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Distinguishing shared ancestral polymorphism from recent introgression

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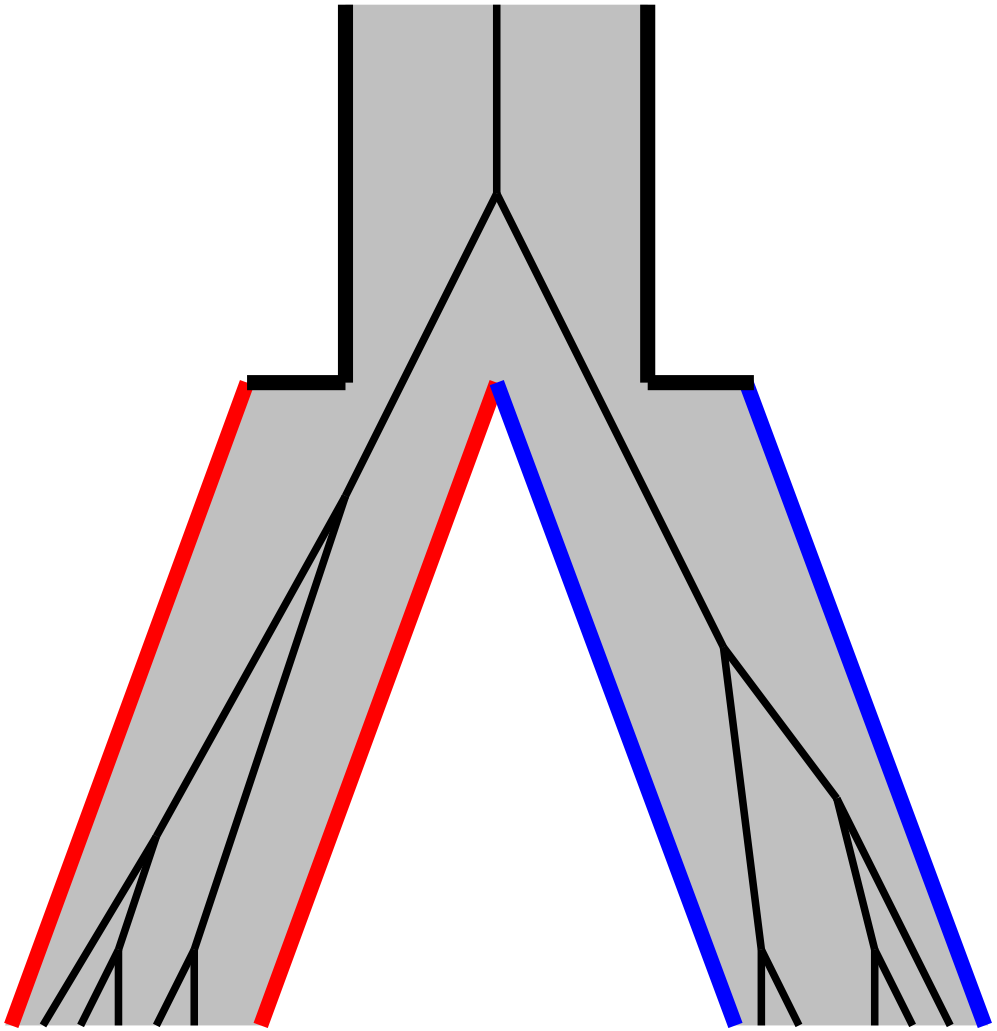
CNRS UMR 7625 Écologie et Évolution (ENS/UPMC)

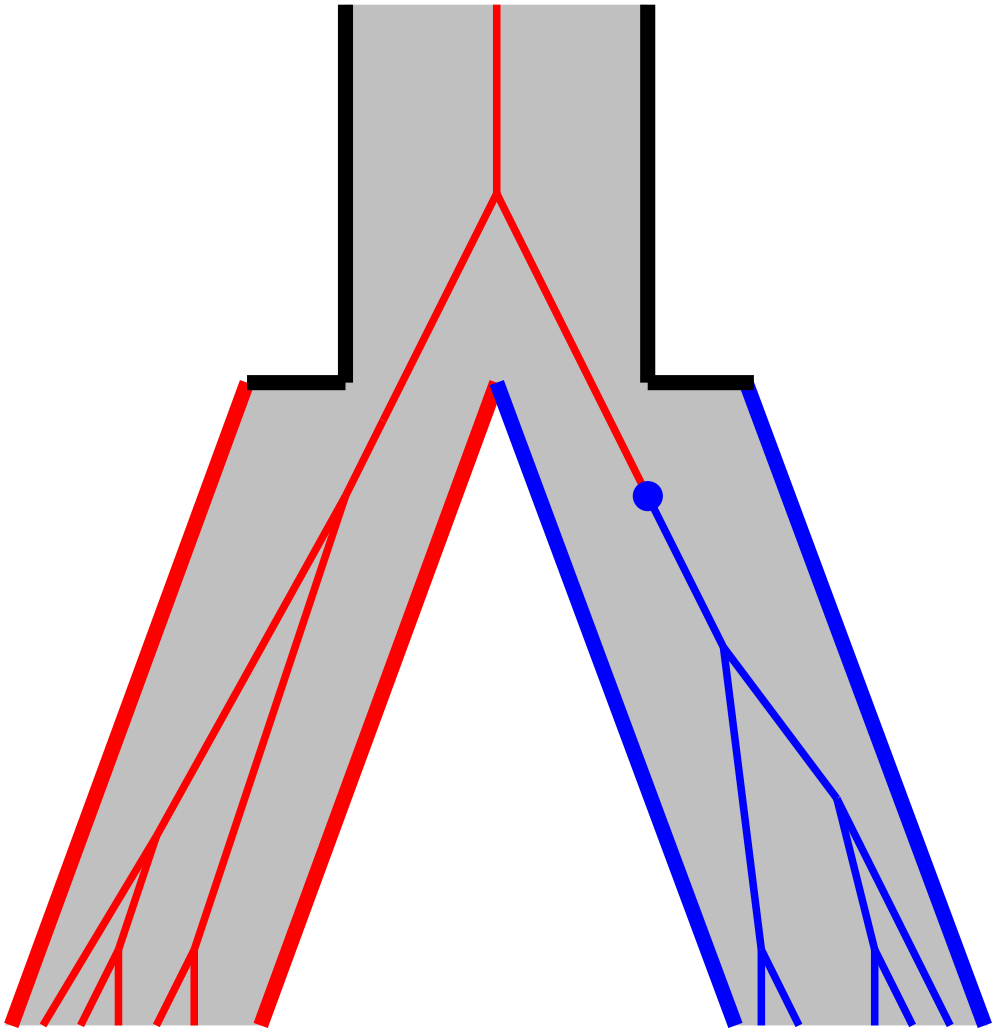
Biodiversité: TRANSBIODIV

Réunion GDR 1928 Génomique des populations et génomique évolutive – Sète, 16 October 2008

