Analysis of population genetic data:

Identifying populations or stocks

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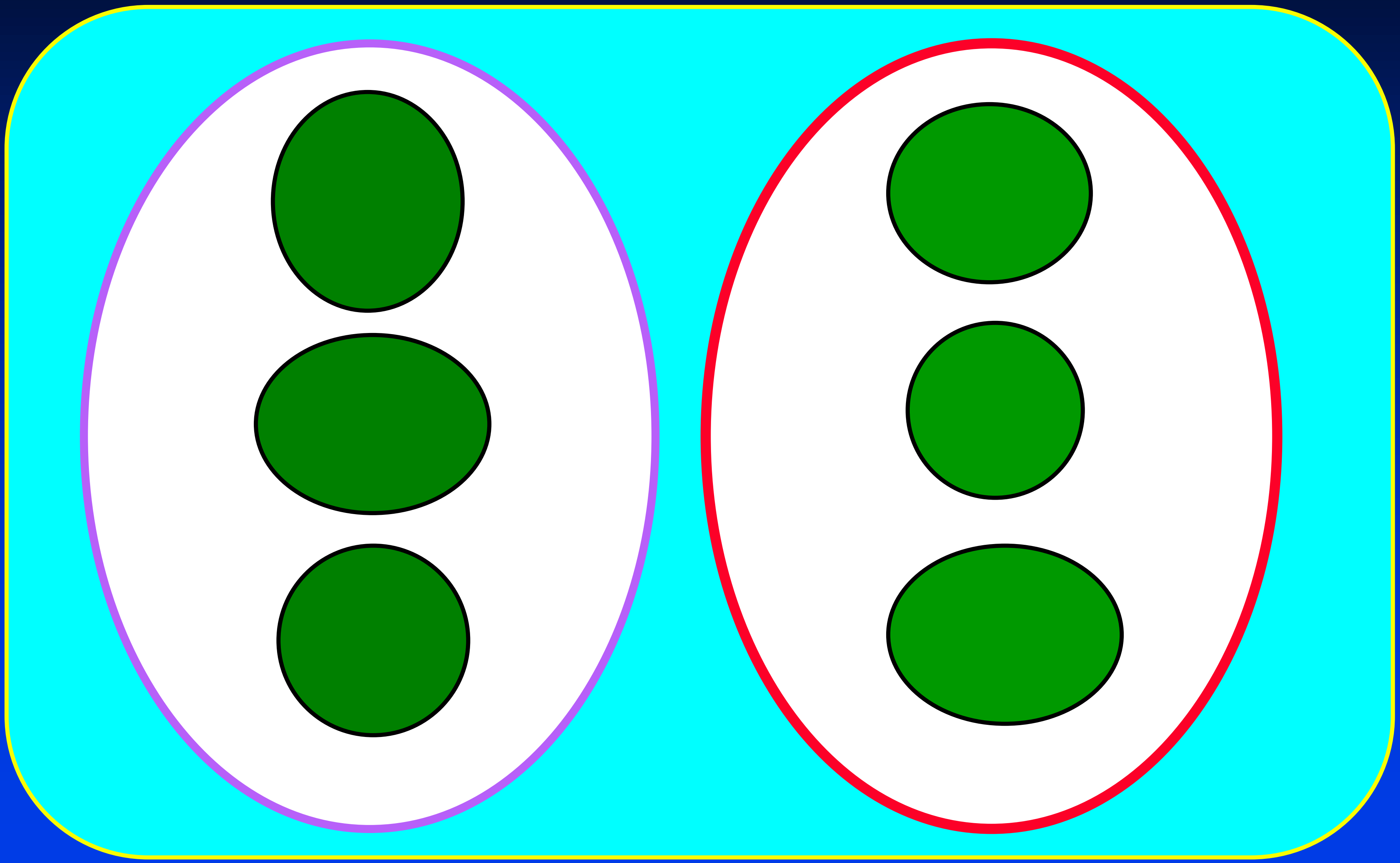
How many ‘populations’ or ‘stocks’?



