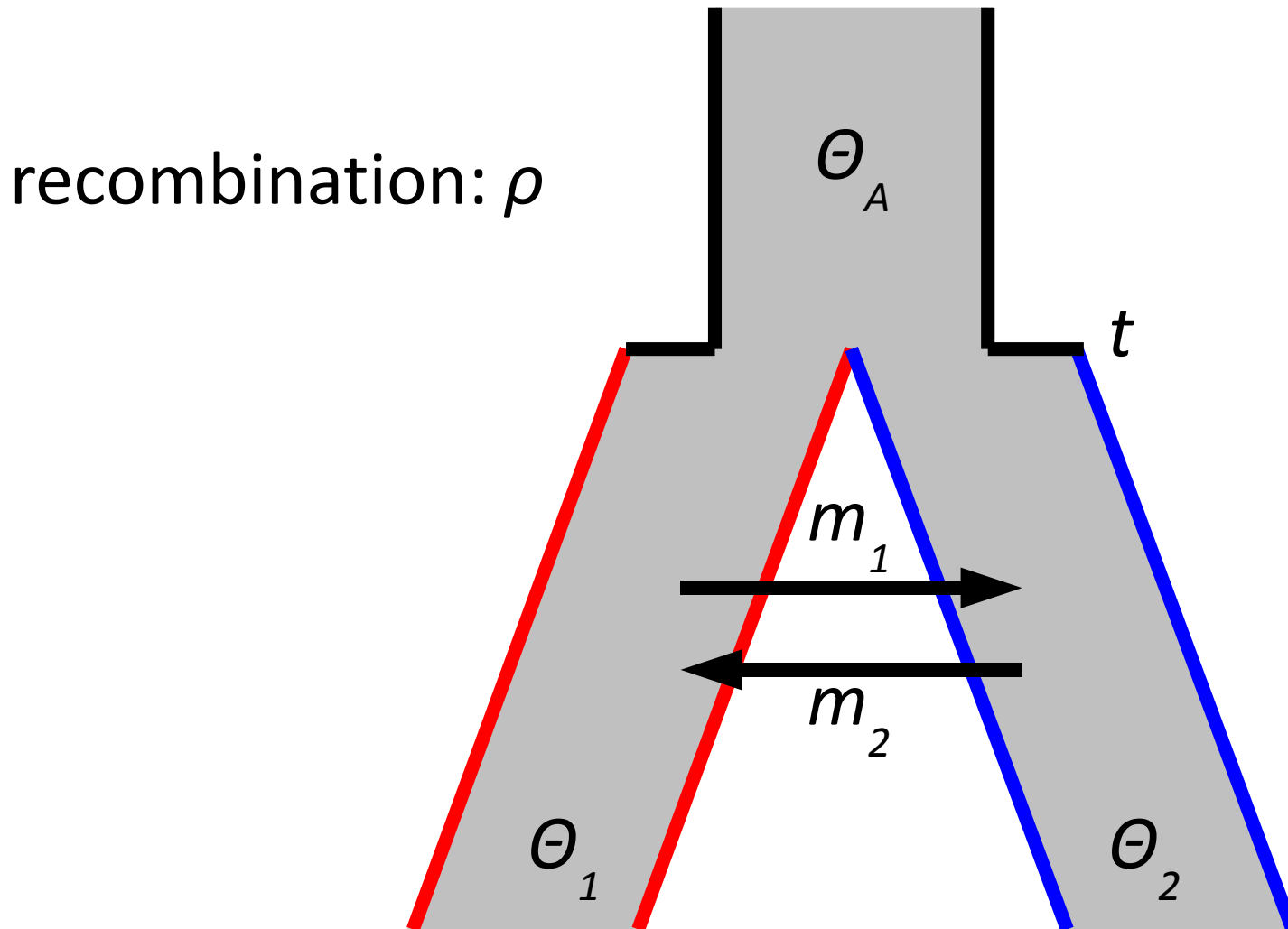
(Nielsen & Wakeley 2001, Hey & Nielsen 2004)

no intragenic recombination



Summary Statistics Coalescent MCMC

(Becquet & Przeworski 2007)

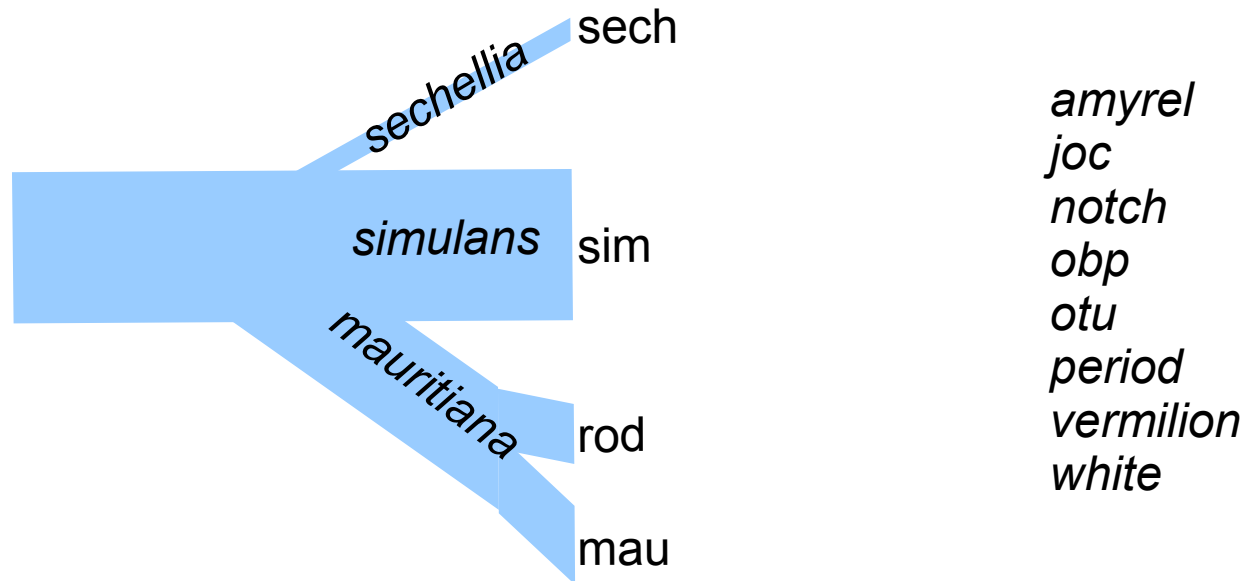


Summary

- Clustering of certain types of polymorphism
- Non-parametric statistics: based on runs
- Statistics sensitive to migration
- Statistics sensitive to direction of migration
- Summary statistics replacing likelihood (e.g. ABC)

Drosophila simulans, sechellia, mauritiana

Marie-Louise Cariou and team



Biodiversité: TRANSBIODIV

Arabidopsis: Xavier Vekemans and team

Millet: Thierry Robert and team

Oaks: Antoine Kremer and team

Mice: Pierre Boursot and team