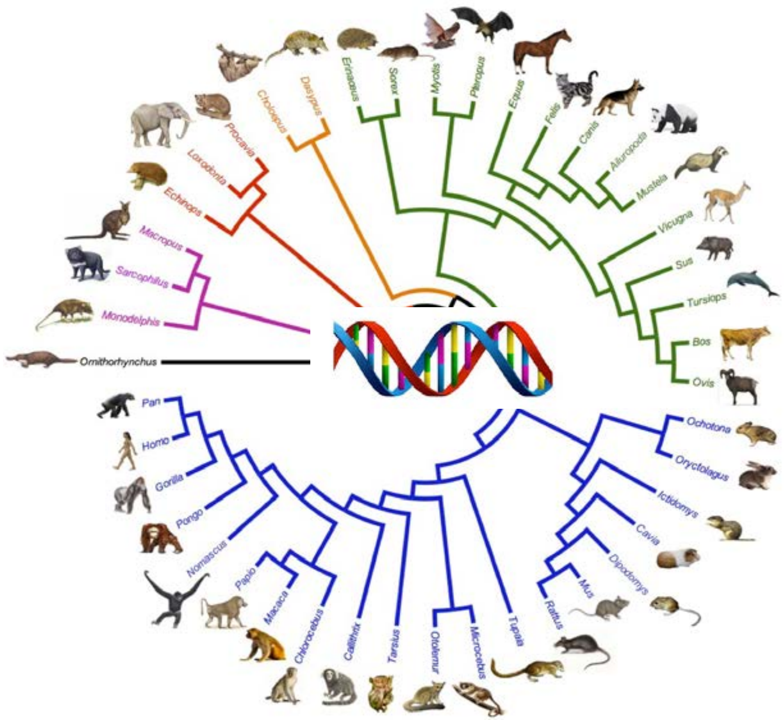
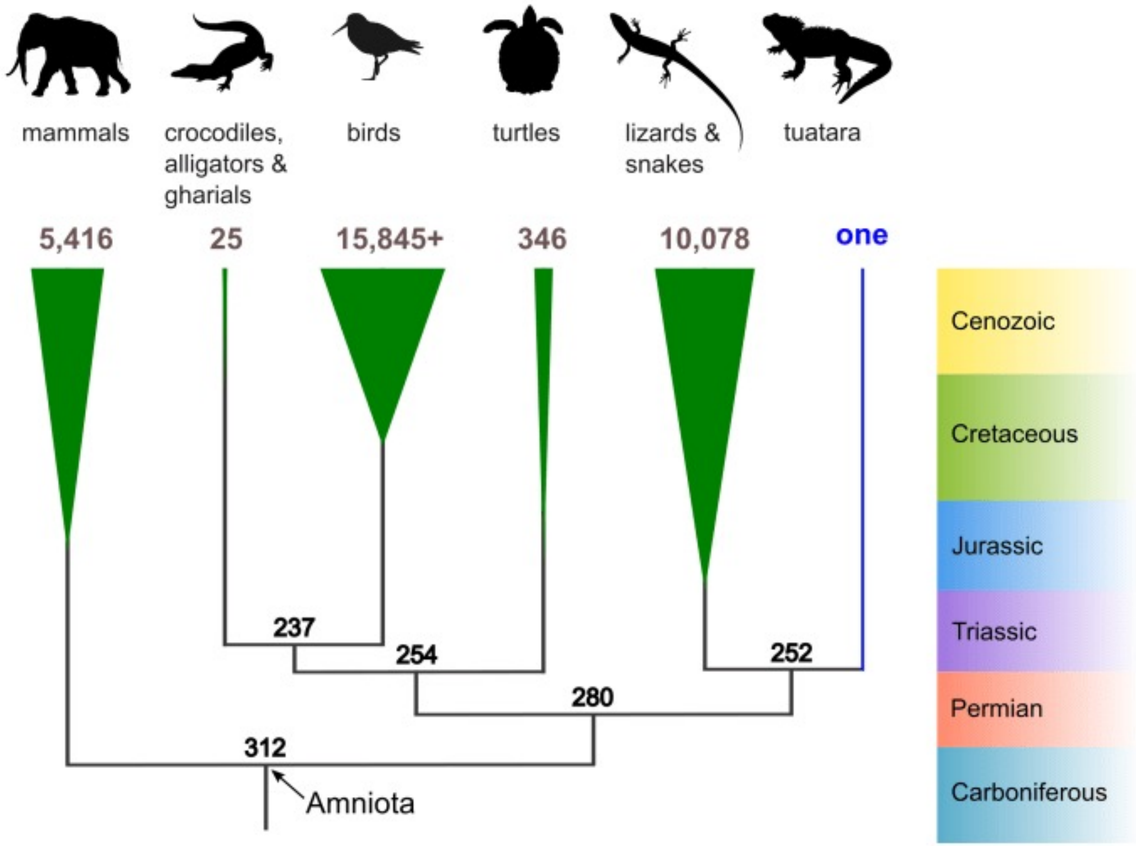
Pourquoi certains groupes d’espèces diversifient-ils plus ou moins rapidement que d’autres?



