Integrating population dynamics and genetics in macroevolutionary diversification models
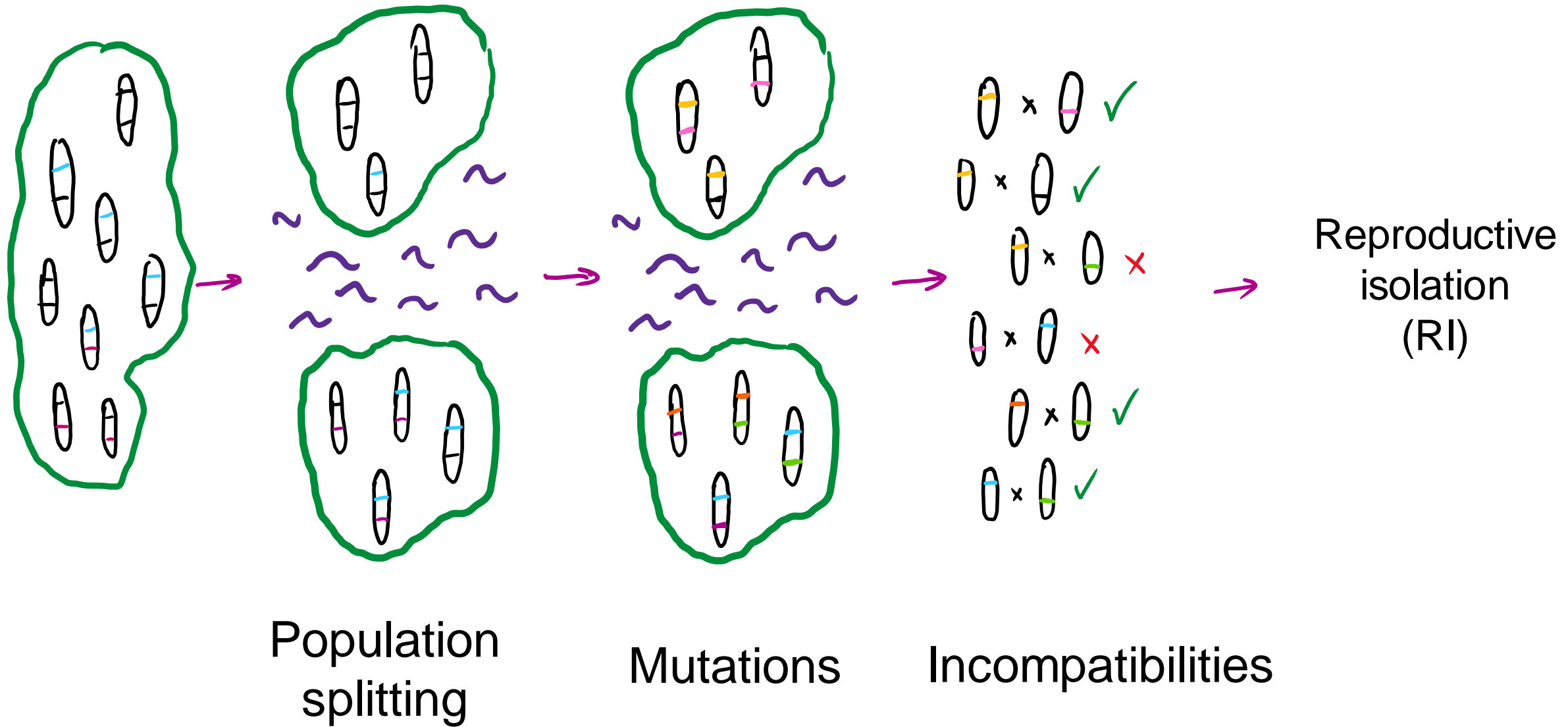
Pierre Veron
PhD student at École Normale Supérieure and IDEEV
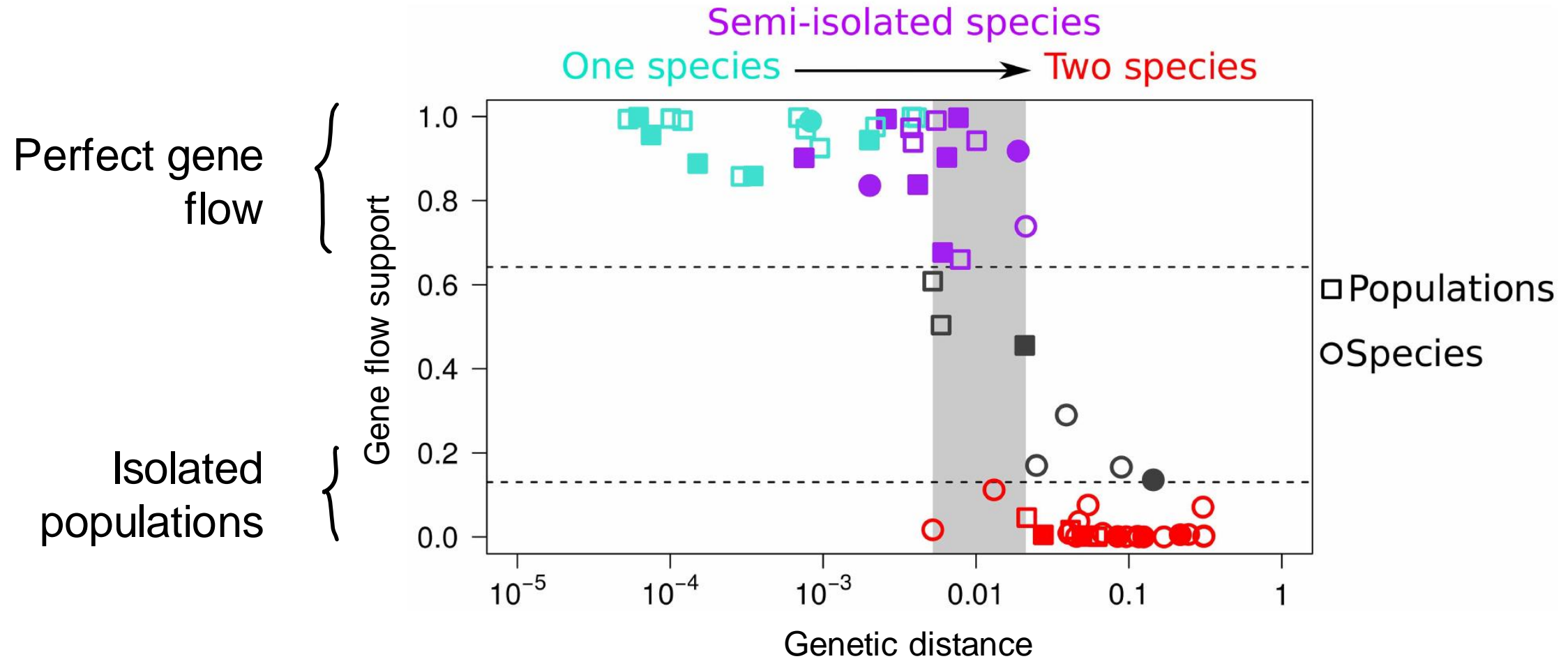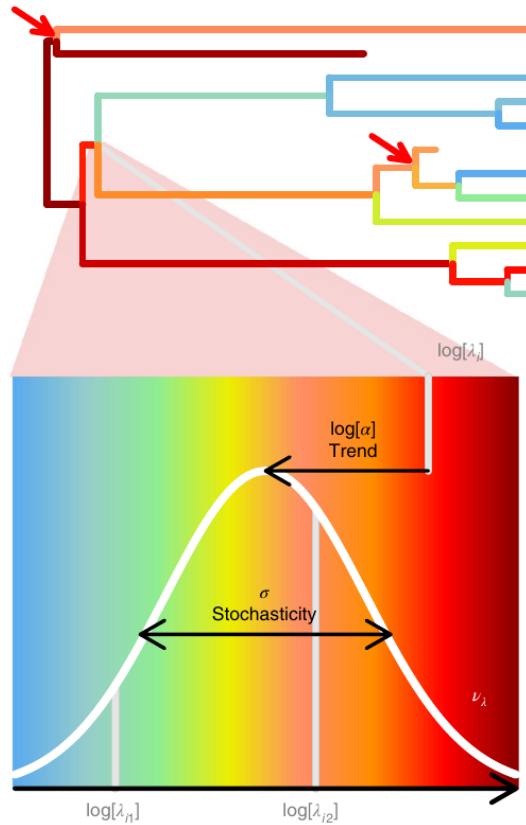
pveron@bio.ens.psl.eu

How does speciation occur?