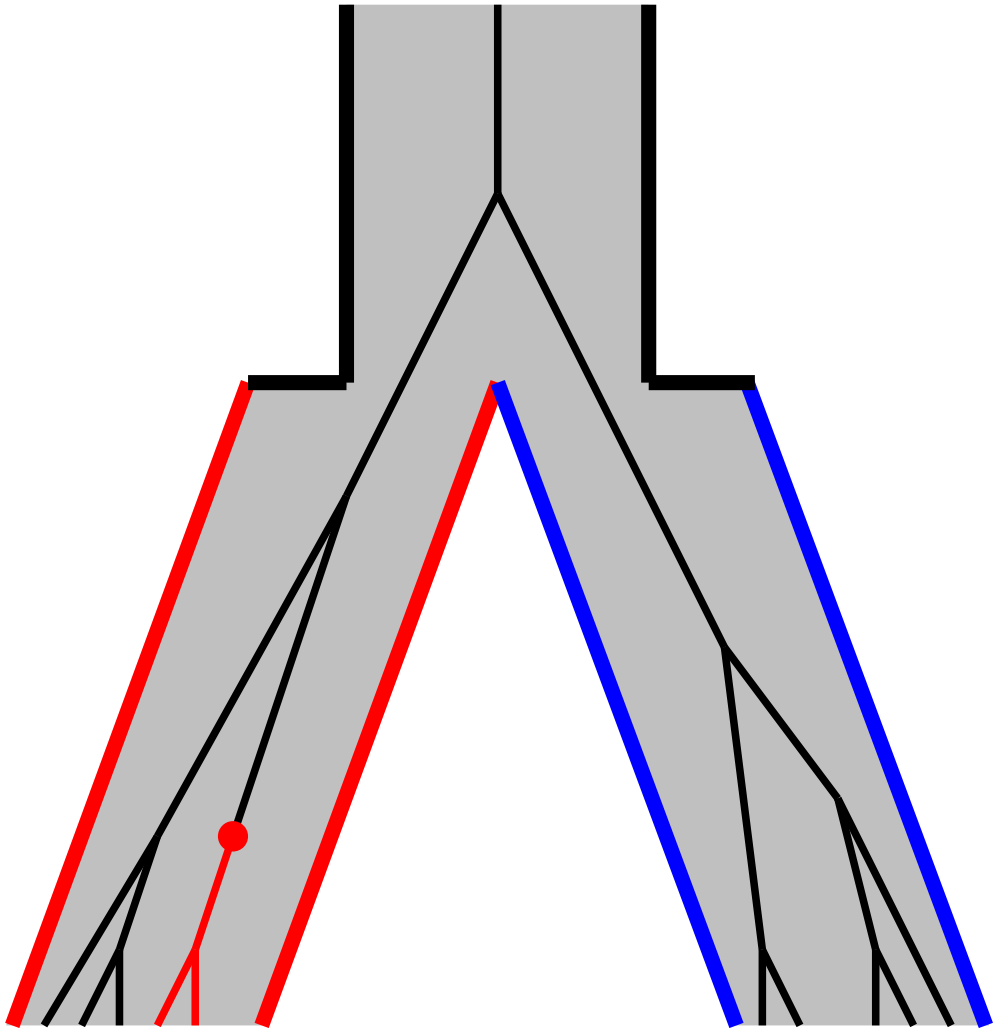
Polymorphisms between two species



Fixed polymorphism

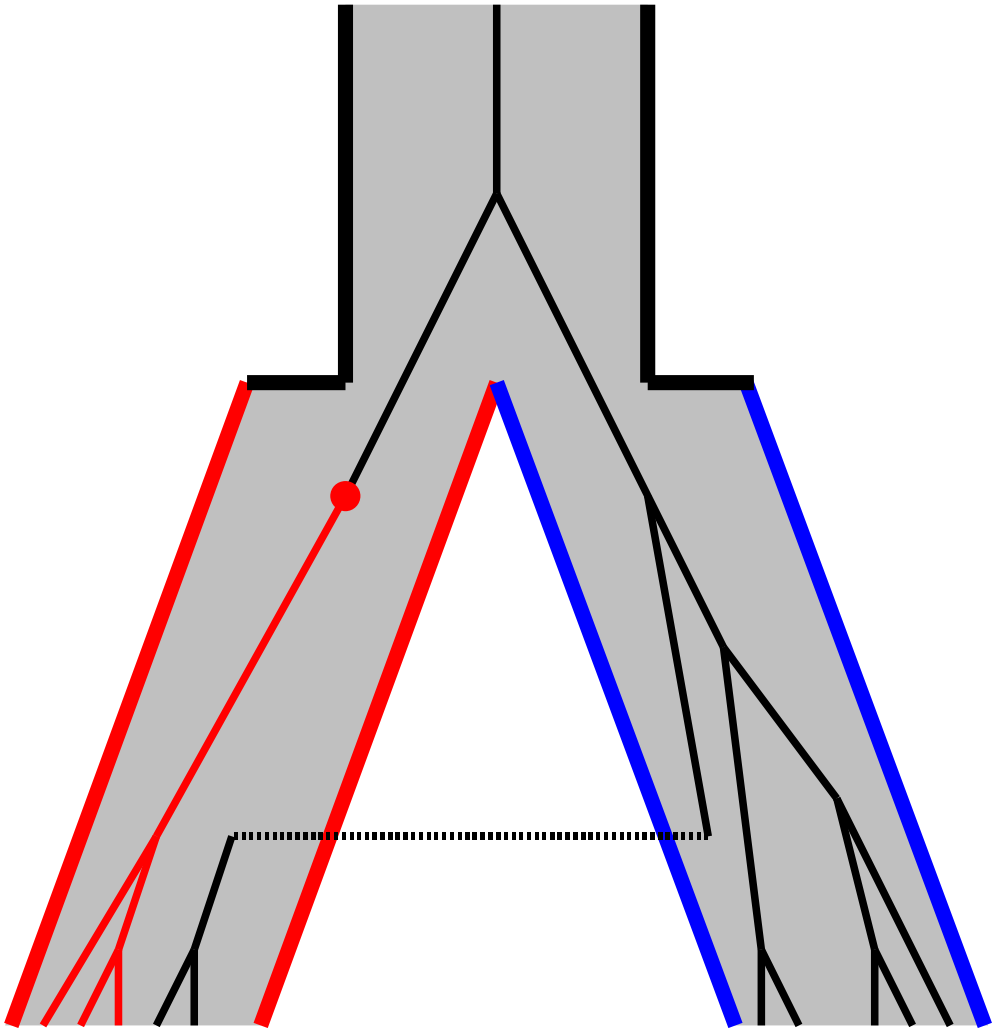


Exclusive polymorphism



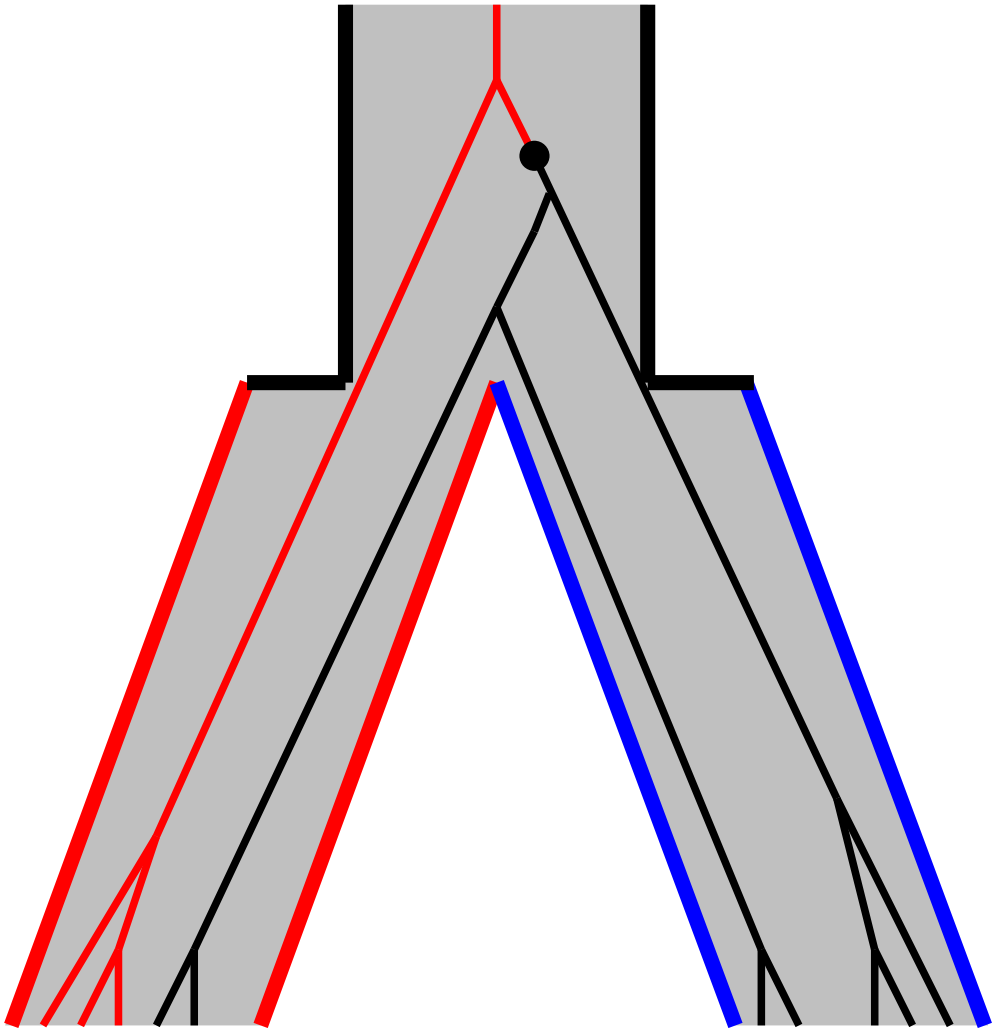
Exclusive polymorphism

Introgression



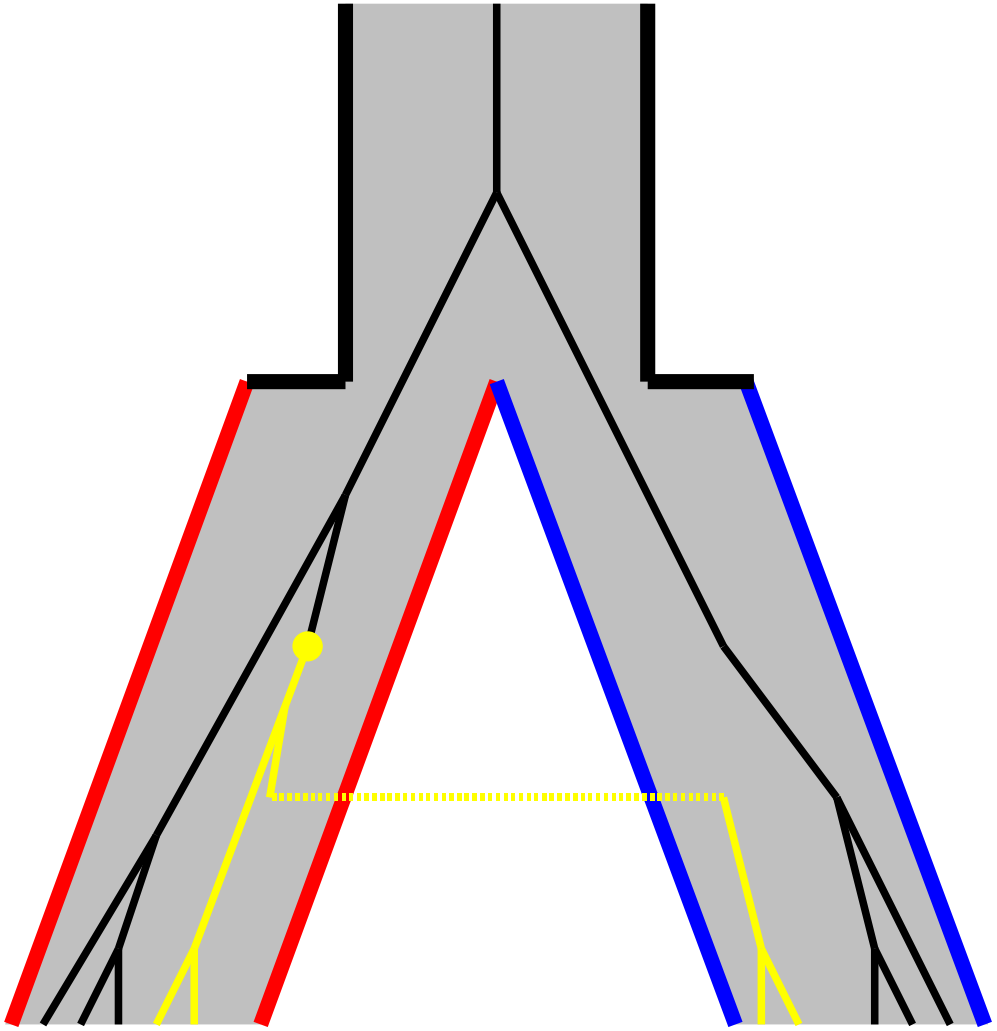
Exclusive polymorphism

Ancestral



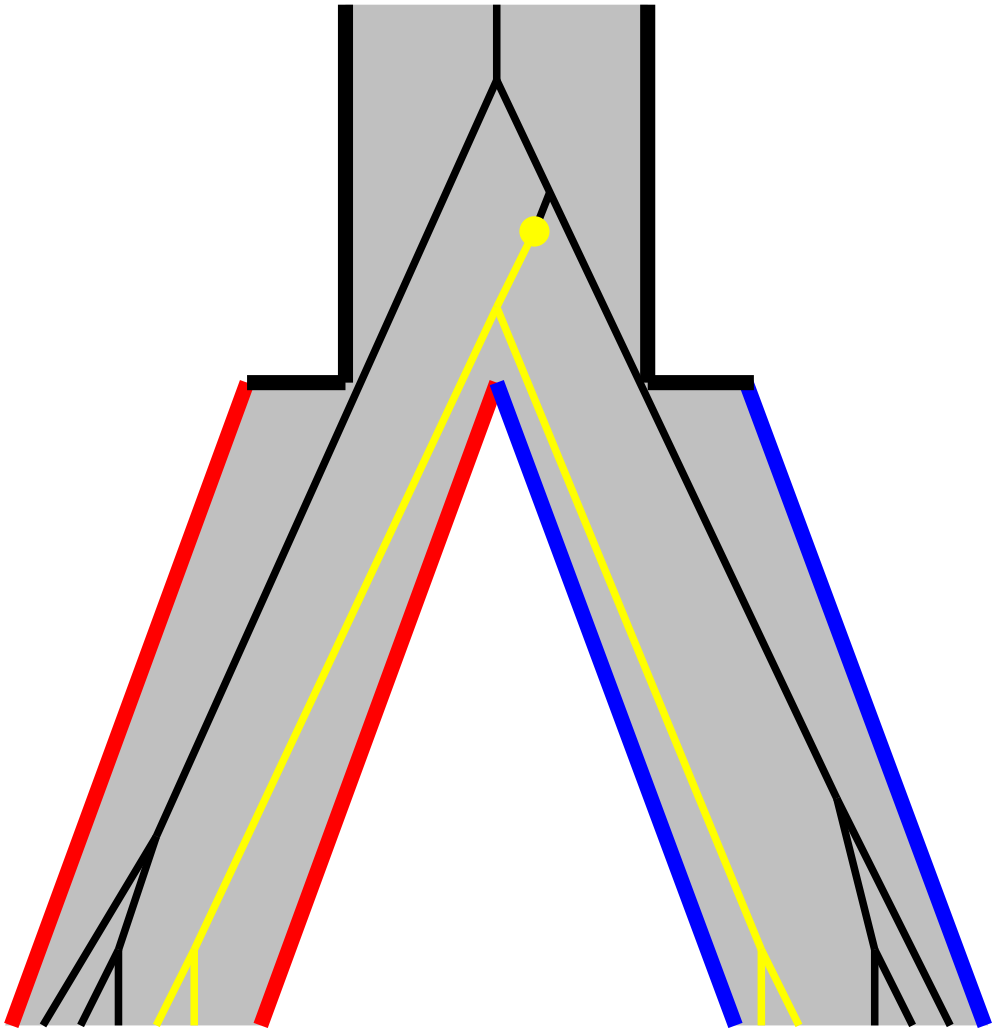