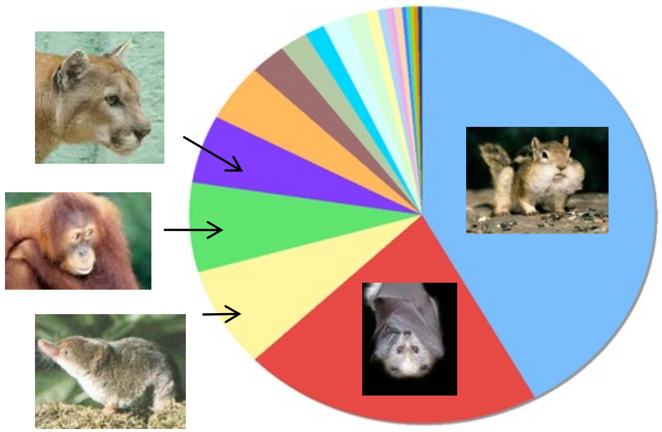
Hélène Morlon
Ecole Normale Supérieure


Life on Earth is tremendously diverse

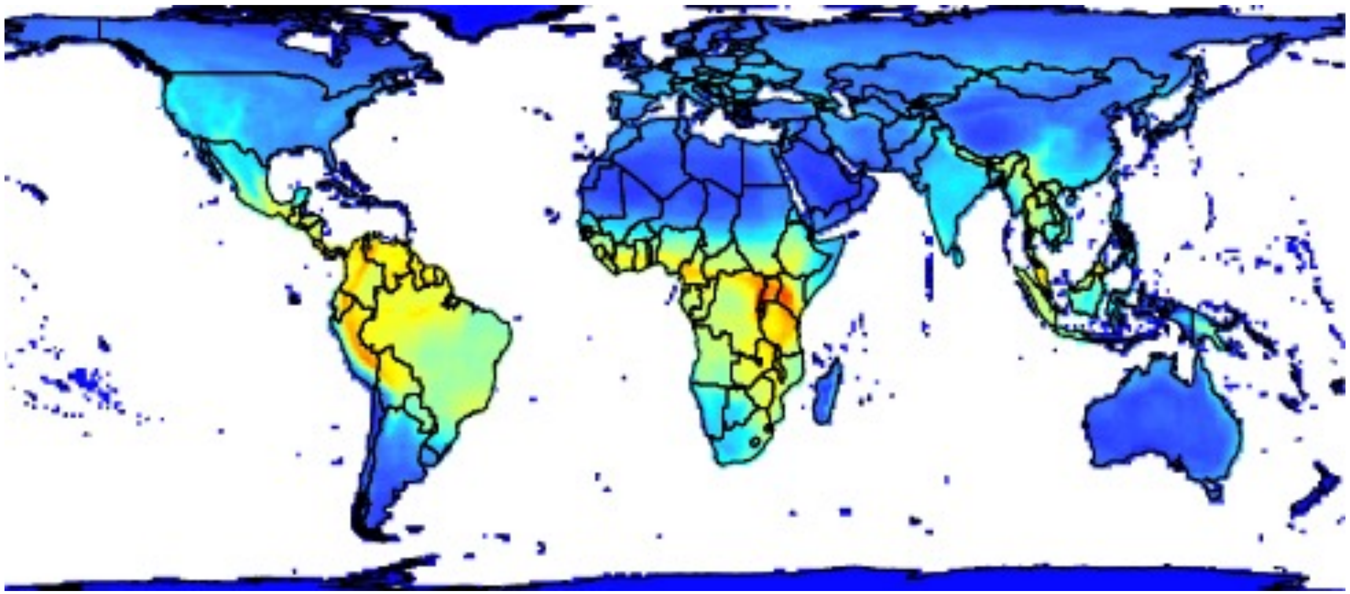
Some species groups are much more species rich than others



Some species groups are much more species rich than others

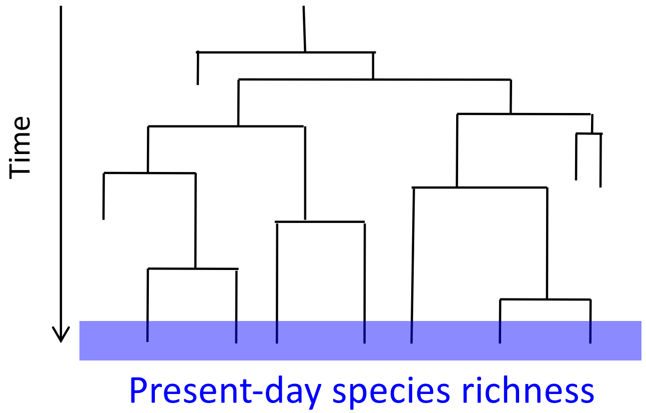


Some regions of the planet are much more species rich than others



Davies *et al*. *PNAS* 2008

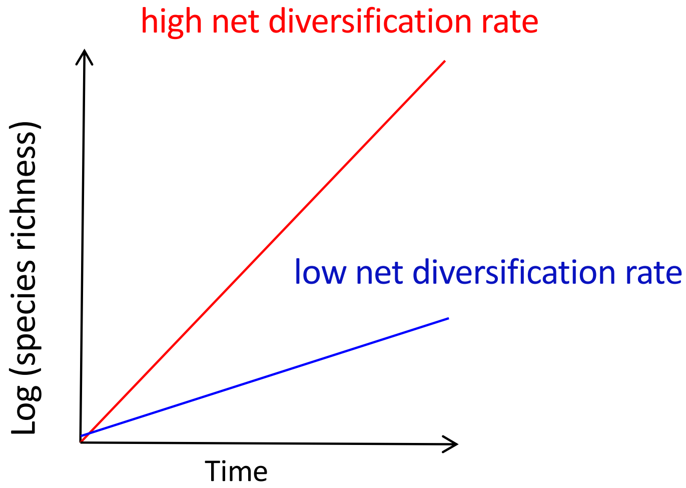
Current levels of species richness result from the balance of speciation and extinction events