Population splitting

Mutations

Incompatibilities

Reproductive isolation (RI)

How does speciation occur?

C. Roux et al., *PLOS Biology*. **14**, e2000234 (2016).
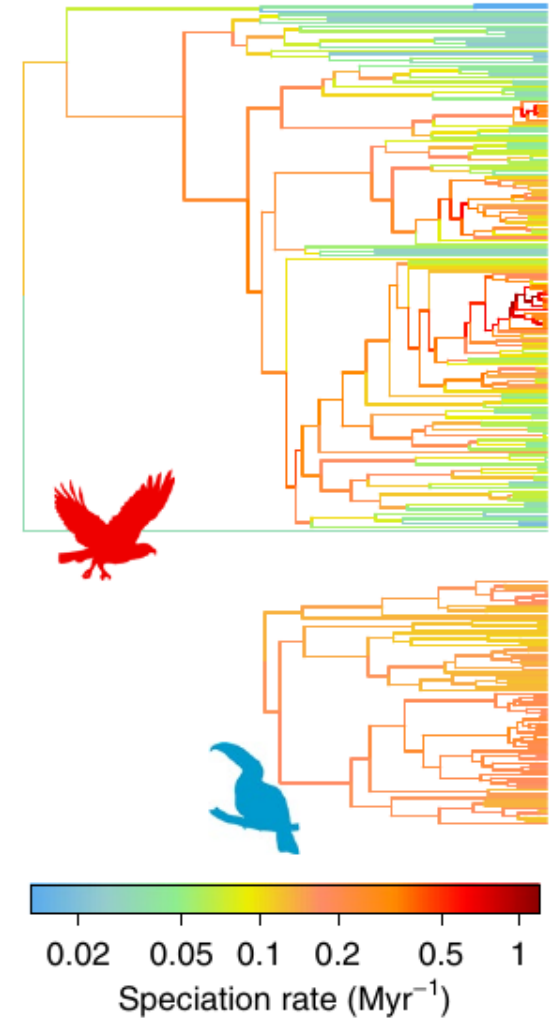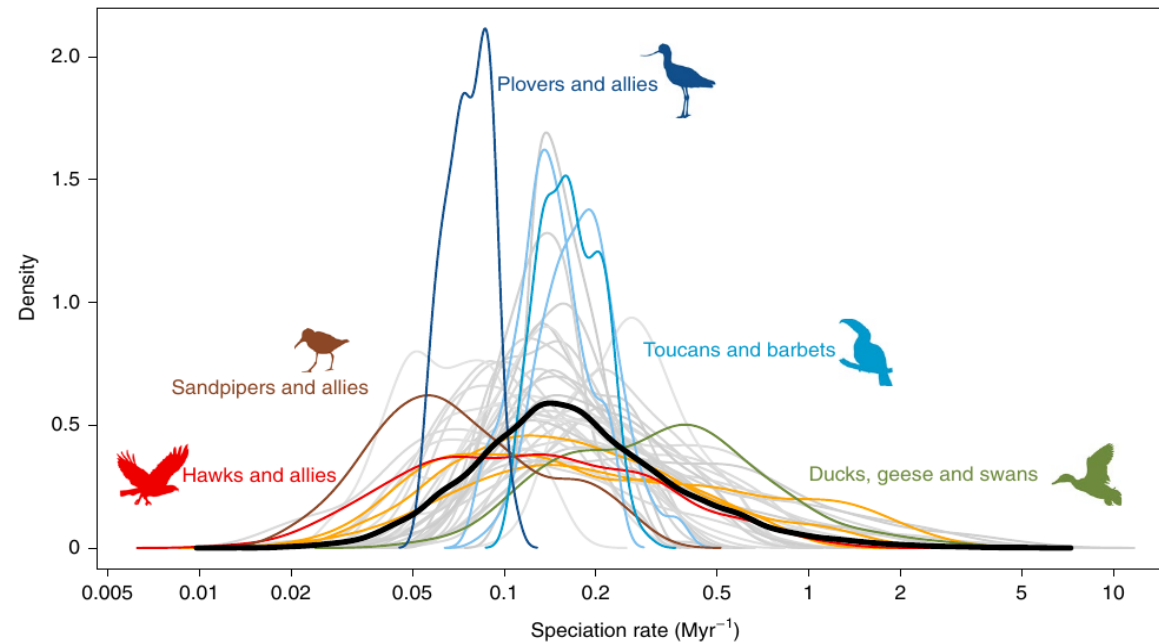
How can we measure speciation rates?

(1) Diversification model with varying rates of speciation
Example ClaDS

(2) Infering the parameters of the model on a true phylogeny

O. Maliet, F. Hartig, H. Morlon, *Nature Ecology & Evolution*. **3**, 1086–1092 (2019).

Speciation rates vary by several orders of magnitude

We know speciation occurs by reproductive isolation

We should find a link between speciation rates and the speed of reproductive isolation

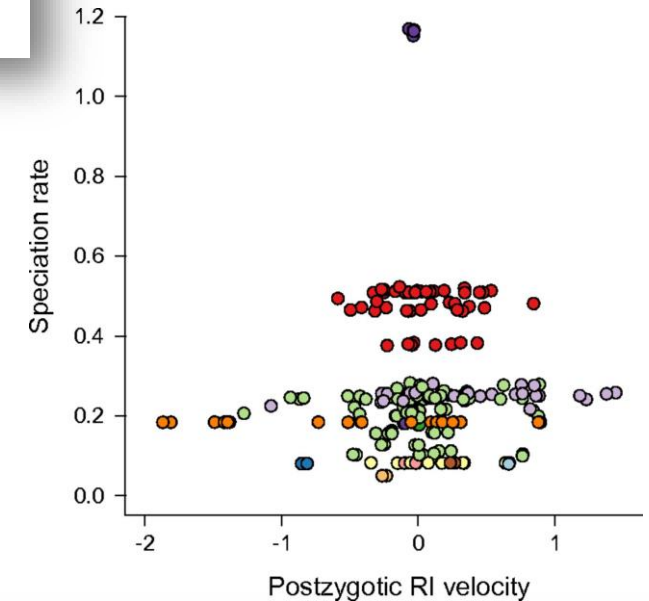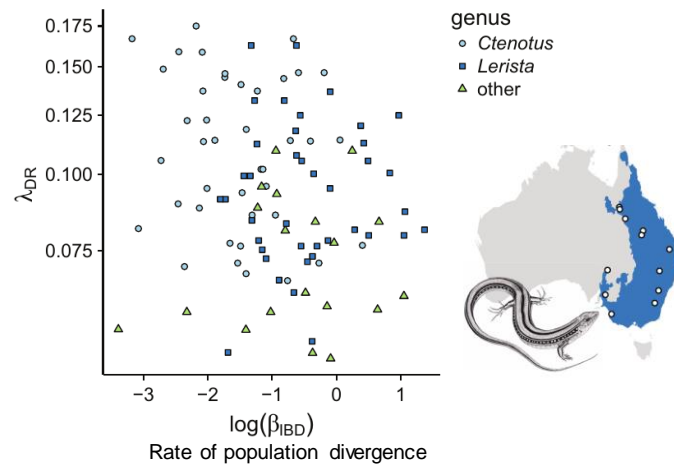# No apparent link between speciation rate and RI

Does Population Structure Predict the Rate of Speciation? A Comparative Test across Australia's Most Diverse Vertebrate Radiation