Shared polymorphism

Introgression



Shared polymorphism

Ancestral

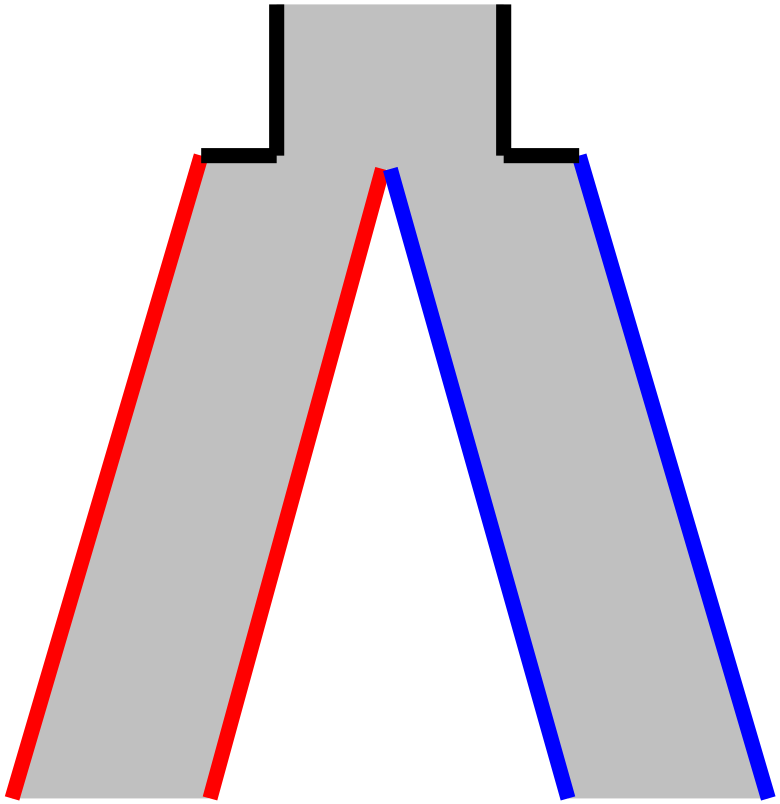


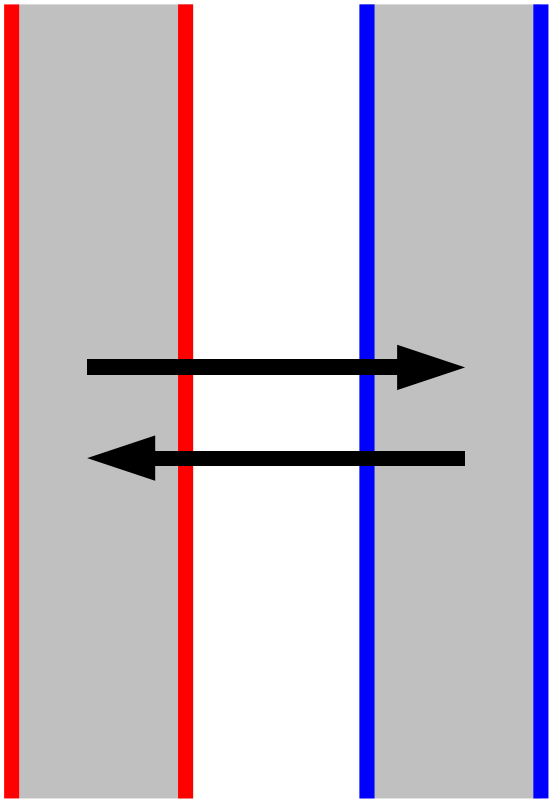
Interpretation of F_{ST}

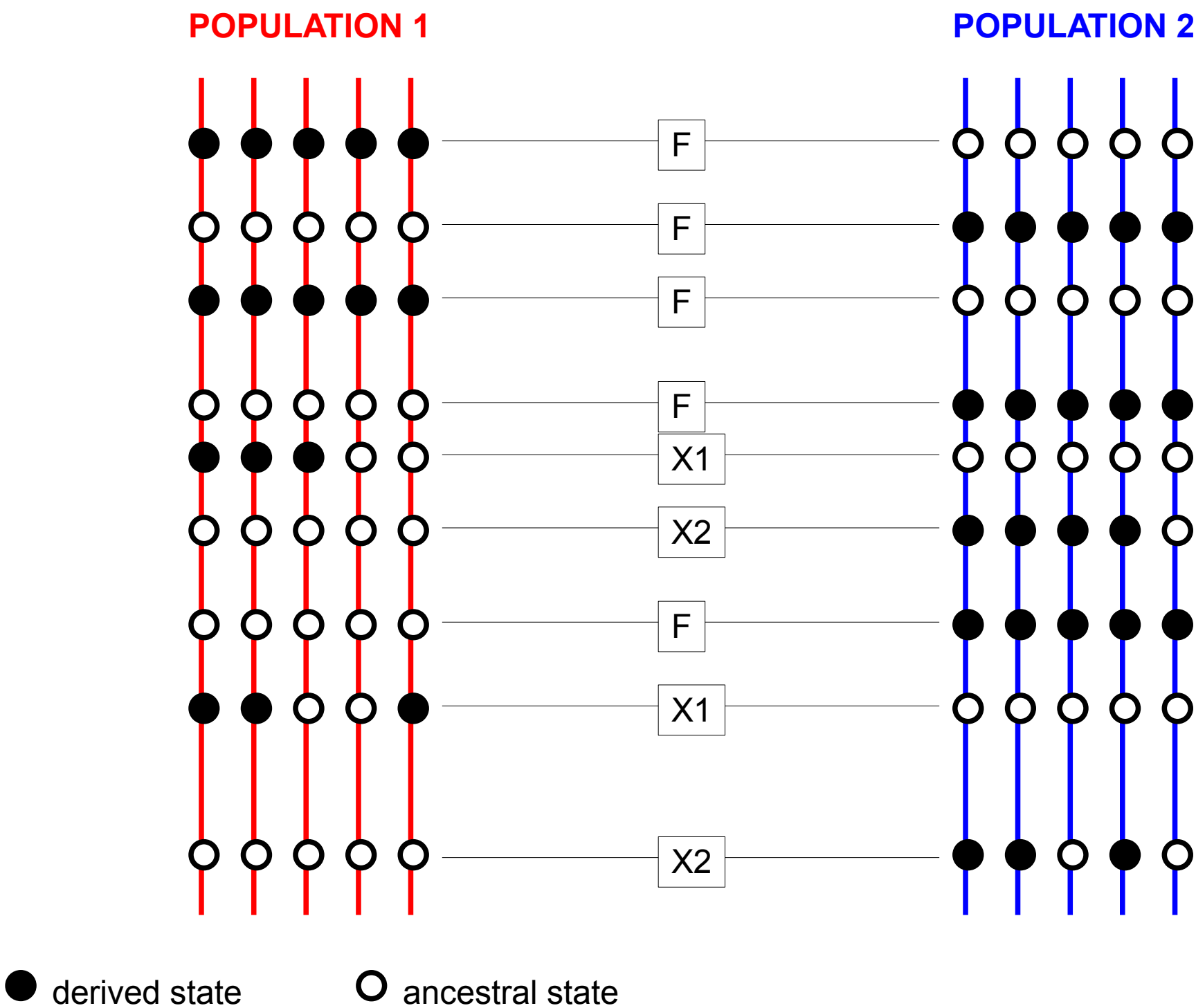
Isolation vs. Migration

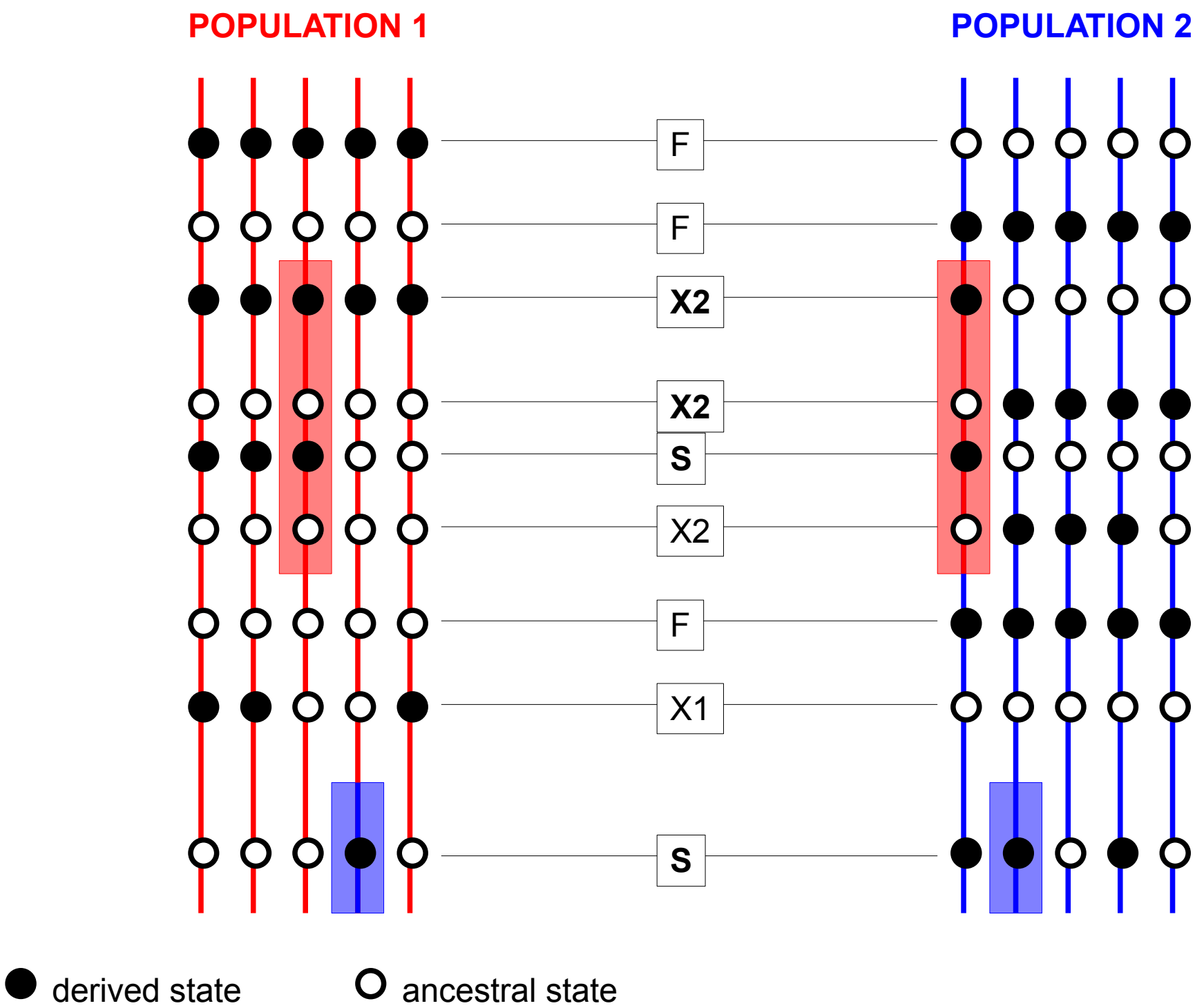
$$F_{ST} \approx 1 - e^{-t/2N}$$

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






POPULATION 1
POPULATION 2
F
F
F
F
X1
X2
F
X1
X2
derived state
ancestral state


POPULATION 1
POPULATION 2
F
F
X2
X2
S
X2
F
X1
S
derived state
ancestral state

Statistics: number of runs

$n^{*}=8$, $n^{-}=7$

```
**--*-****-*---    NR=8    random
1  2  345    678

********-------    NR=2    clustered
1         2
```