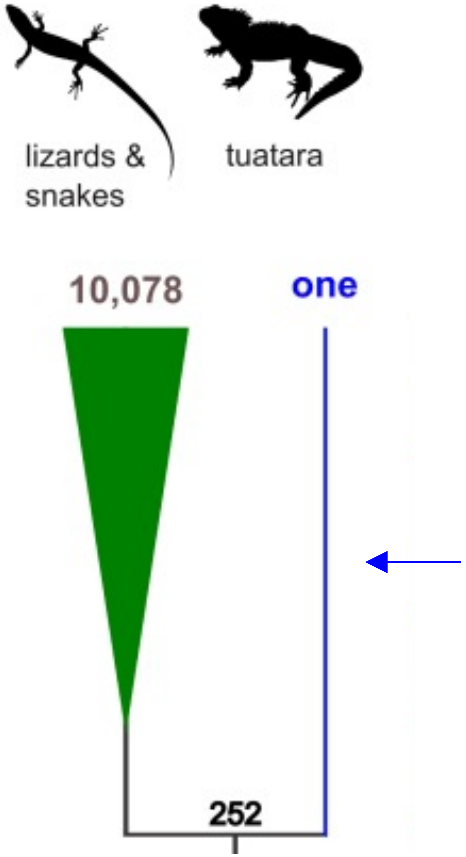
Speciation rate
average number of speciation events per Myr per lineage

Extinction rate
average number of extinction events per Myr per lineage

Net diversification rate
speciation rate – extinction rate



Have species poor groups always been poor or are they the remnants of a diverse past?

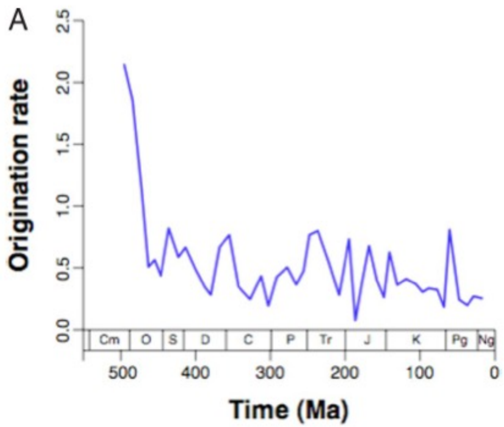


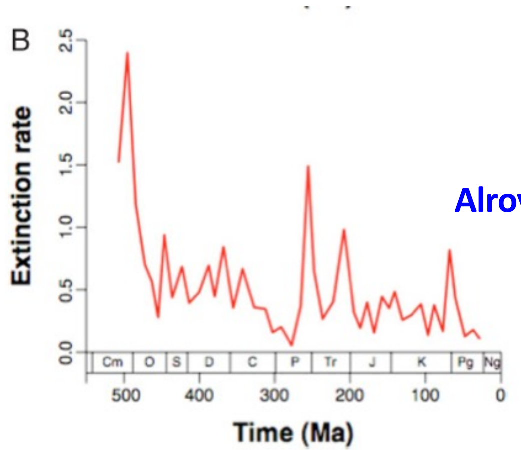
Few speciation events

OR

Many extinction events?

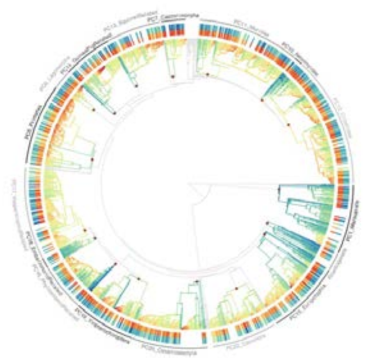
Historically, processes of speciation and extinction have been studied through the fossil record



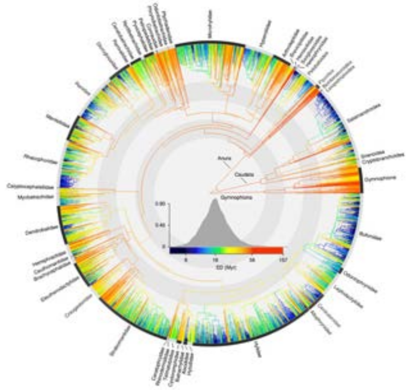


Alroy *PNAS* 2008

Studying deep time variations in biodiversity using the phylogenies of present-day species

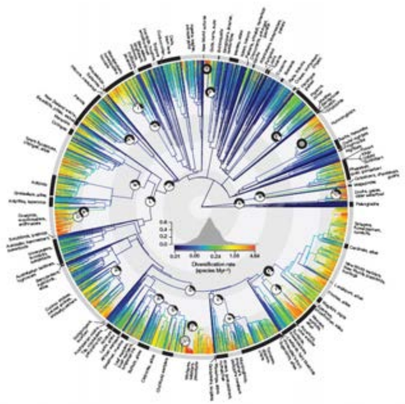


6 000 mammal species
Upham *et al. PloSB 2019*



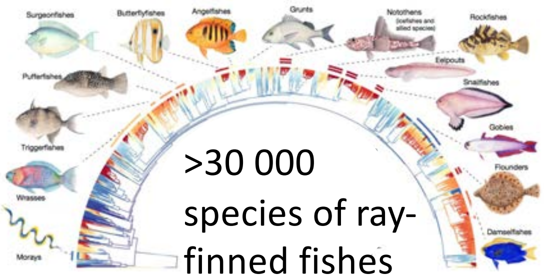
\> 7 000 amphibian species
Jetz & Pyron *Nat Ecol Evol* 2018