Sonal Singhal,[1,2,*] Huateng Huang,[1,3] Maggie R. Grundler,[1] María R. Marchán-Rivadeneira,[4]
Iris Holmes,[1] Pascal O. Title,[1] Stephen C. Donnellan,[5] and Daniel L. Rabosky[1]

Daniel L. Rabosky[a,1] and Daniel R. Matute[b]

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Edited by David B. Wake, University of California, Berkeley, CA, and approved August 6, 2013 (received for review March 22, 2013)

# No apparent link between speciation rate and RI

We understand much about the genetic basis for reproductive isolation, which plays a critical role in maintaining species diversity. However, until we understand the relative contribution of reproductive isolation (and other factors) to taxonomic speciation rates, we cannot claim to have answered the most basic questions about the diversity of life that surrounds us.
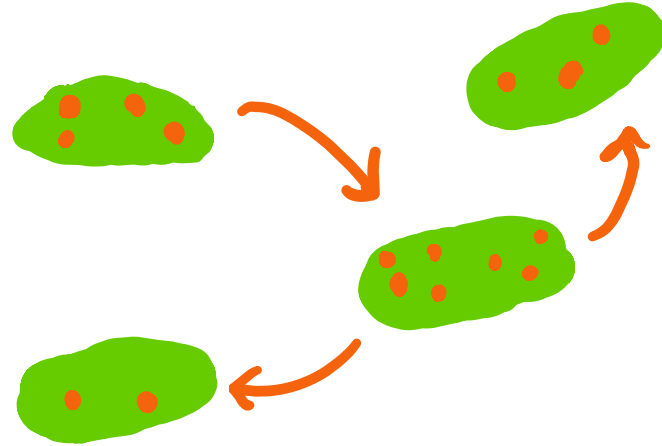
D. Rabosky, 2016, Biol. J. Linn. Soc.

- Demography,
- population structure,
- external splitting events,
- population extinction

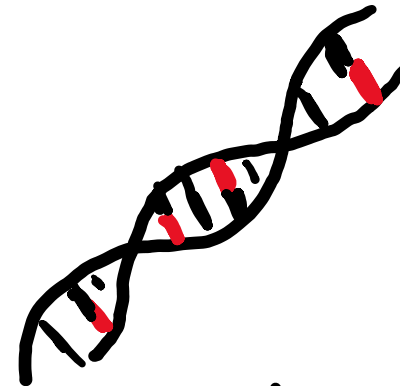may be more limiting than RI in the speciation rate
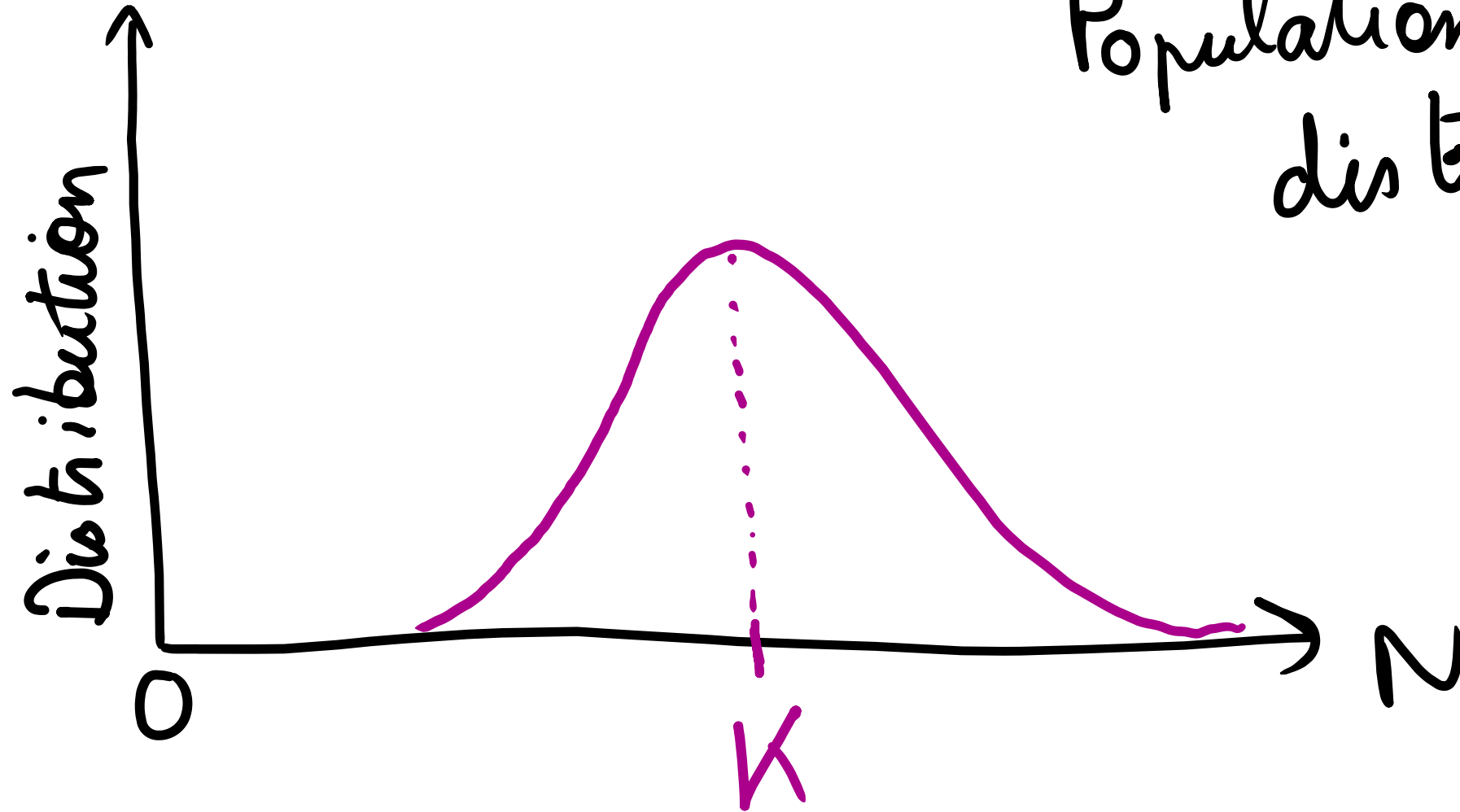
Building an explicit model of speciation
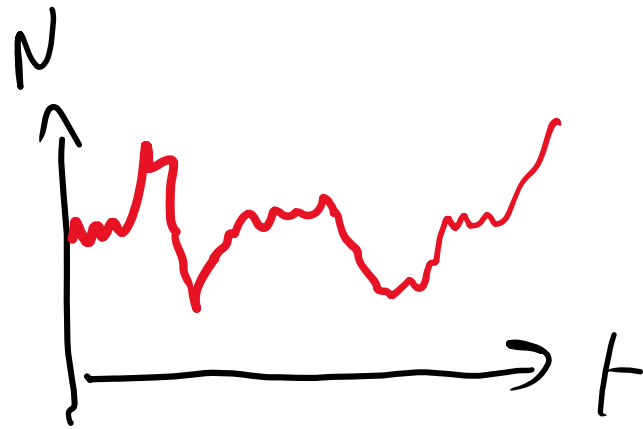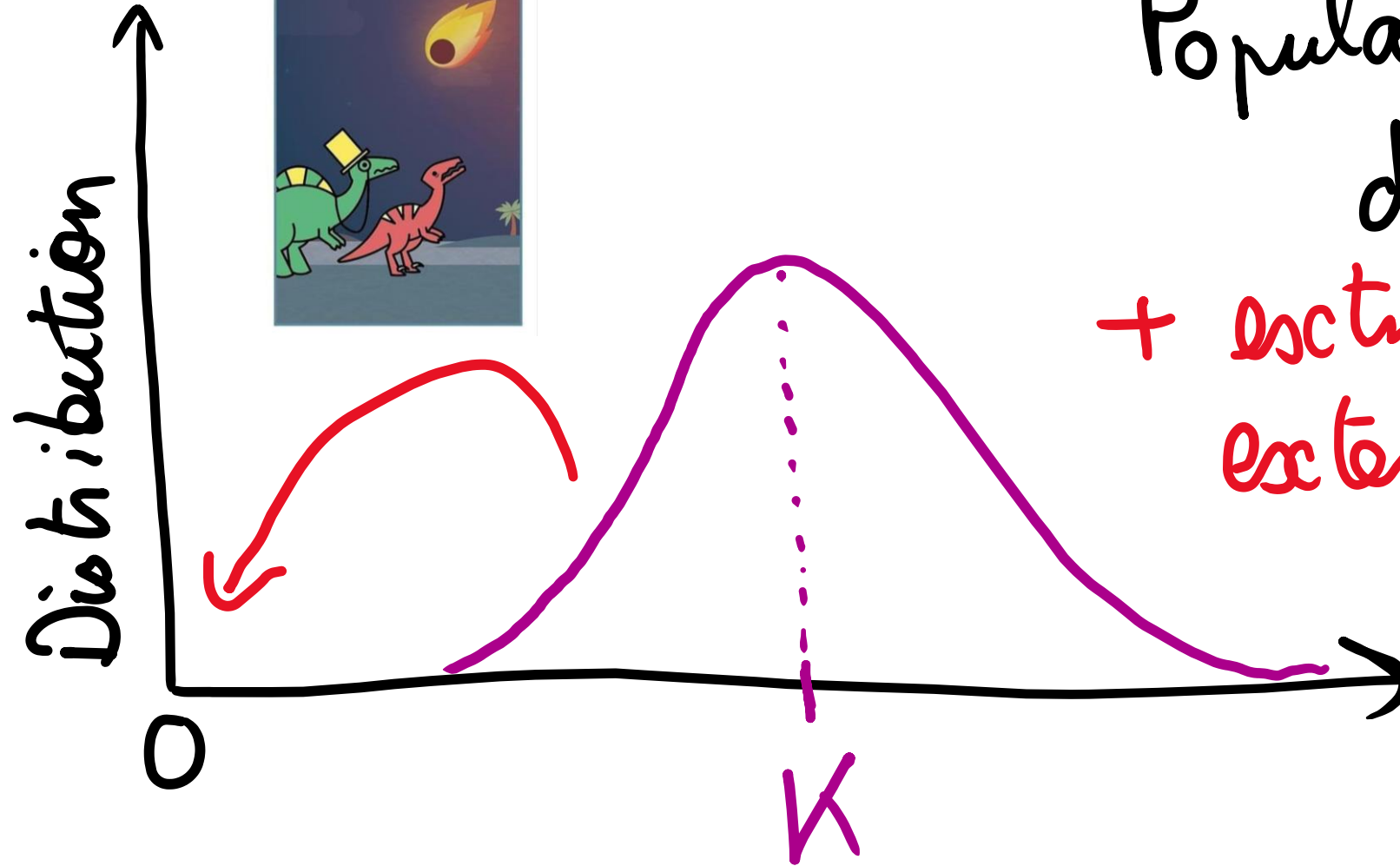
Populations