Statistics: length of runs

$n^{*}=7$, $n^{-}=8$

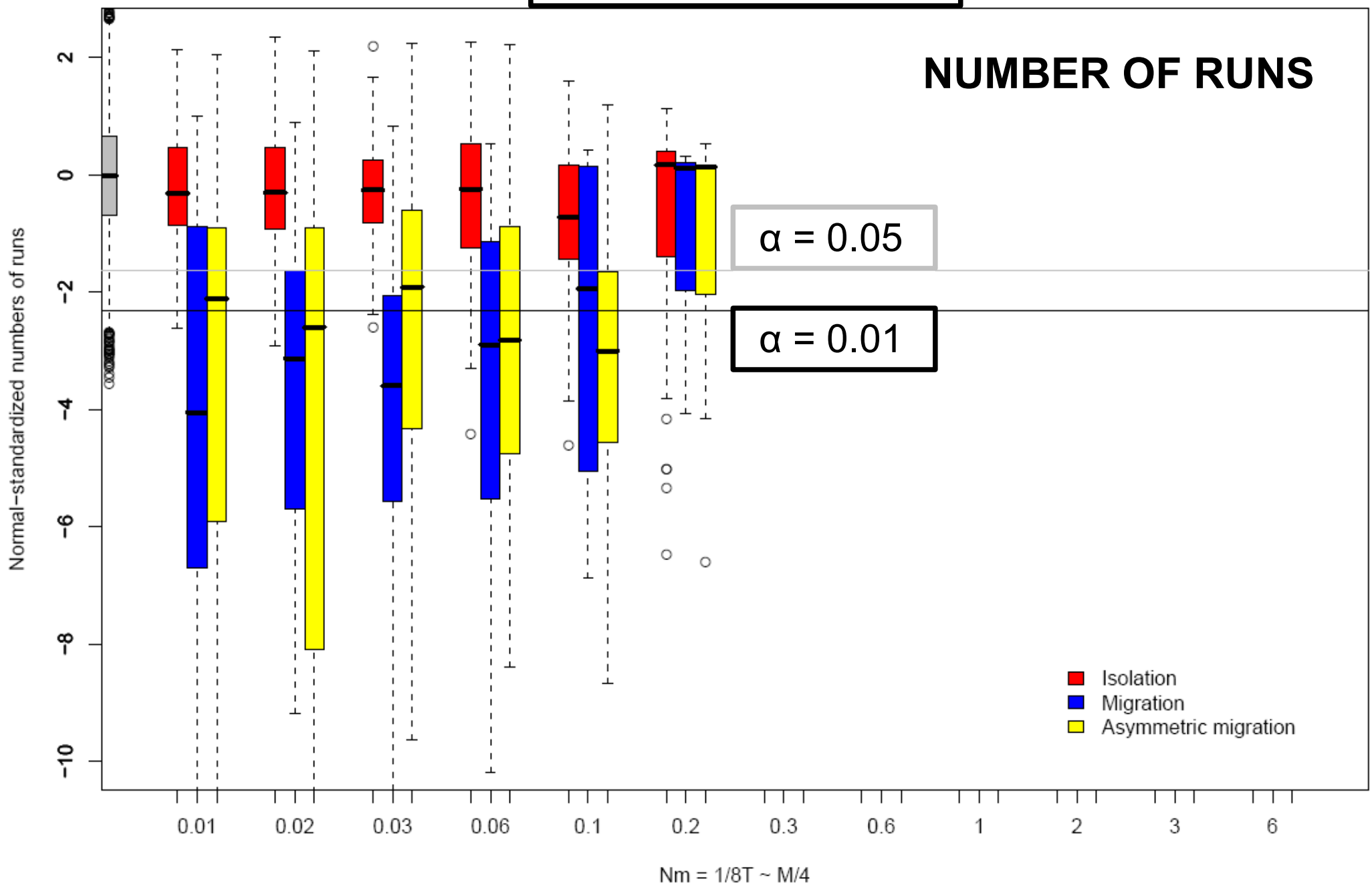
"−−−−−−−−−" + 7 random cuts (*) =

−*−**−−−*−−**−* Lengths (−): 1, 1, 0, 3, 2, 0, 1, 0

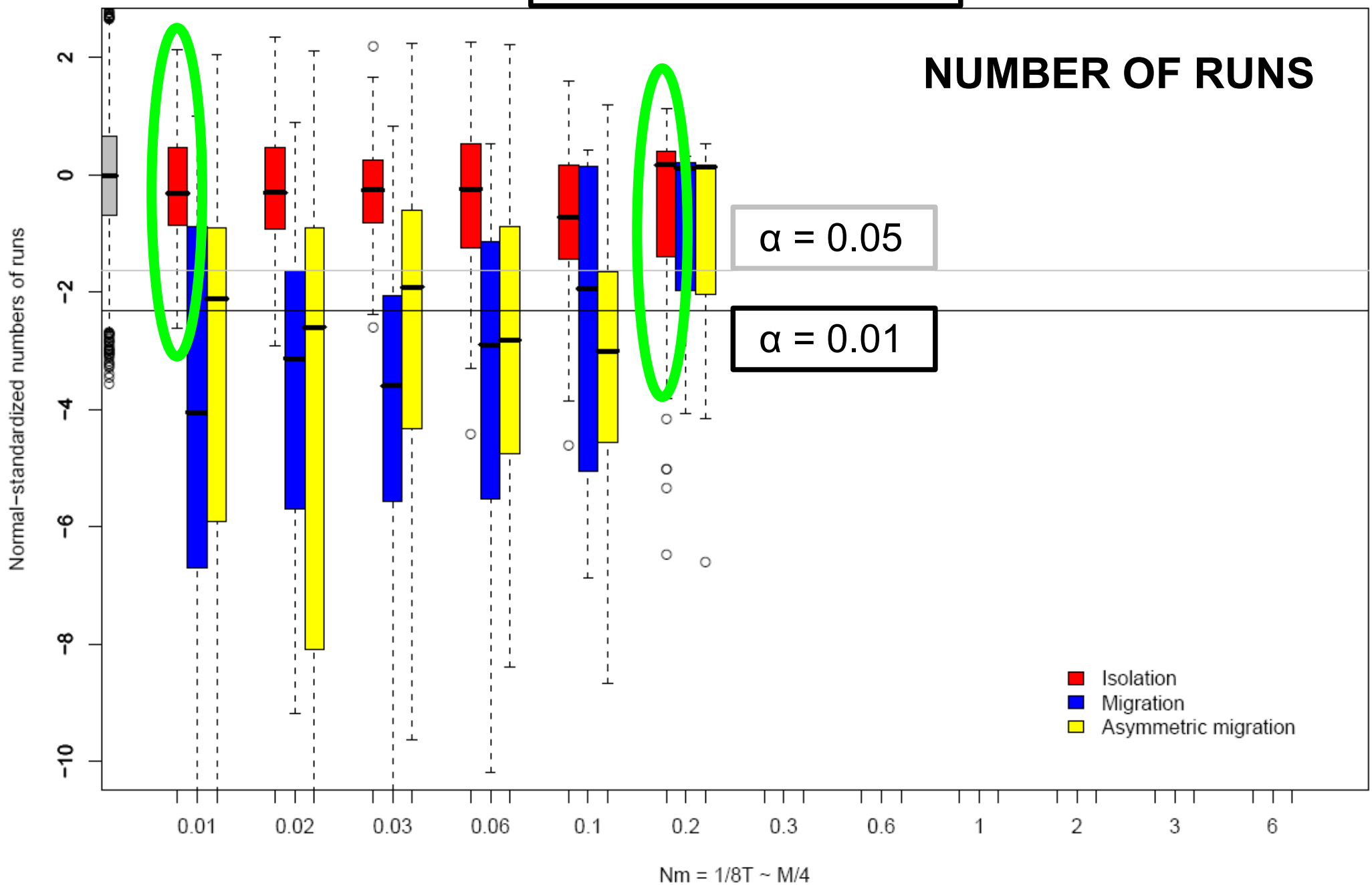
"−−−−−−−−−" + 7 clustered cuts (*) =

−−−−−*******−−− Lengths (−): 5, 0, 0, 0, 0, 0, 0, 3

F(*) vs. S+X(−)


NUMBER OF RUNS
α = 0.05
α = 0.01
Isolation
Migration
Asymmetric migration
Normal−standardized numbers of runs
2
0
−2
−4
−6
−8
−10
0.01
0.02
0.03
0.06
0.1
0.2
0.3
0.6
1
2
3
6
Nm = 1/8T ~ M/4

F(*) vs. S+X(–)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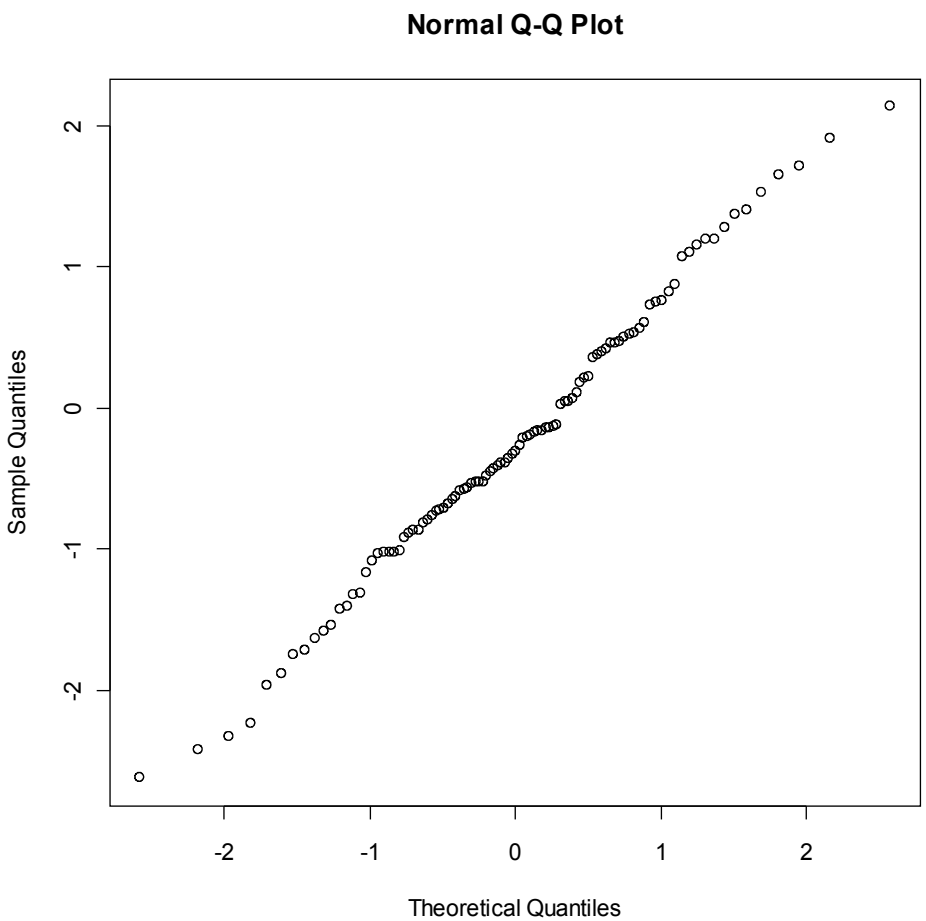
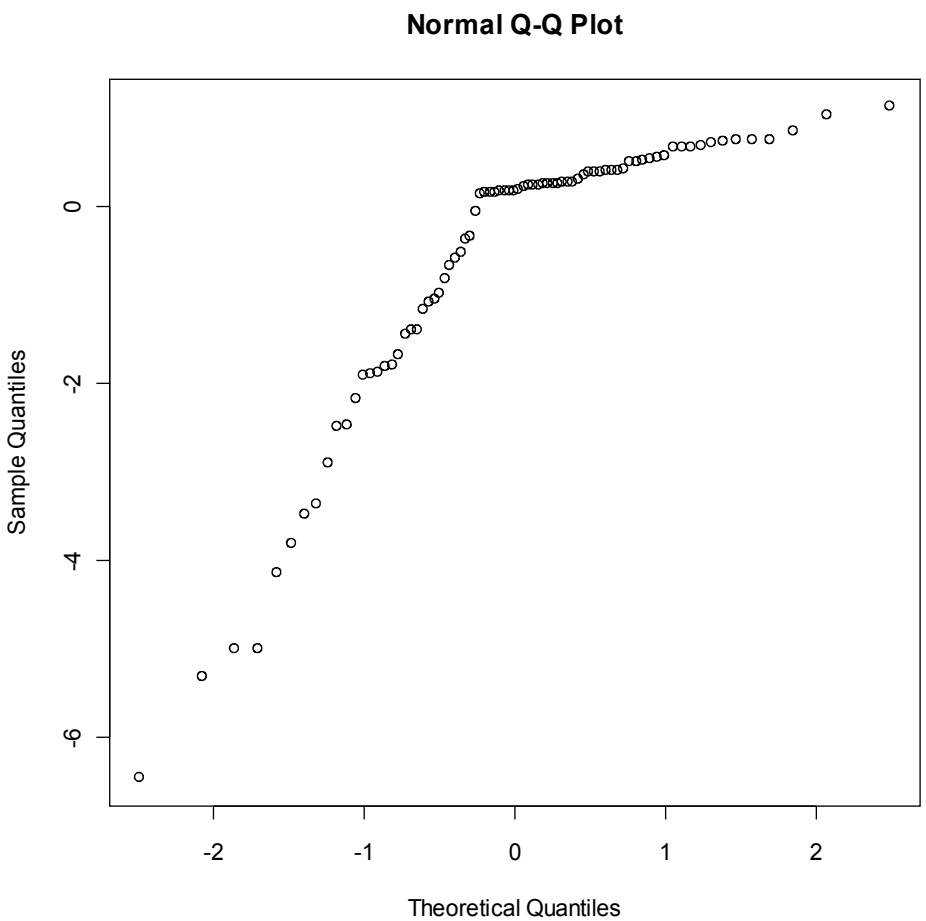
0.01
0.02
0.03
0.06
0.1
0.2
0.3
0.6
1
2
3
6
Nm = 1/8T ~ M/4