2.2 Million species on a single tree



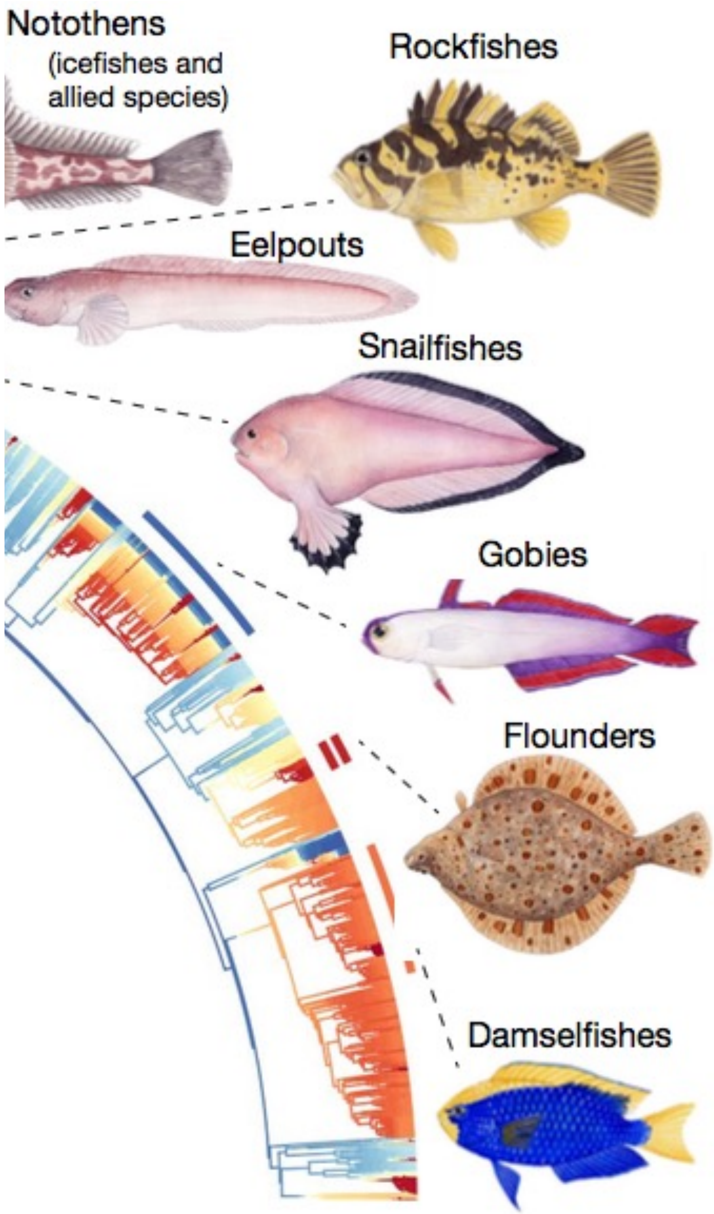
10 000 bird species

Jetz *et al. Nature* 2012



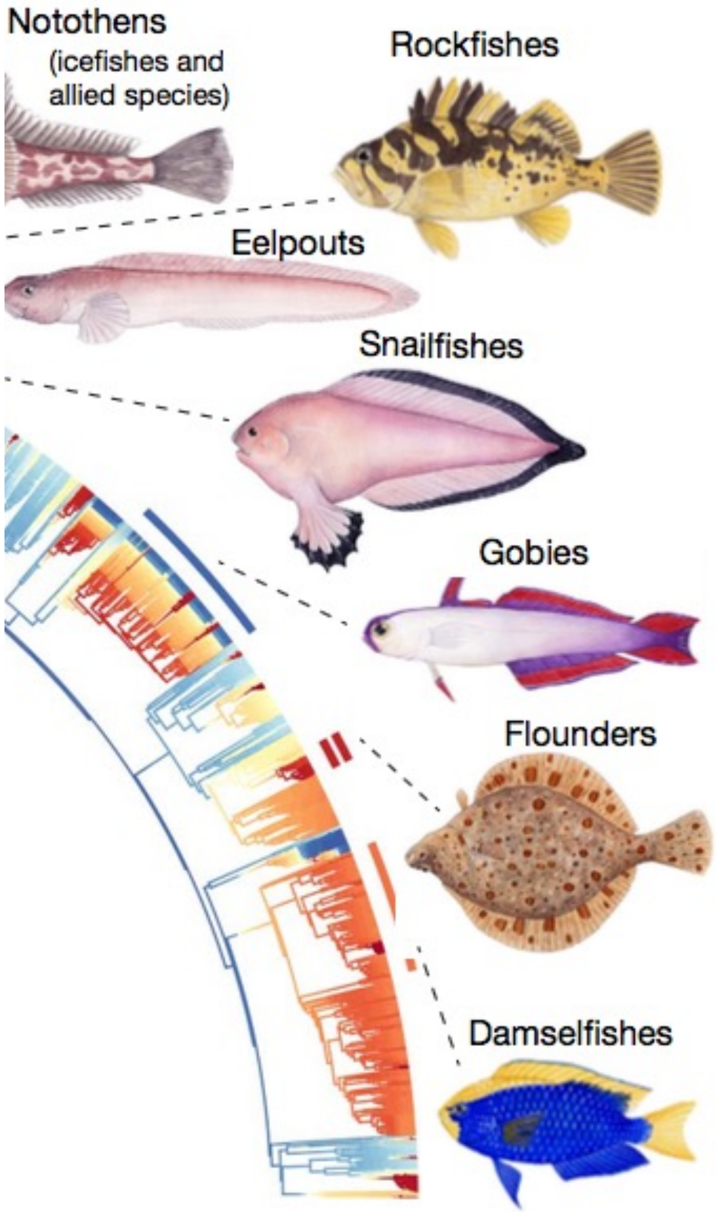
\>30 000 species of ray-finned fishes

Rabosky *et al. Nature* 2018

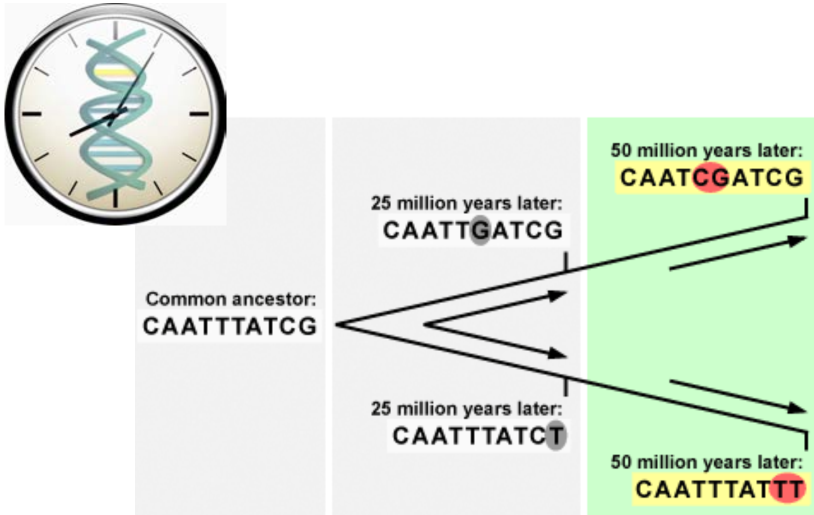


Phylogenies represent the order and timing of divergences between ancestral species that led to present-day species

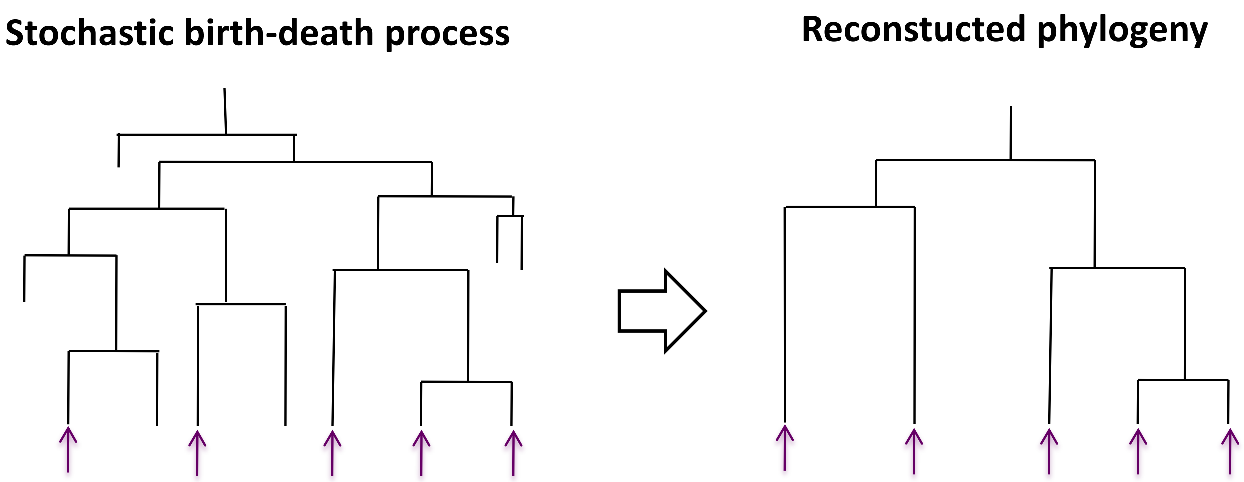
Phylogenies are constructed from the genetic (and sometimes phenotypic) similarity between present-day species



The datation is performed with fossil calibrations and the molecular clock