Demography

Genetic divergence

Clustering

Demography

Population normally distributed
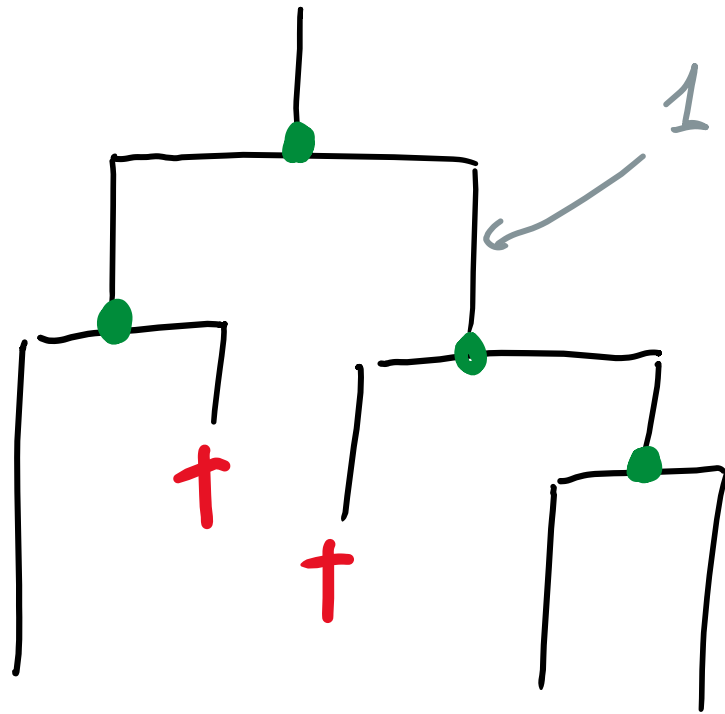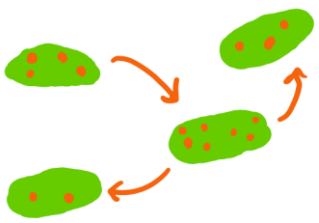
Demography

Distribution (y-axis)

N (x-axis)

O

K

Population normally distributed

+ extinction by external factor at rate μ_{ext}

1 population

• splitting event : rate b_{init}

✝ extinction event : rate μ_{ext}
   or by demographic fluctuations

Genetics

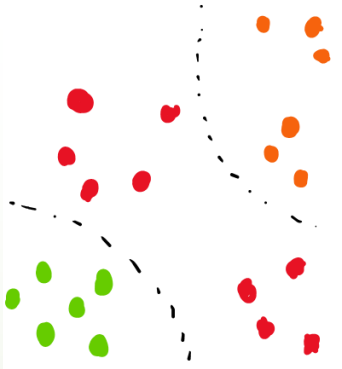substitution $\Big\{$ mutation rate $\quad m$

$\hspace{4cm} \longrightarrow$ mutation fixation time
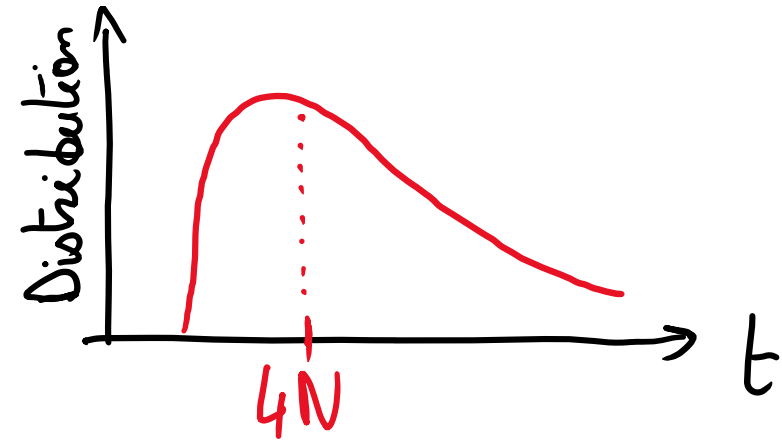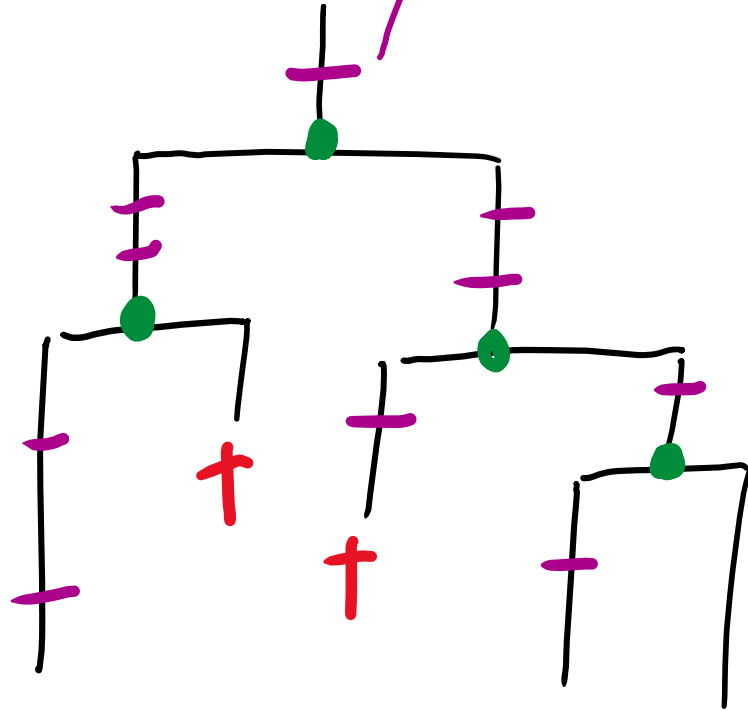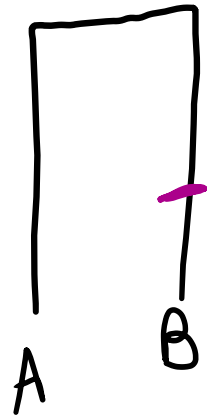

Kimura, *Genet. Res.* **15**, 131-133 (1970).