Two population concepts:

(Andrewartha & Birch 1984; Waples & Gaggioti 2006)

Ecological paradigm

A group of individuals that co-occur in space and time and have an opportunity to interact

(cohesive forces are demographic)

Evolutionary paradigm

A group of interbreeding individuals that exist together in time and space

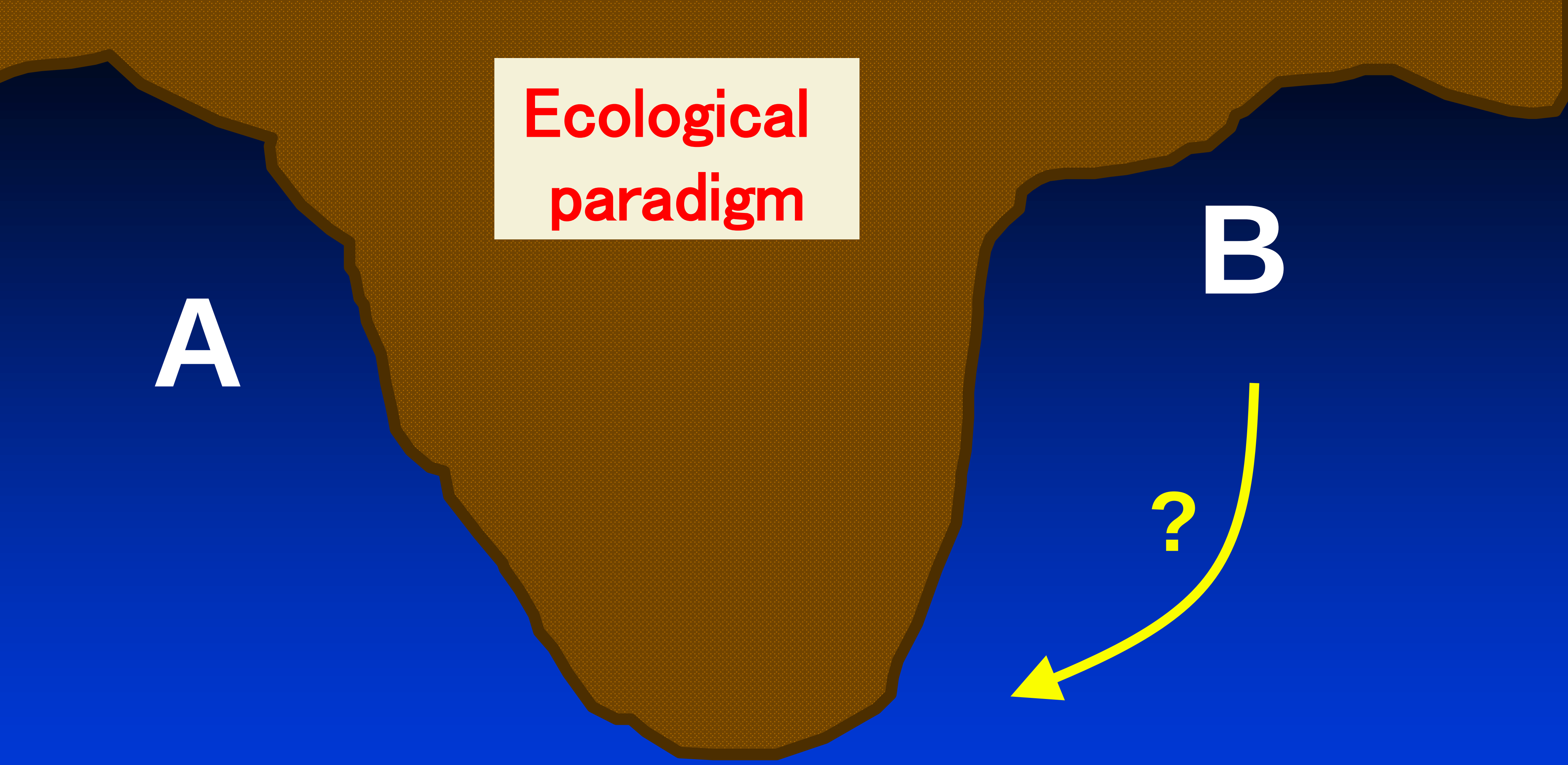
(cohesive forces are genetic)

Matching the population concept with management objectives

We want to minimize impacts on “weak” stocks, because

- Locally depleted stocks take a long time to rebuild (Ecological paradigm)
- Local extirpation might represent an irreversible loss of biodiversity (Evolutionary paradigm)

Ecological paradigm



If we overharvest area A, will it be replenished by immigration from B?