Isolation as null hypothesis



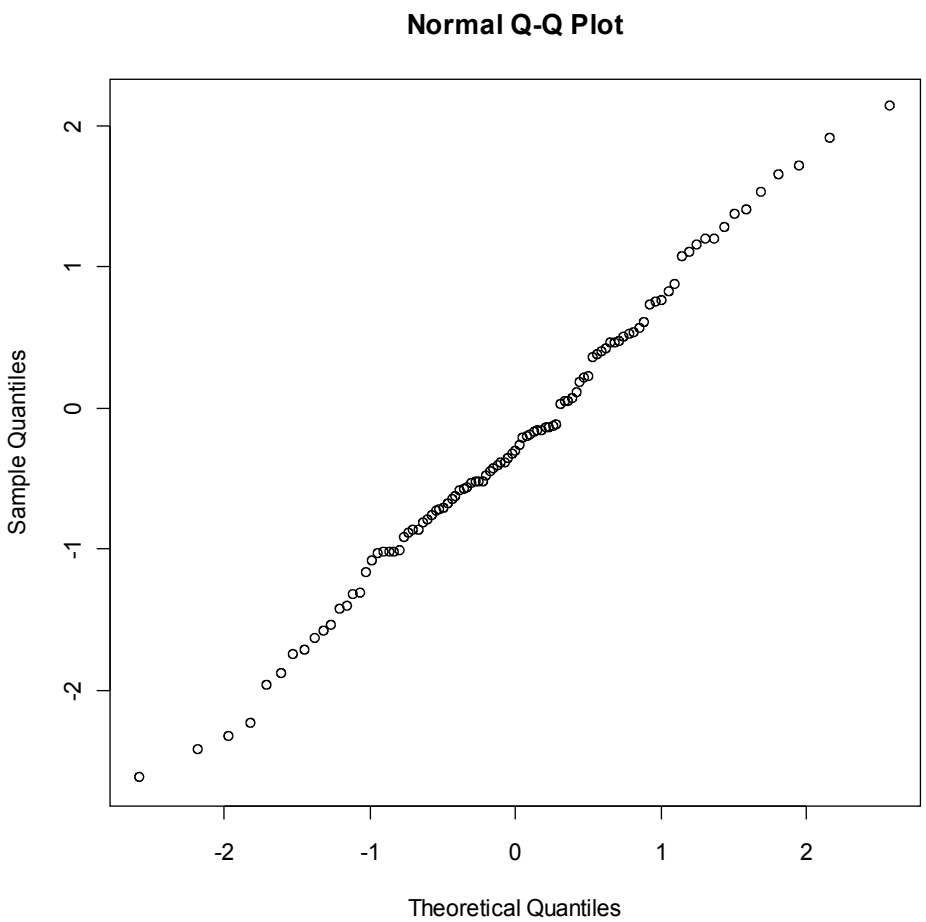


Isolation: T=12.5

Isolation: T=0.625

(T: time scaled to population size)