Species clustering

Threshold model   +   Transitive closure

A × B ✗
A × C ✓   *clustering* →
B × C ✓
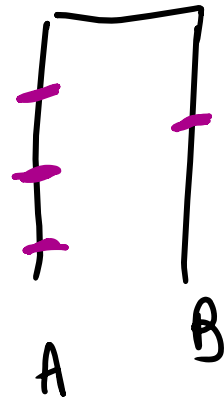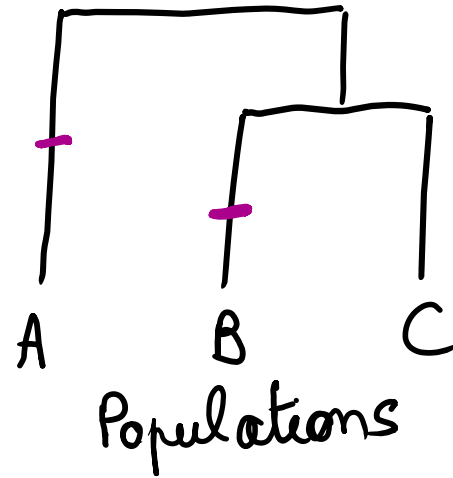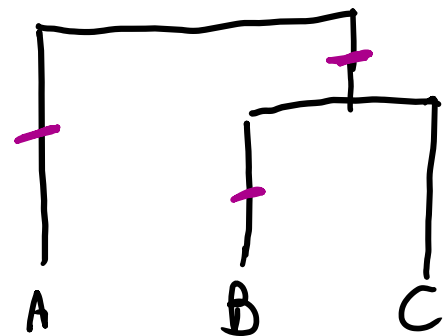
A · B - C
Species

A × B ✗
A × C ✗   *clustering* →
B × C ✓

Populations

A × B   ✓
A × B   ✗

A   B   C

A - B-C
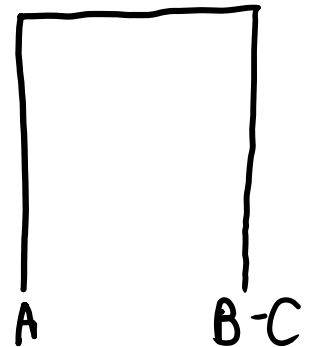
Predicting the macroevolutionary rates

Protracted birth-death model (PBD)

1 lineage

+ extinction rate μ_{PBD}

● initiation rate λ_1

● completion rate λ_2

✓ Simpler model

✓ Mean time for speciation already known

Predicting the macroevolutionary rates

Protracted birth-death model (PBD)
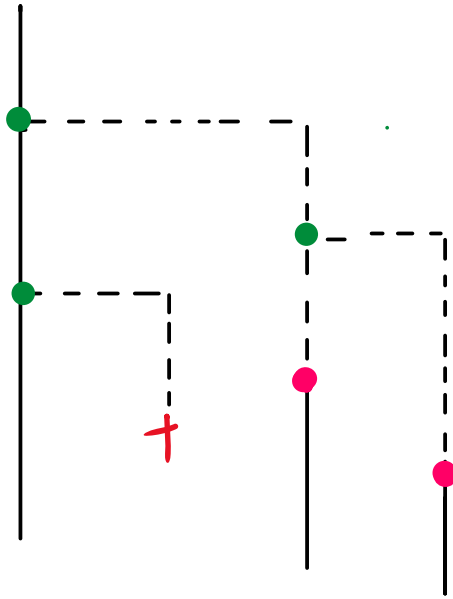
| lineage

+ extinction rate μ_{PBD}

● initiation rate λ_1

● completion rate λ_2

JOURNAL ARTICLE

Prolonging the Past Counteracts the Pull of the Present: Protracted Speciation Can Explain Observed Slowdowns in Diversification 🔓
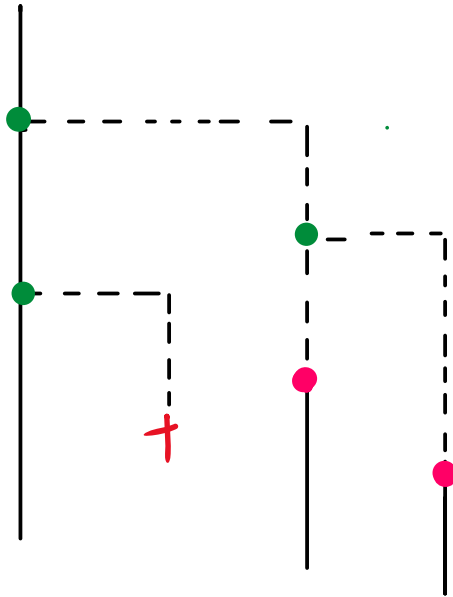
Rampal S. Etienne ✉, James Rosindell   Author Notes

Systematic Biology, Volume 61, Issue 2, March 2012, Page 204, https://doi.org/10.1093 /sysbio/syr091

Published: 01 March 2012   **Article history** ▾

① Deriving $\mu_{PBD}, \lambda_1, \lambda_2$
as functions of the model
parameter
② Predicting the expected
speciation and extinction rates