By fitting birth-death models of cladogenesis to phylogenies, we can estimate speciation and extinction rates and how they vary through time and species groups



Nee *et al. PTB* 1994

Ecology Letters, (2014) doi: 10.

REVIEW AND SYNTHESIS

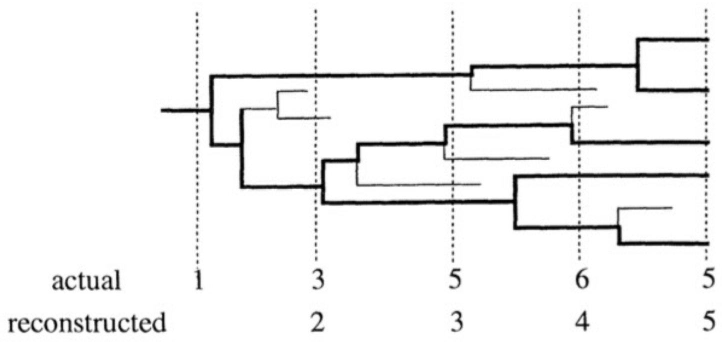
Phylogenetic approaches for studying diversification

Morlon *Eco Lett* 2014

Stadler *JEB* 2013

Pennel & Harmon *Ann NY Acad Sci* 2013

Under the homogeneous constant rate birth-death process with speciation rate λ and extinction rate μ, extinction leaves a distinctive signal in reconstructed phylogenies even though extinct taxa are not observed