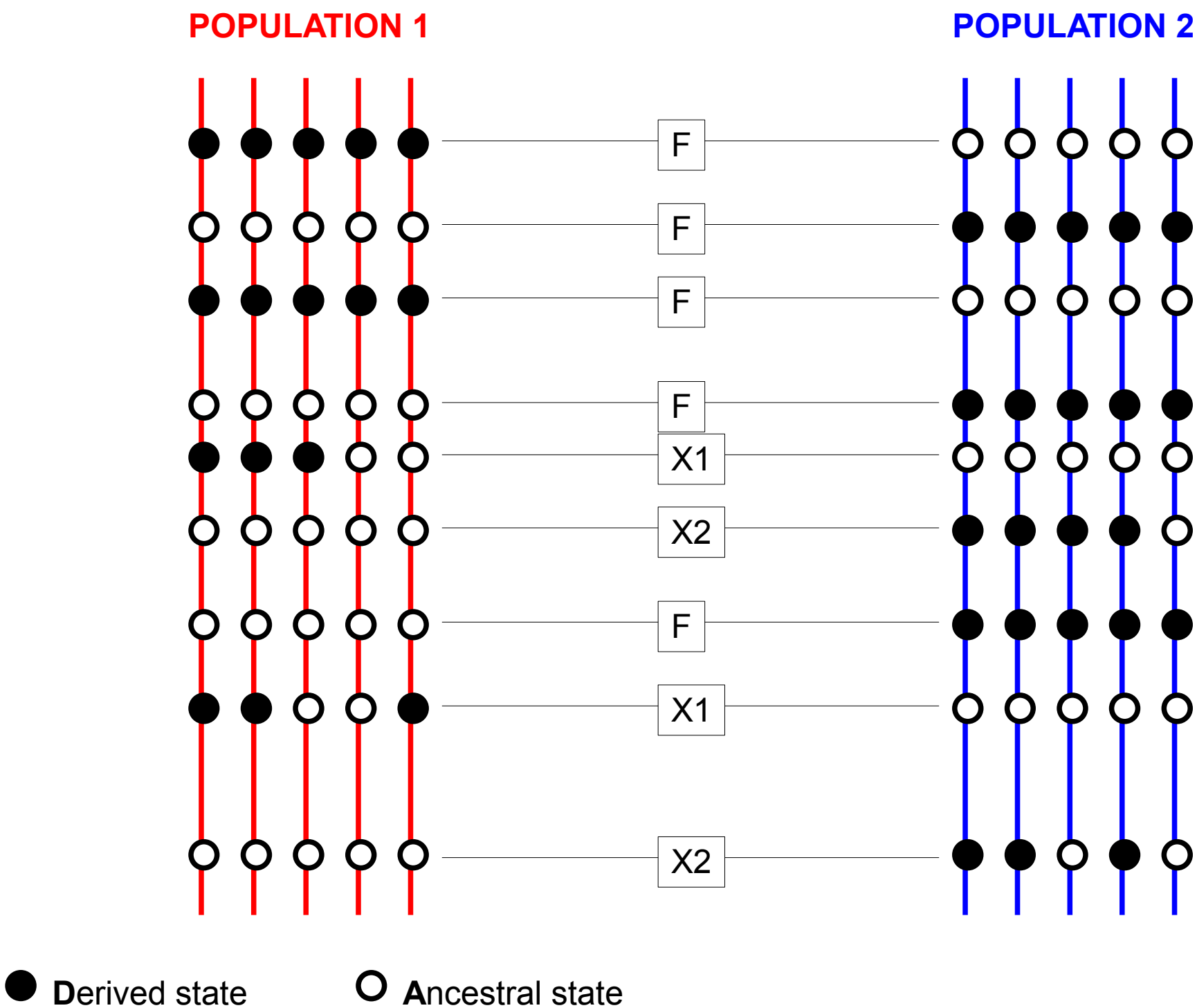
Test with several loci

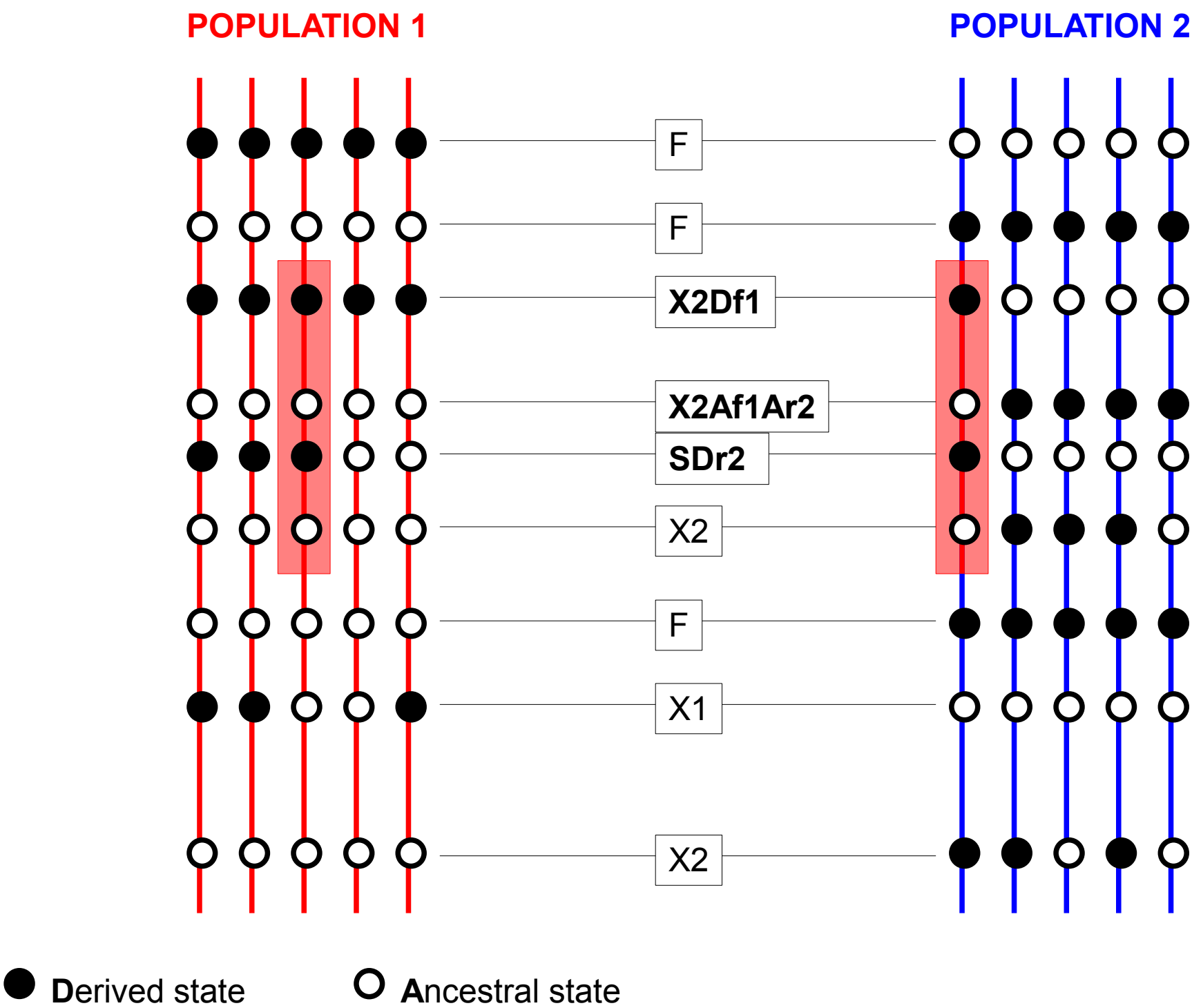


Kolmogorov–Smirnov test (on 10 loci)

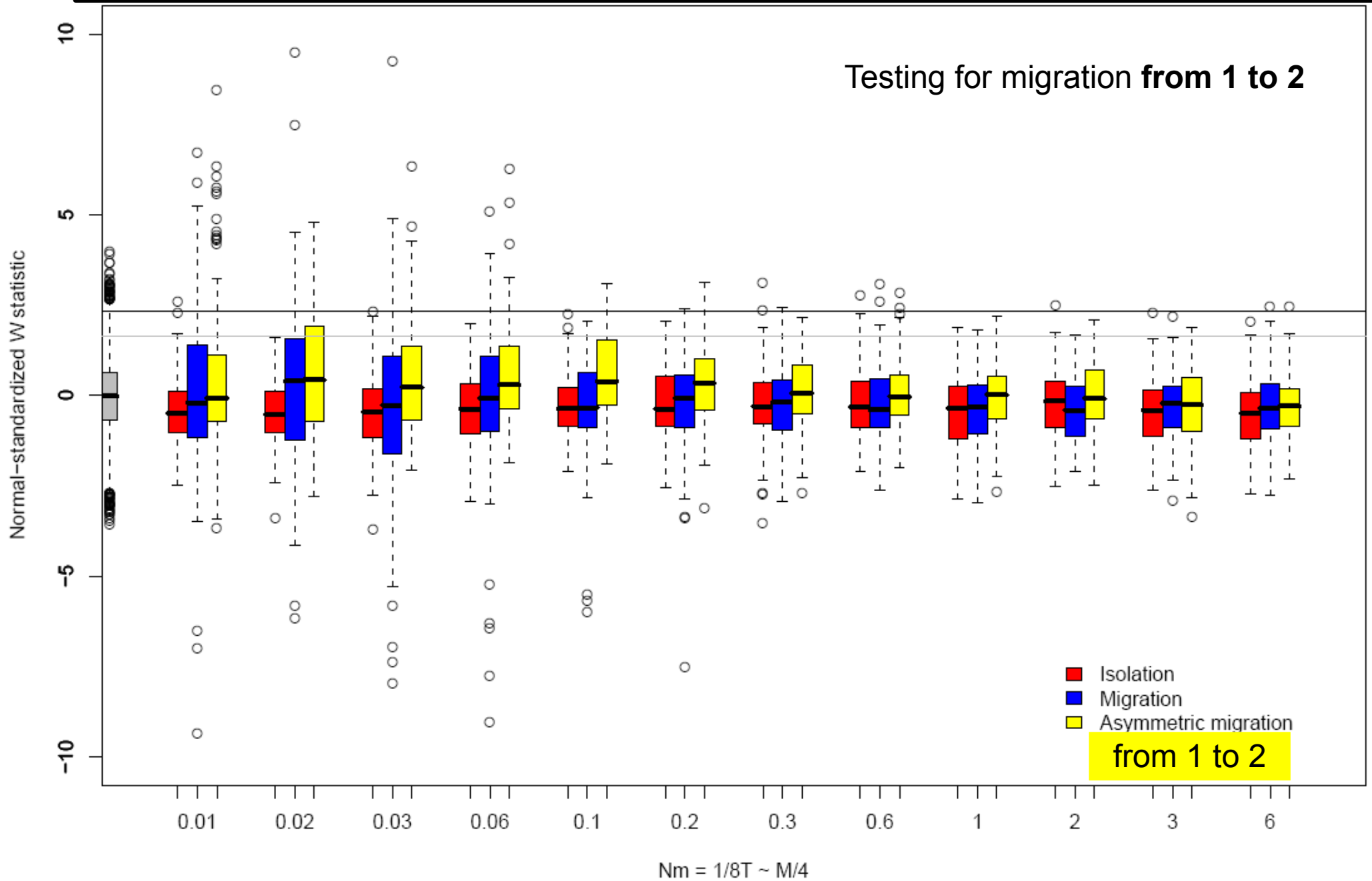
Isolation:	1/10
Migration:	9/10
Asymmetric mig.:	10/10

Asymmetric migration

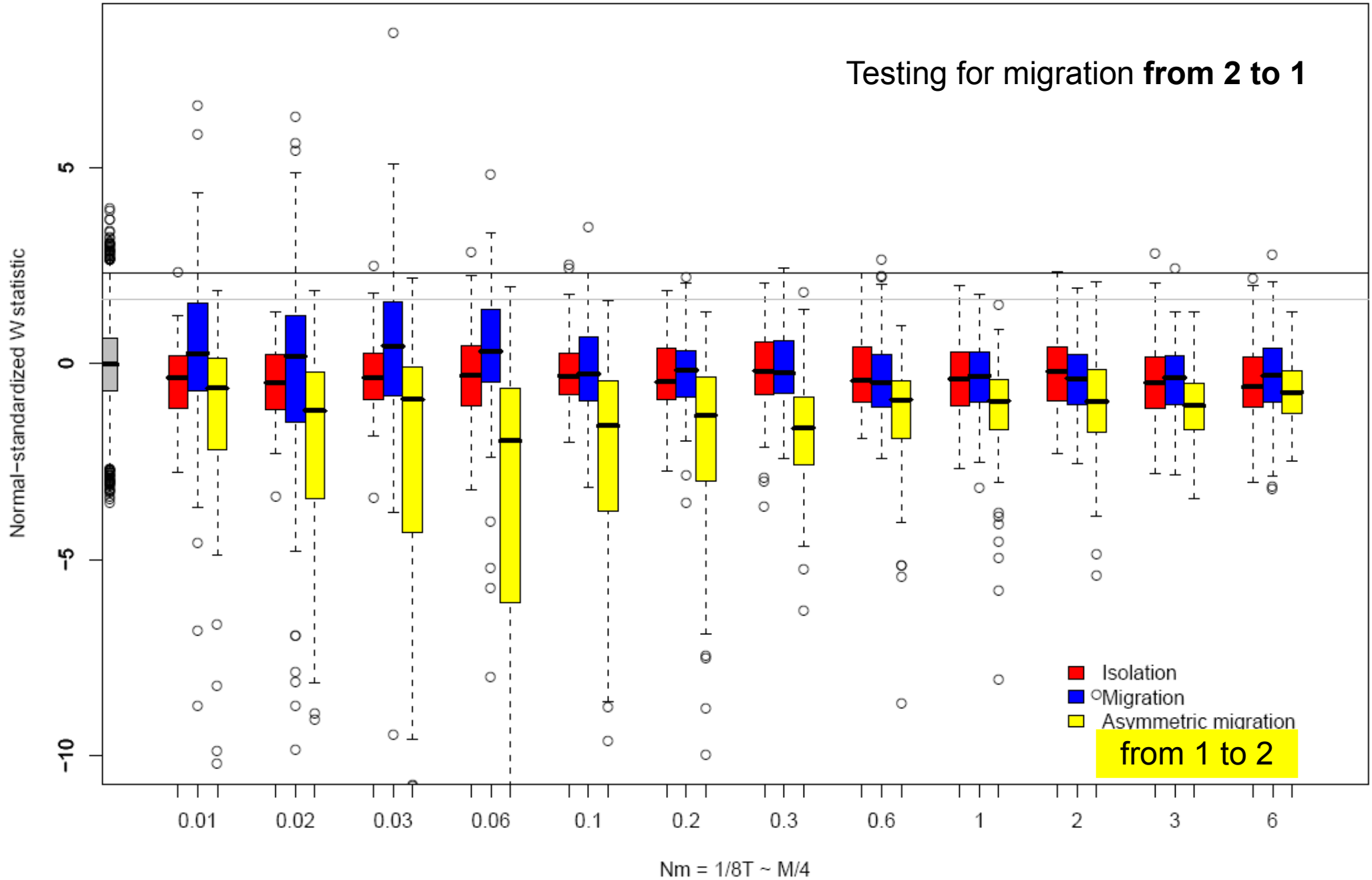

POPULATION 1
POPULATION 2
F
F
F
F
X1
X2
F
X1
X2
Derived state
Ancestral state


POPULATION 1
POPULATION 2
F
F
X2Df1
X2Af1Ar2
SDr2
X2
F
X1
X2
Derived state
Ancestral state