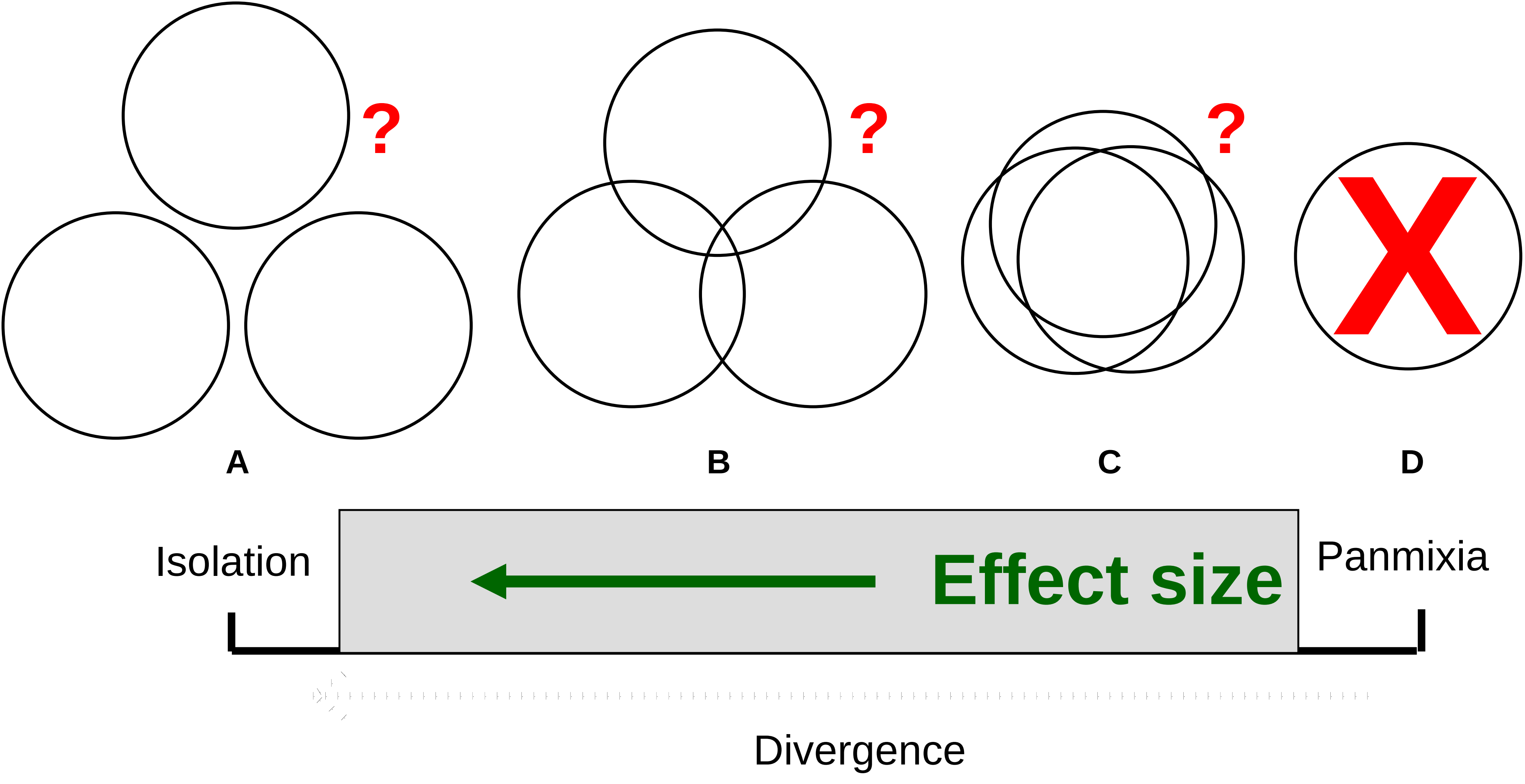
Ecological paradigm

Demographic independence—population dynamics driven more by local births and deaths than by immigration