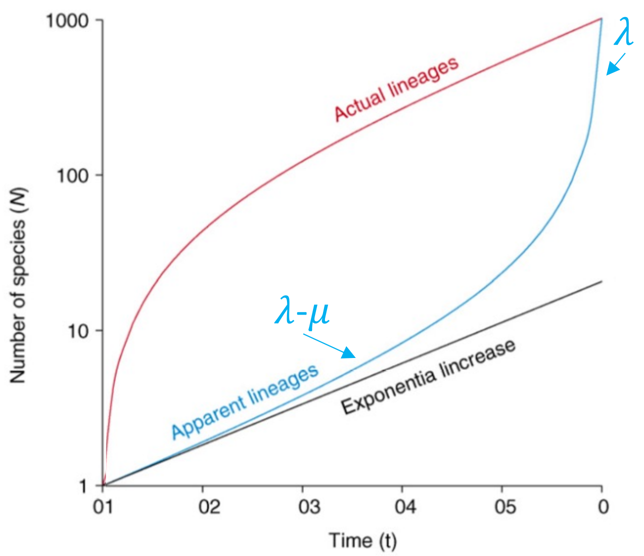


Figure from Ricklefs TREE 2007

Nee *et al. PTB* 1994

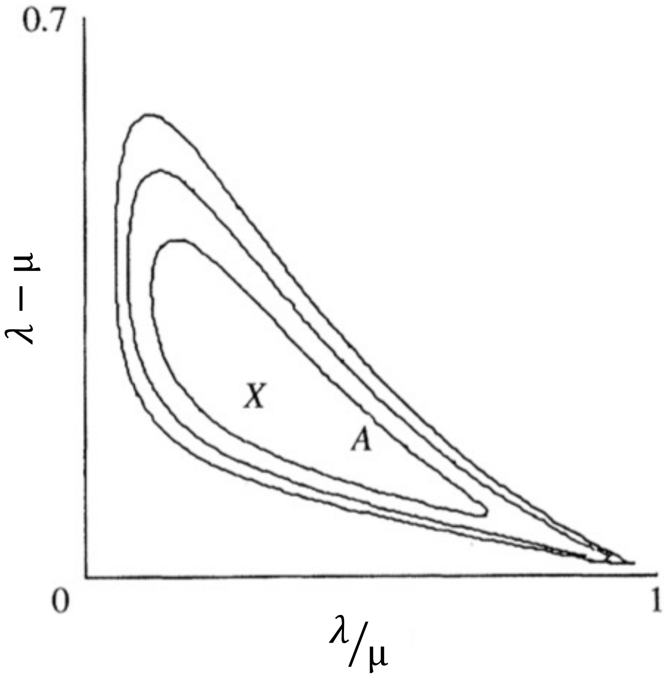
Given an empirical phylogeny, we can compare the statistical support of different diversification models, and estimate parameters of these models, i.e. λ and μ, using likelihood-based statistical inference

The likelihood is defined as

$$\mathcal{L}_x(\theta) = f_\theta(x)$$

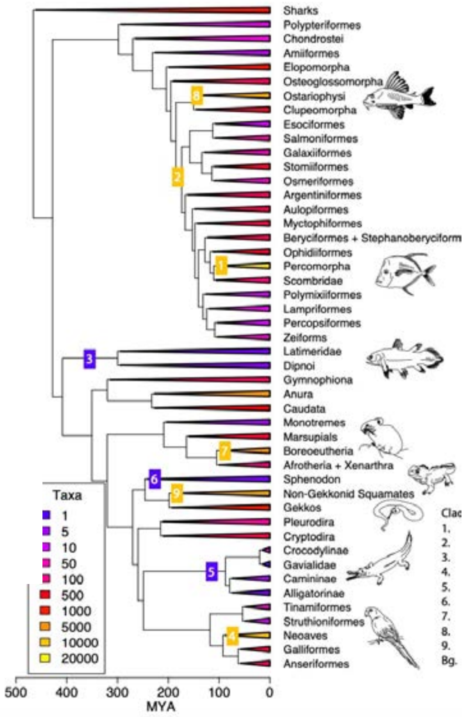
where $f_\theta(x)$ is the probability of observing x under the model for parameters θ

The ML estimate is the parameter θ that maximizes $\mathcal{L}_x(\theta)$

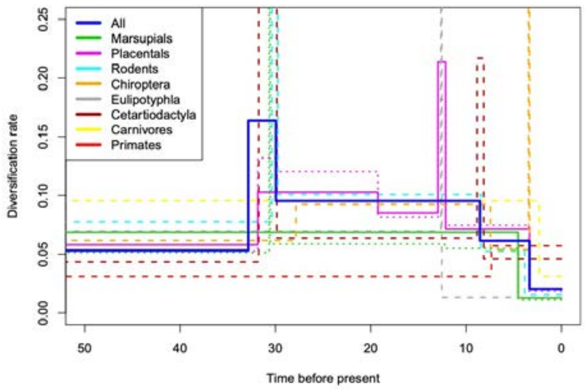


From the 90's to today:
a battery of new models to quantify how diversification rates vary…