✓ Simpler model

✓ Mean time for speciation already known

15

Influence of the parameters on the diversification rates
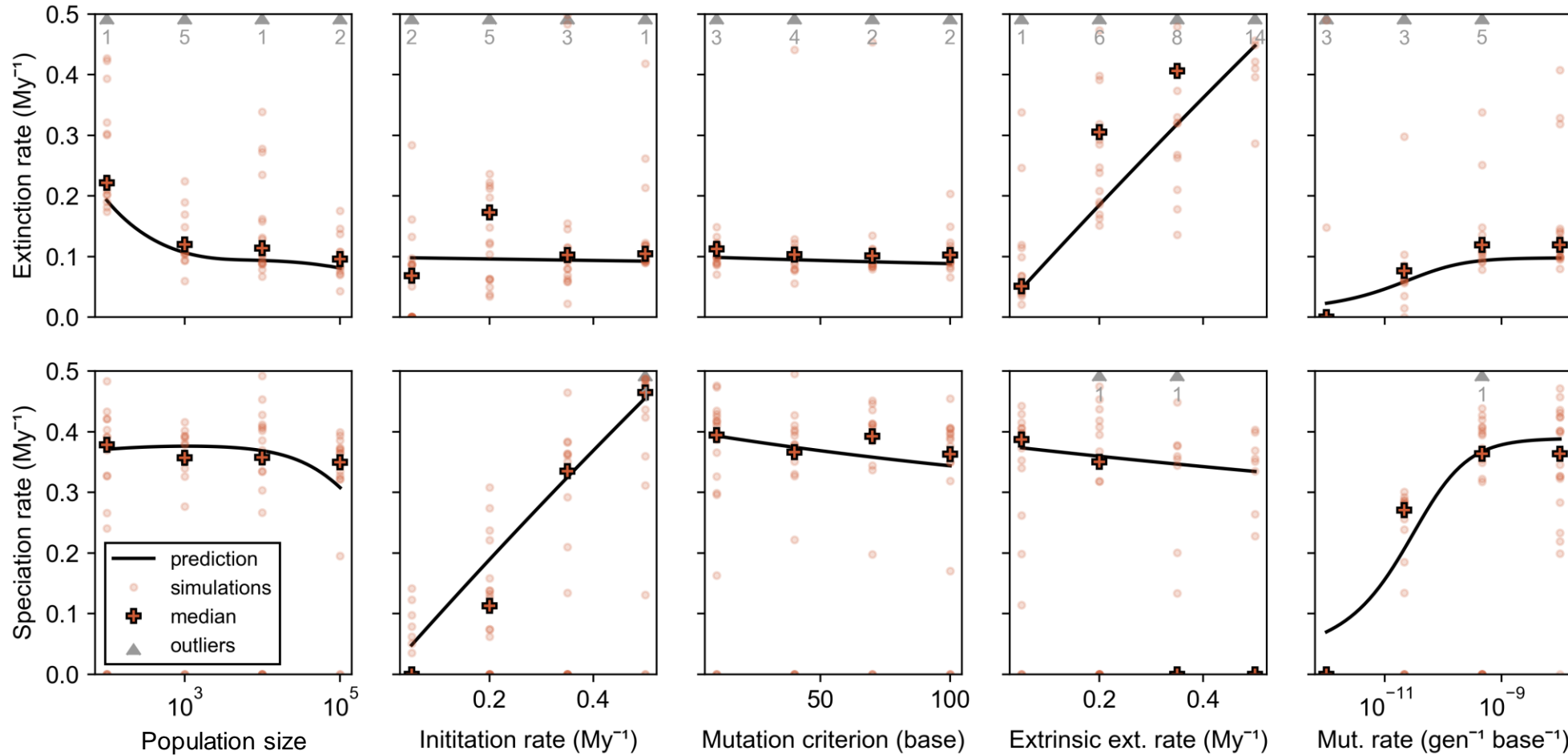
Yes, but ...

- All populations are not demes (polymorphism)
- One mutation at the time → not very realistic
- Not fixed mutations may play a role in the reproductive isolation

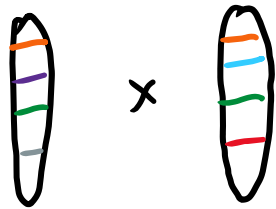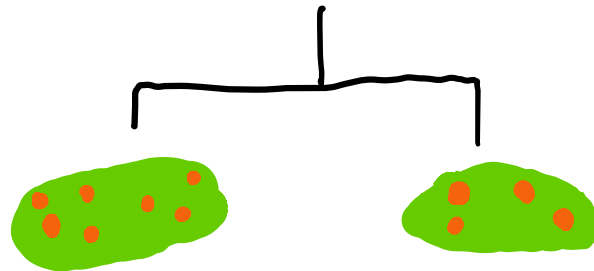## A Dynamical Theory of Speciation on Holey Adaptive Landscapes

Sergey Gavrilets[*]

$d = \#$ different loci

$D_w = \pi =$ mean of d across pairs of individuals in a population

$D_b = D_{XY} =$ mean of across pairs of individuals between 2 populations

$D_w(t)$

$D_b(t)$.

✓ if $d < K$

✗ if $d \geqslant K$

fitness

1

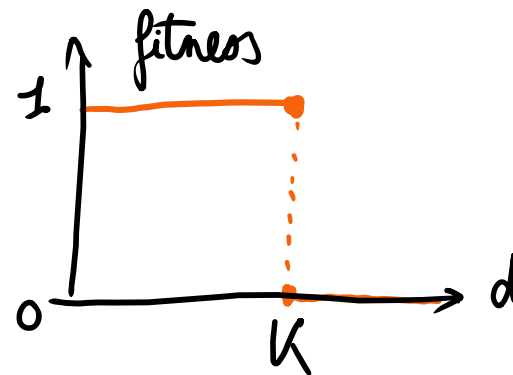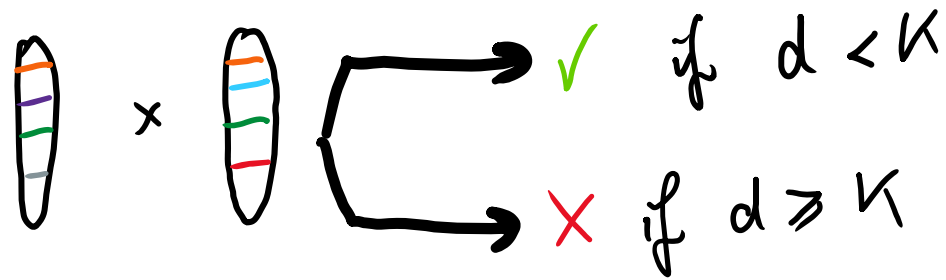0 · K · d