Key metric is migration rate (*m*) = fraction of individuals that are migrants

Threshhold for demographic independence poorly studied, but thought to be ~ 0.1

A significant test rejects only one extreme of the population continuum



$$F_{ST} = \frac{\mathrm{var}(P)}{\bar{P}(1-\bar{P})}$$

$$\mathrm{range}\,(F_{ST}) = [0,1]$$

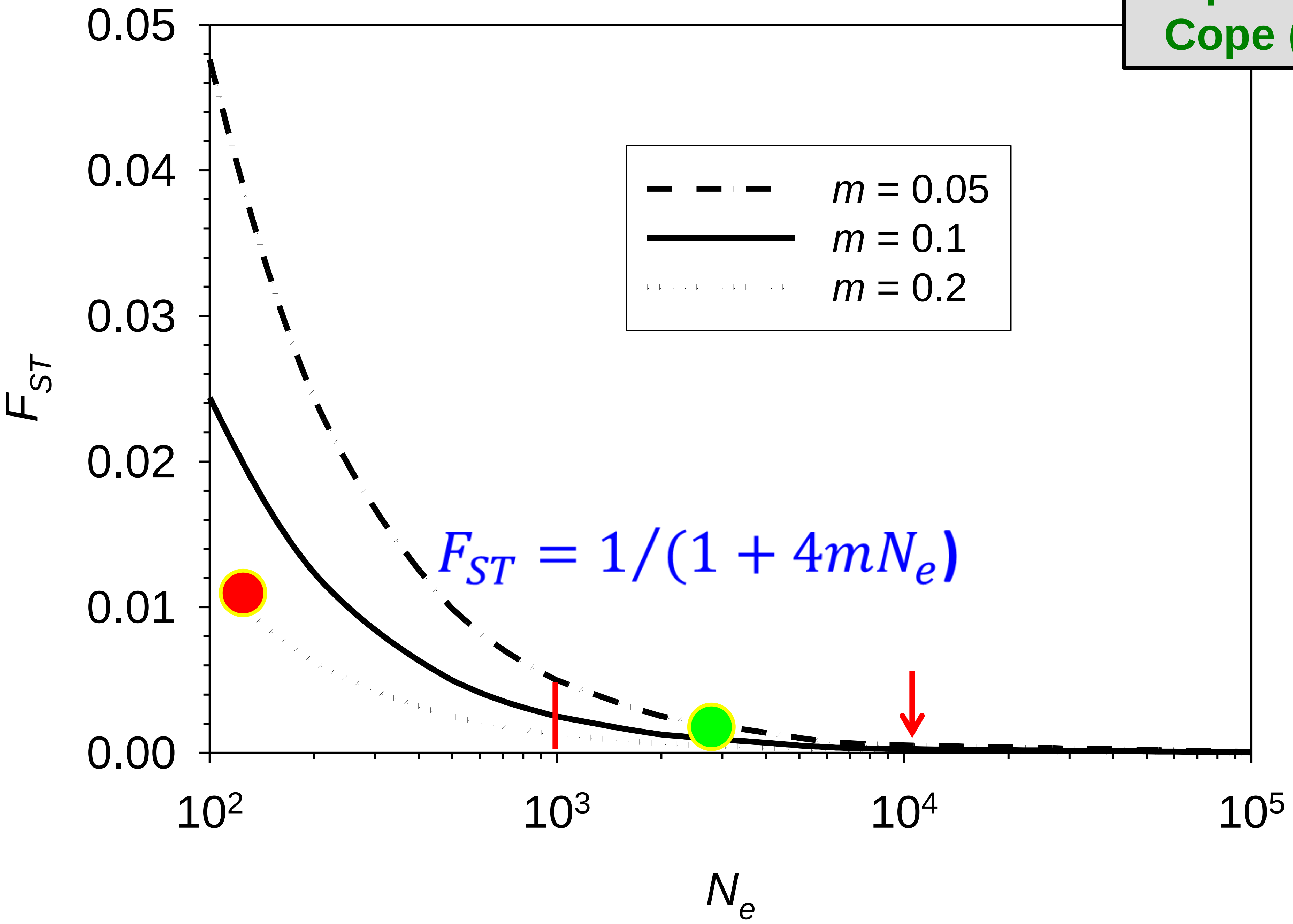
$$E(F_{ST}) \approx \frac{1}{1 + 4mN_e}$$