… across lineages



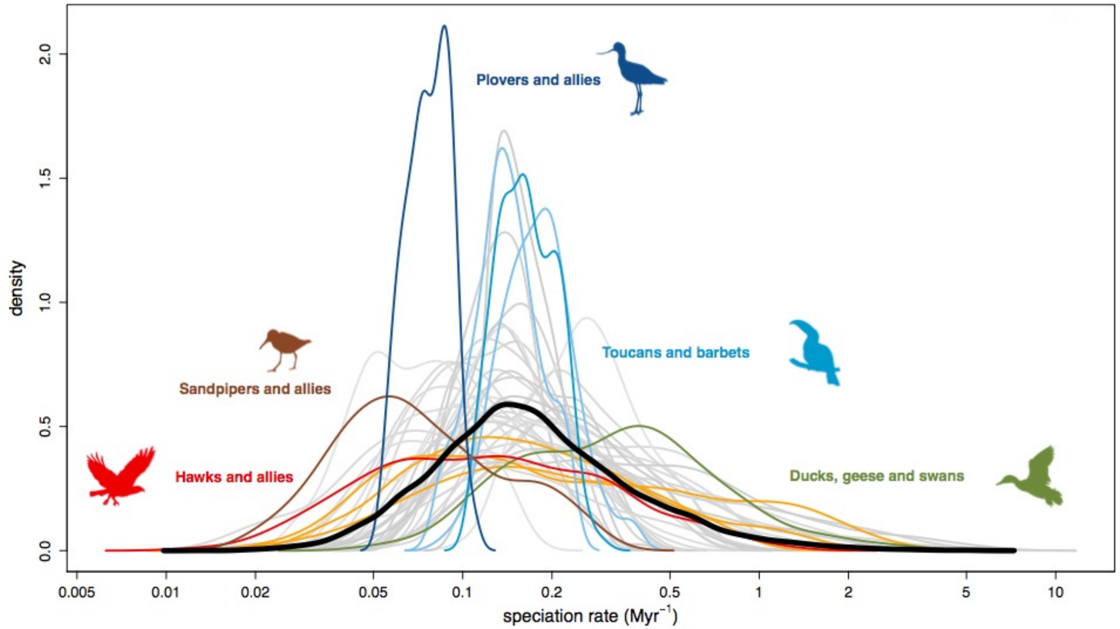
… through time



Stadler *et al.* PNAS 2011,
Morlon *et al.* PNAS 2011,
May *et al.* MEE 2016, etc…

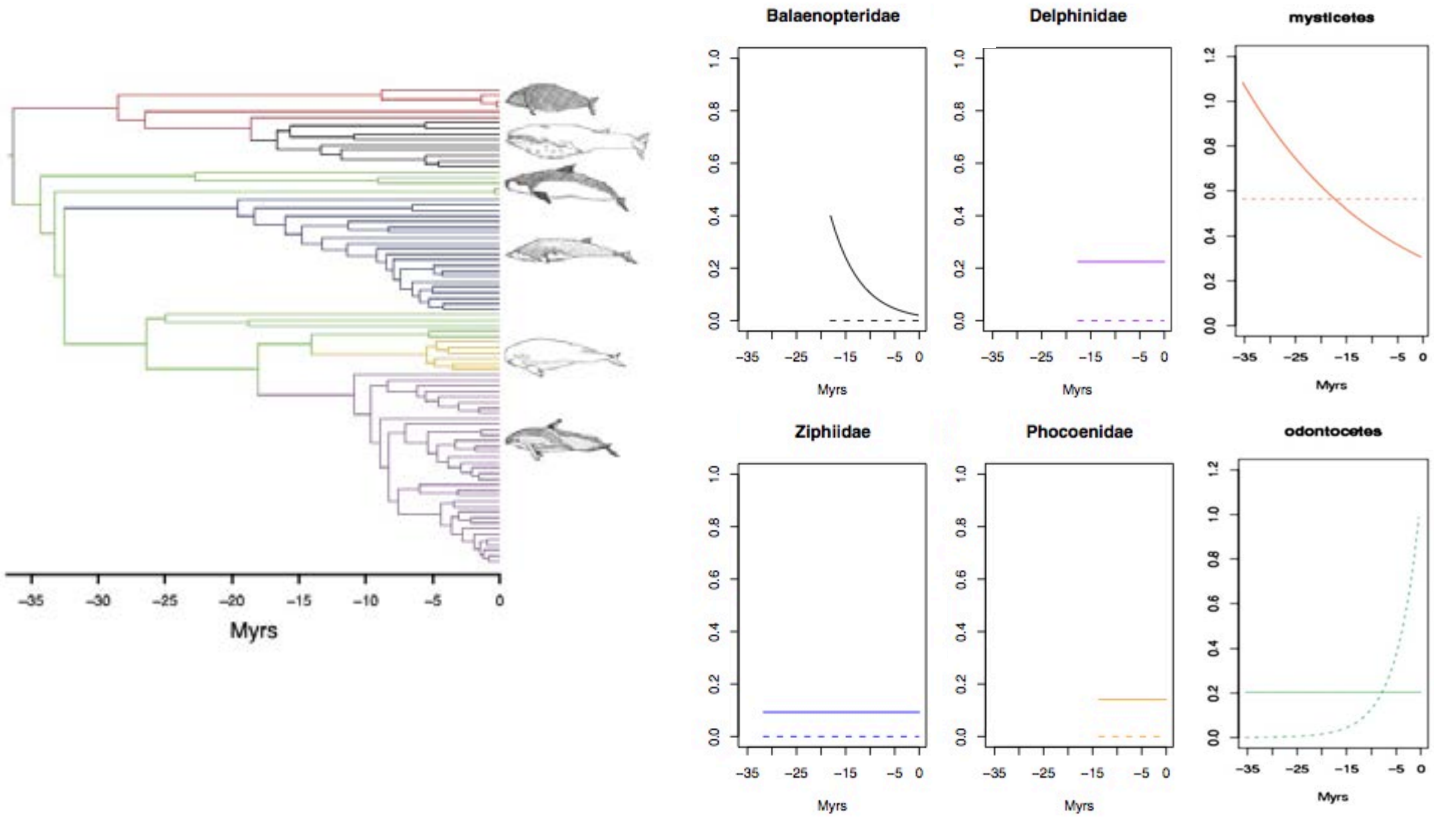
Alfaro *et al.* PNAS 2009,
Rabosky *et al.* PloS One 2014,
Maliet *et al.* NEE 2019,
Barido-Sottani *et al.* Syst Bio 2020,
etc…