1 new allele → mean fitness depends on D_w

$$s(D_w) = \frac{e^{-D_w} D_w^K}{\Gamma(K+1, D_w)}$$

with $\Gamma(s, x) = \int_x^{+\infty} t^{s-1} e^{-t} dt$

Selection coefficient

more negative selection

more neutral

K

D_w

S. Gavrilets, The American Naturalist. 154, 1–22 (1999).
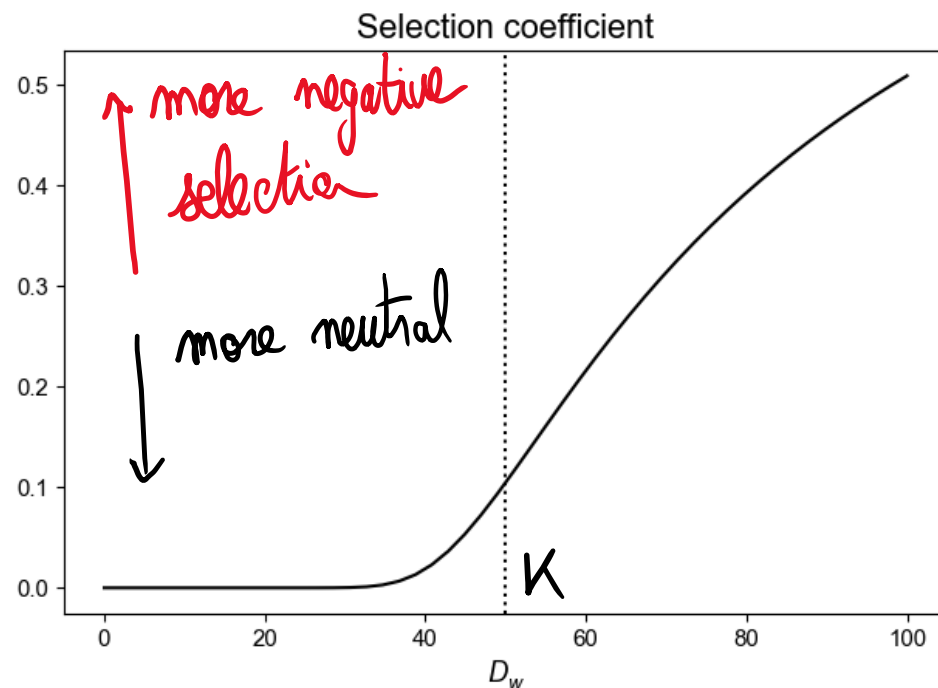
Genetics

Polymorphism

$$\frac{dD_w}{dt} = mut^\Theta + sel^\Theta + drift^-$$

Divergence

$$\frac{dD_b}{dt} = mutations$$

S. Gavrilets, The American Naturalist. 154, 1–22 (1999).

Genetics

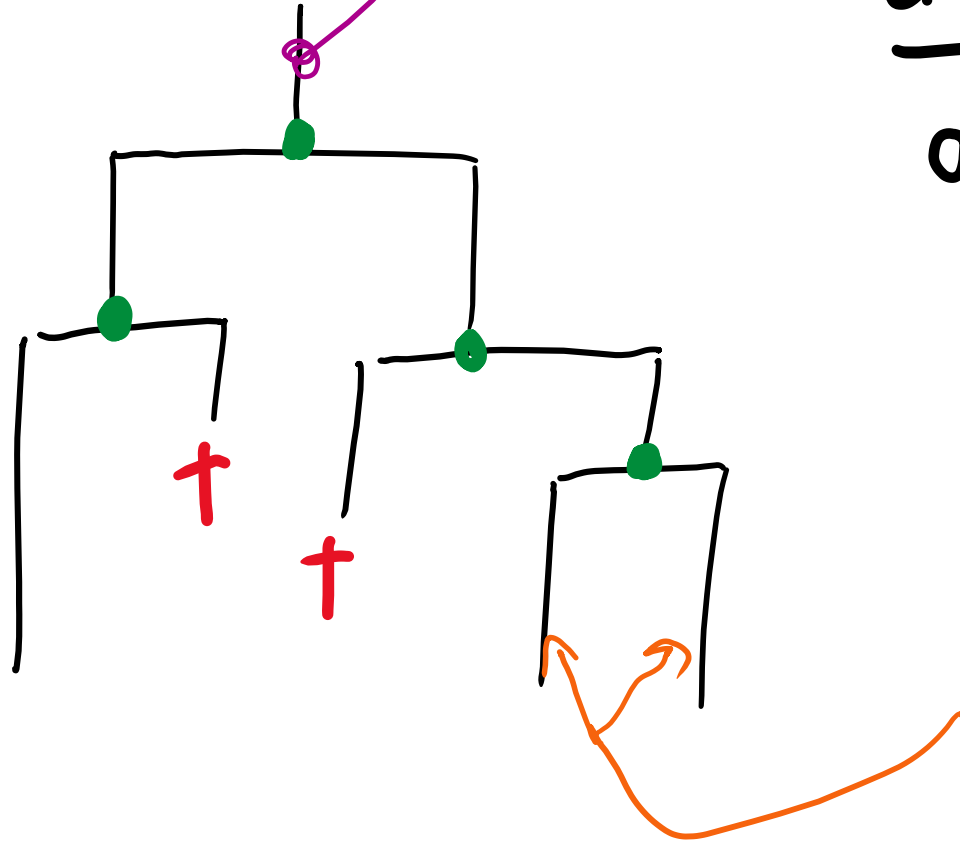$$\frac{d\,D_w(t)}{dt} = \frac{1}{t_g}\left(-s\,D_w + 2\nu - \frac{D_w}{N}\right)$$

selection   mutation   drift

$$\frac{d\,B_b(t)}{dt} = \frac{1}{t_g}\,2\nu R$$

with $R = f(D_w)$ a rate of divergence

ν mutation rate

t_g generation time

N population size

S. Gavrilets, The American Naturalist. 154, 1–22 (1999).

21
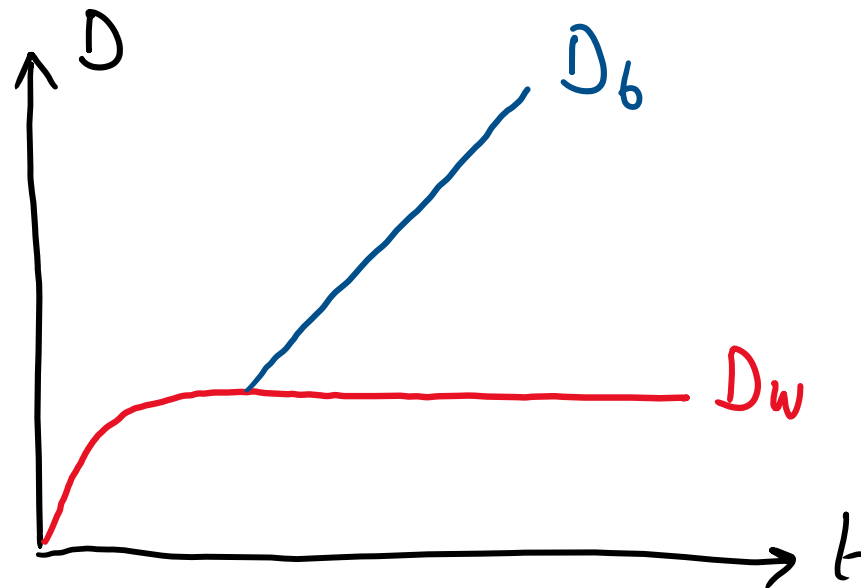
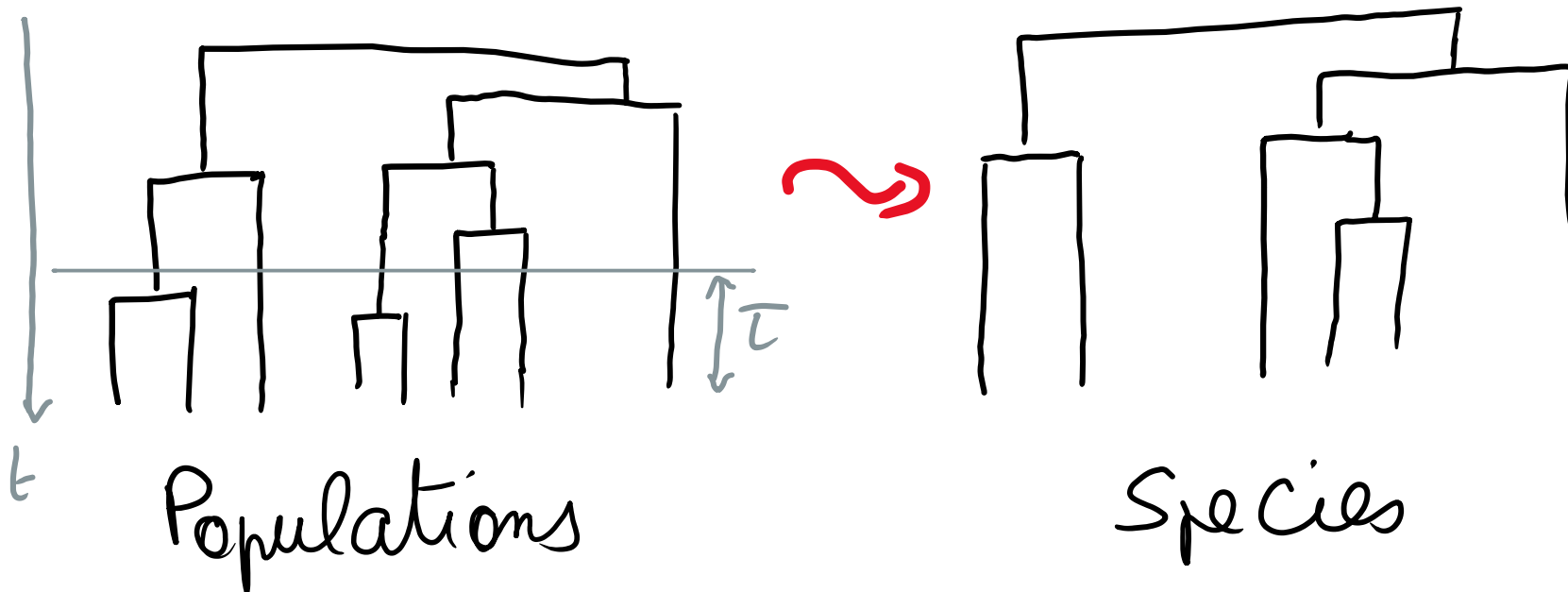# Clustering in the holey adaptive landscapes
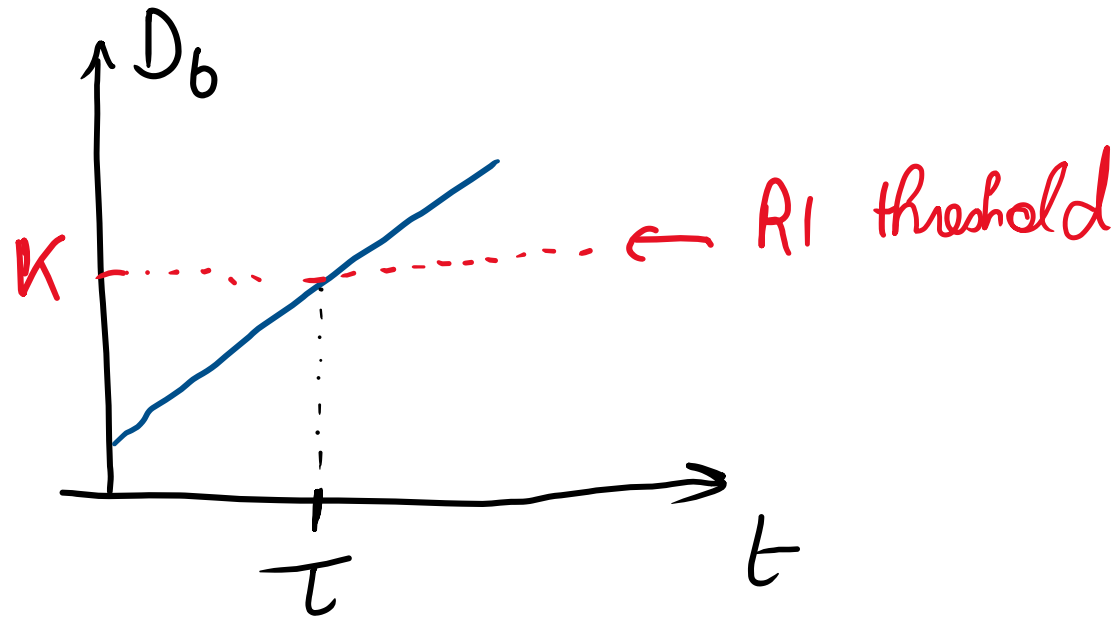
Clustering in the holey adaptive landscapes
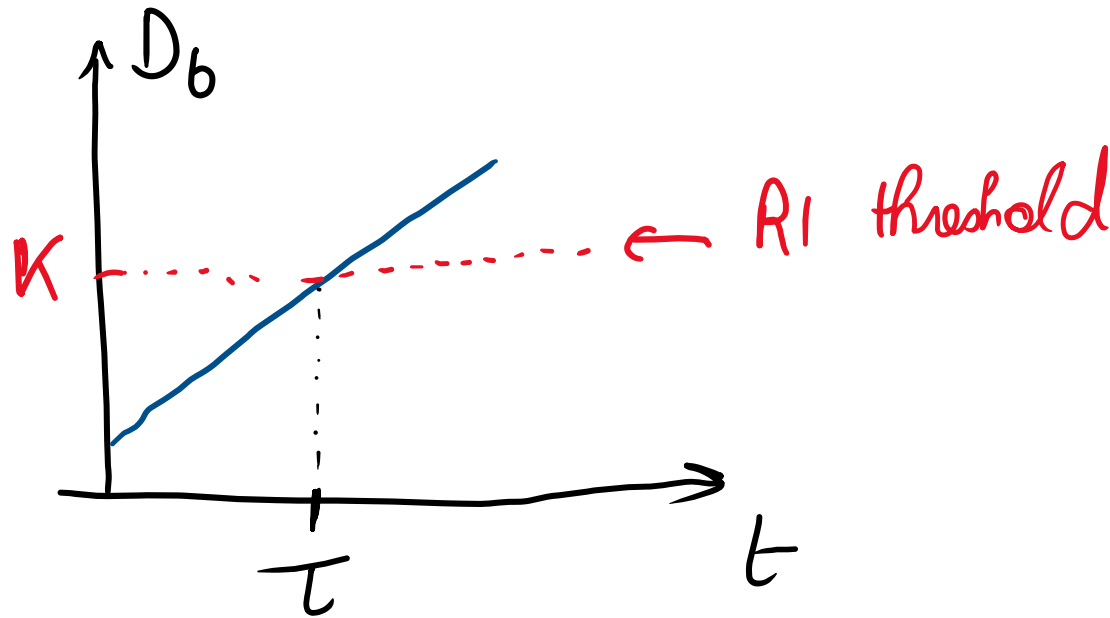
- A deterministic approach of the genetic divergence
- τ depends on population size, mutation rate, K, generation time