Genetic marks: *Ecological paradigm*

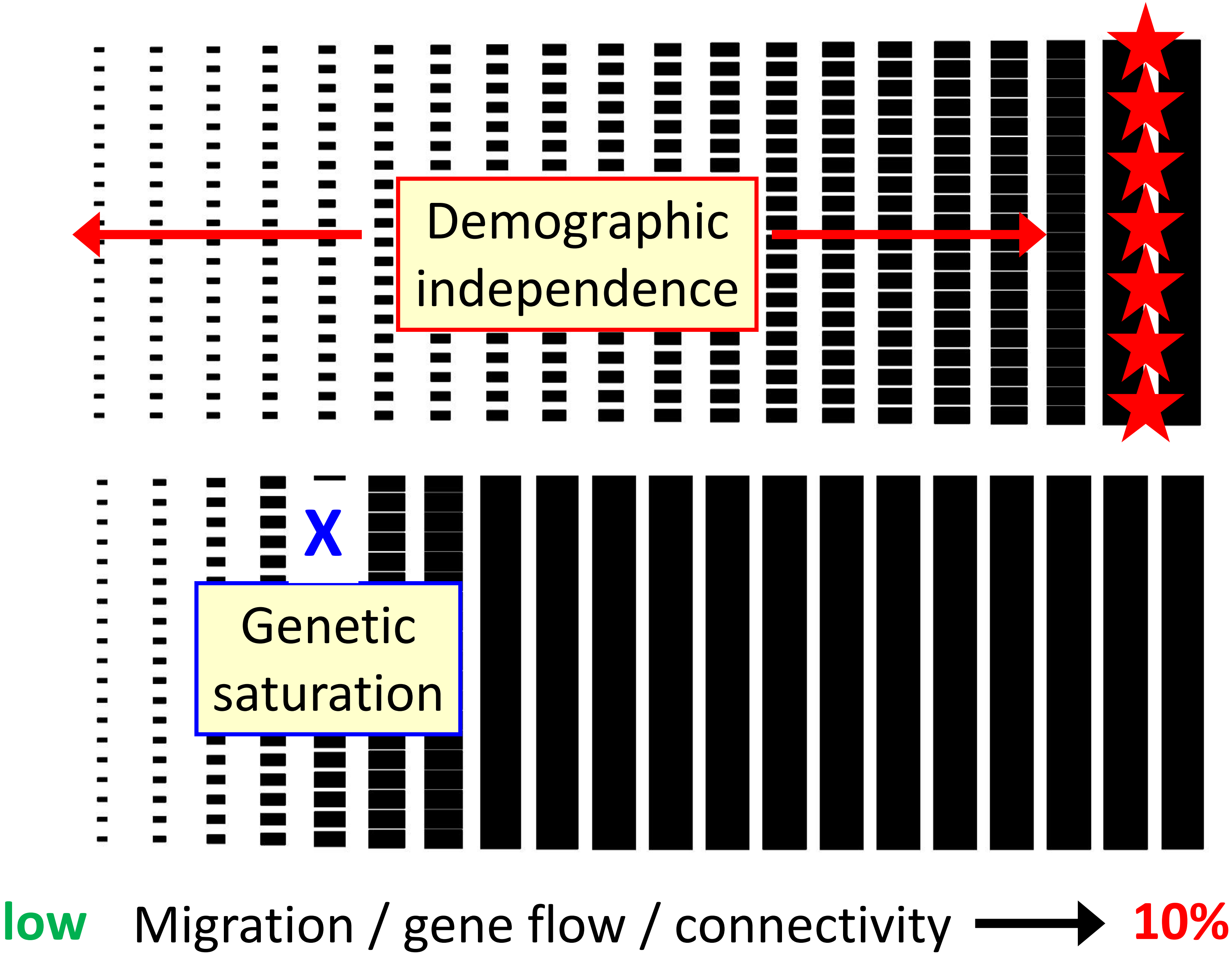
Fundamental problems:

1. Genetic indices yield information about mN_e but need information about m
2. Transition to demographic independence occurs in region of high gene flow (m ~ 10%) where genetic methods have little power
3. When genetic signal is weak, small artifacts can be mistaken for a signal
4. Above model assumes migration-drift equilibrium