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

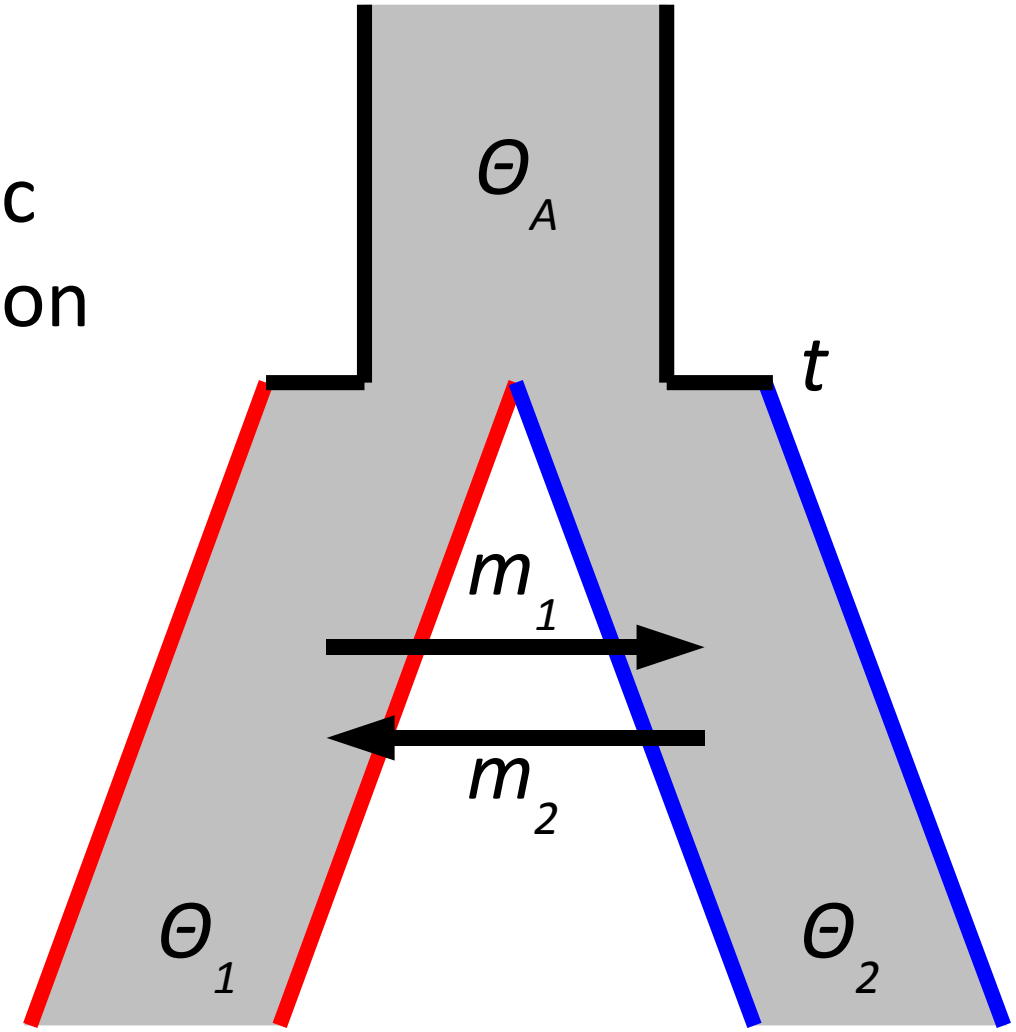


SDr1+X1Df2+X1Af2Ar1 vs. SDr2+X2Df1+X2Af1Ar1



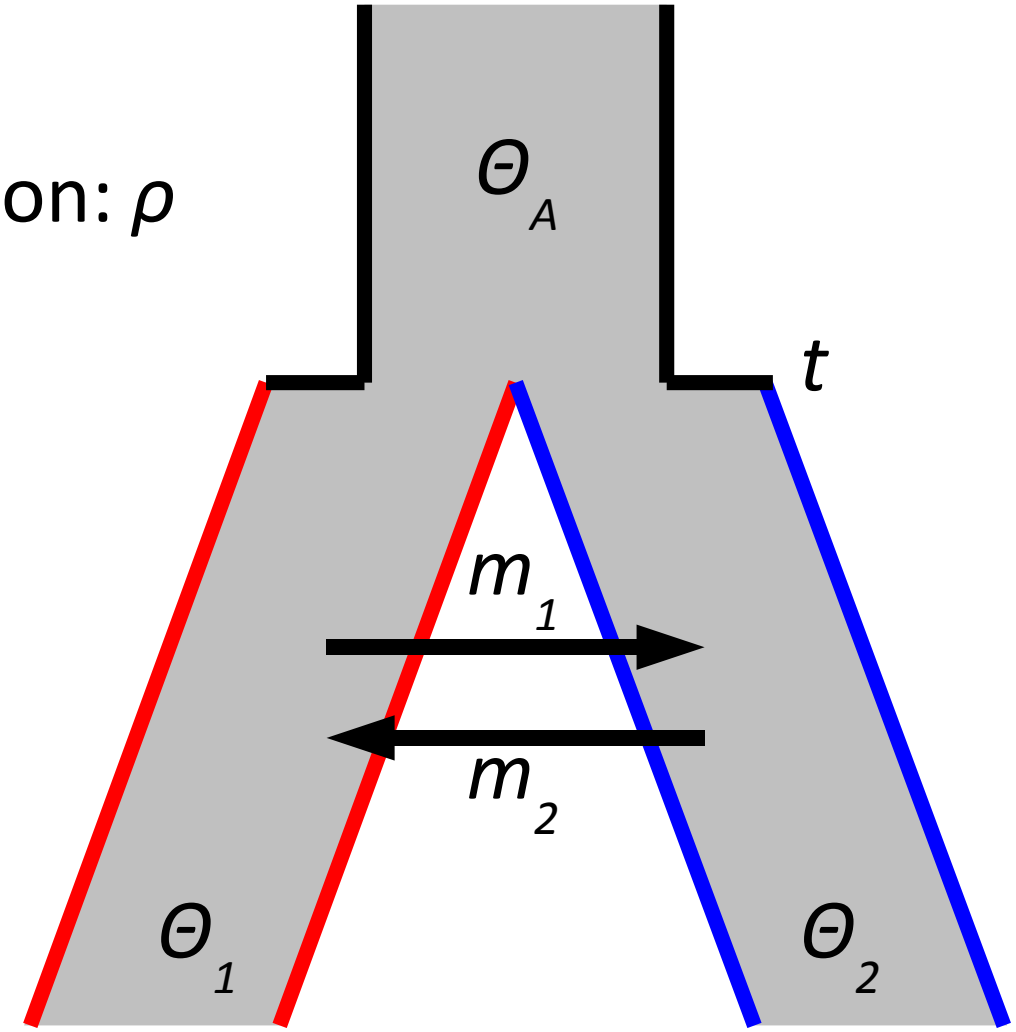
Likelihood Coalescent MCMC
(Nielsen & Wakeley 2001, Hey & Nielsen 2004)

no intragenic recombination



Summary Statistics Coalescent MCMC
(Becquet & Przeworski 2007)

recombination: ρ

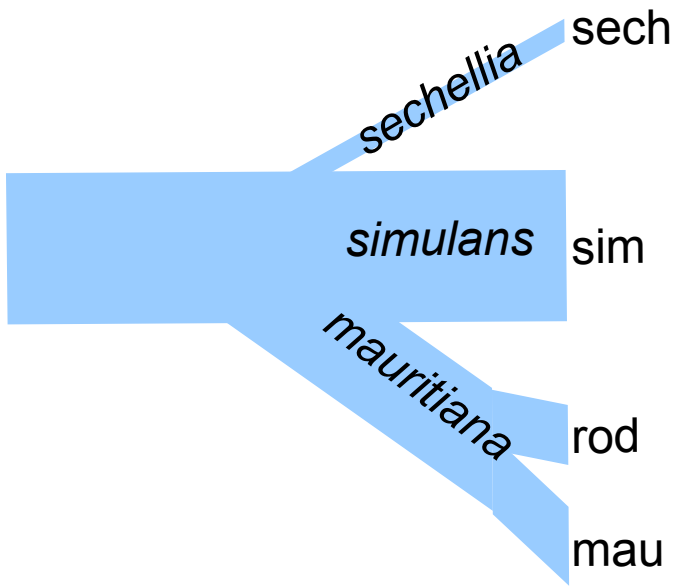


Summary

- 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, mauritiania

Marie-Louise Cariou and team



amyrel
joc
notch
obp
otu
period
vermilion
white

AGENCE NATIONALE DE LA RECHERCHE ANR Biodiversité: TRANSBIODIV

Arabidopsis: Xavier Vekemans and team

Oaks: Antoine Kremer and team

Millet: Thierry Robert and team

Mice: Pierre Boursot and team