- What if N varies across populations, or generation times?

Conclusions

We have built an explicit model of speciation to predict the processes that are limiting the speciation and extinction speed

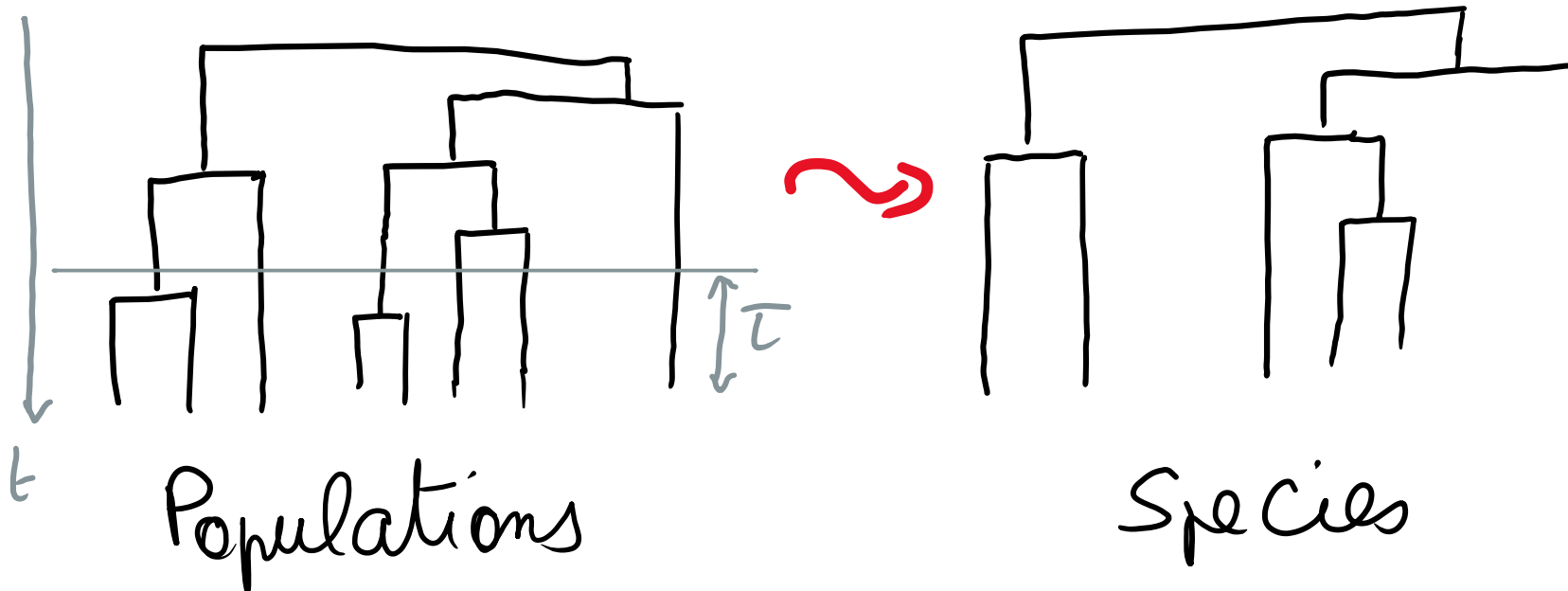# Conclusions

We have built an explicit model of speciation to predict the processes that are limiting the speciation and extinction speed

Population structure dynamics is the most relevant factor to predict speciation rate

Conclusions

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Population dynamics and mutation rates are not always limiting processes

Conclusions

We have built an explicit model of speciation to predict the processes that are limiting the speciation and extinction speed

Population structure dynamics is the most relevant factor to predict speciation rate

Population dynamics and mutation rates are not always limiting processes

Holey adaptive landscape can provide a more accurate model of accumulation of genetic divergence

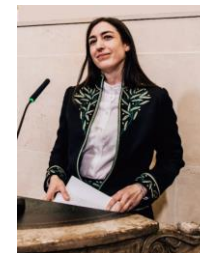Thank you for your attention

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