Waples, Punt, Cope (2008)



$$F_{ST} = 1/(1 + 4mN_e)$$



Demographic independence

X

Genetic saturation

low Migration / gene flow / connectivity → 10%

Possible genetic artifacts

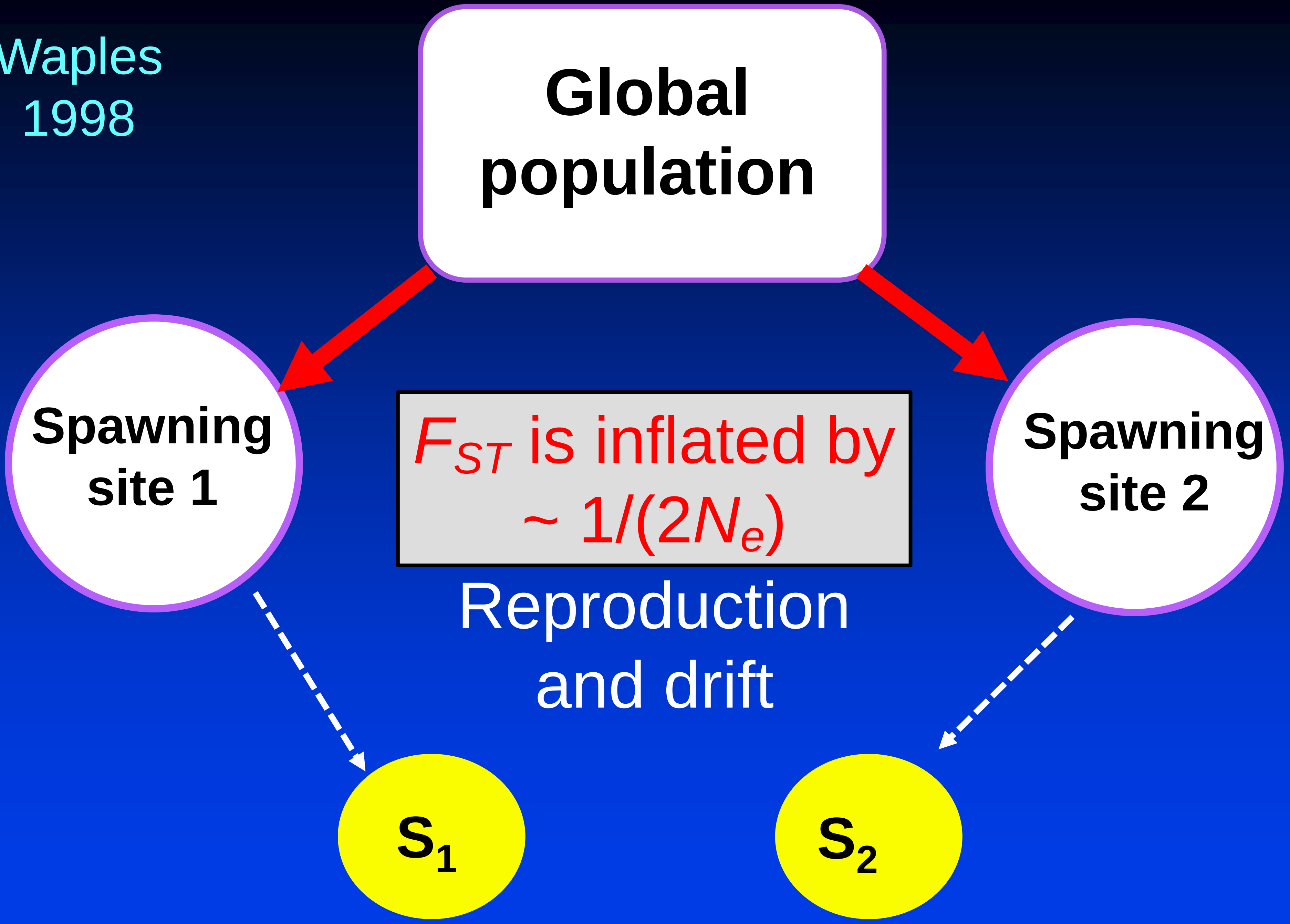
Genotyping errors

Non-random sampling

Recruitment variability

Chaotic patchiness

Waples
1998



Global population

Spawning site 1

Spawning site 2

F_{ST} is inflated by ~ $1/(2N_e)$

Reproduction and drift

S_1

S_2

Some strategies for dealing with high gene flow species (Waples 1998)

Clarify objectives and research questions

Get more data (individuals, samples, loci)

Careful attention to sampling protocols

  Departures from randomness

  Understand life history

  Temporal replication

Go beyond statistical tests

Combine information from different methods

Summary

Relatively high F_{ST} (> 0.01) generally implies separate stocks unless:

- N_e is very small
- Artifacts and/or chaotic patchiness

Relatively low F_{ST} (<< 0.01) is often inconclusive without additional information