Speciation rates vary widely across lineages



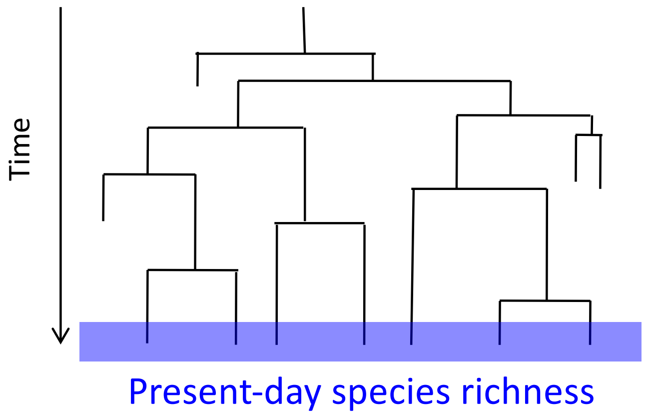
Maliet *et al. Nature Ecol Evol* 2019

Extinction rates are harder to estimate, but evidence suggests they can vary widely across lineages



Morlon *et al. PNAS* 2011

Levels of species richness result from the balance of speciation and extinction events: reconstructing paleodiversity curves

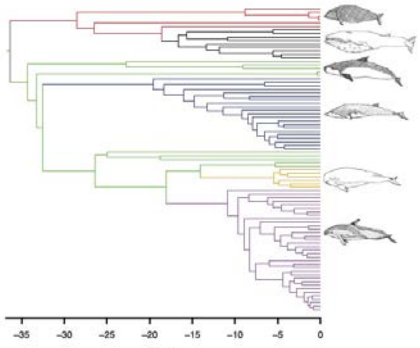


speciation rate

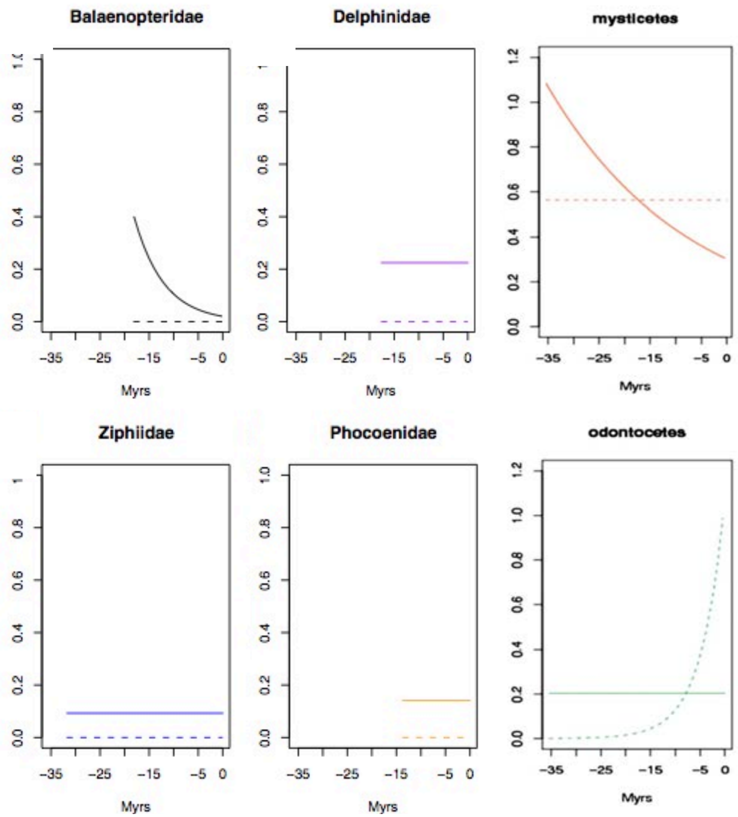
extinction rate

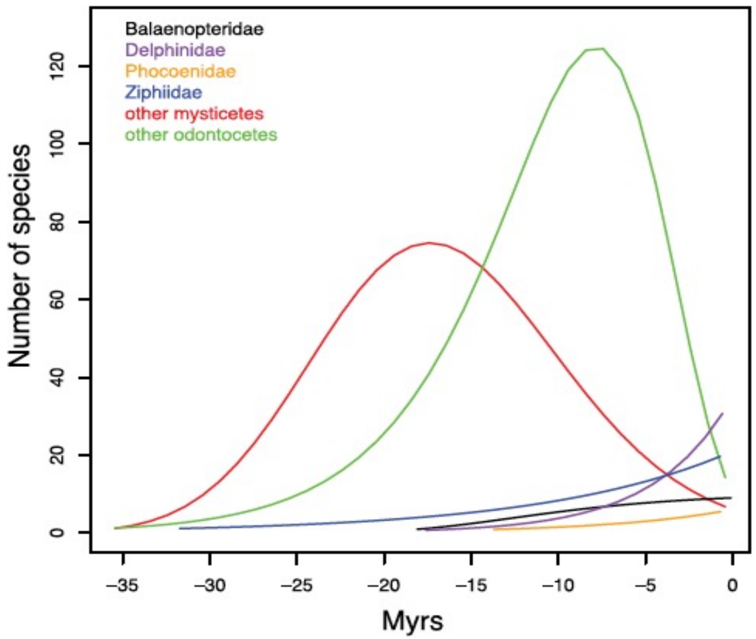
$$N(t) = N_0 e^{\int_0 (-\lambda(s)+\bar{\mu}(s))ds}$$

number of species today



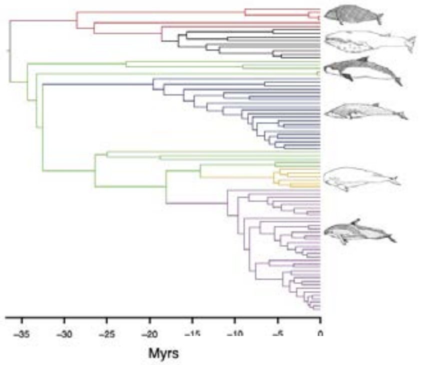
Current levels of species richness result from the balance of speciation and extinction events



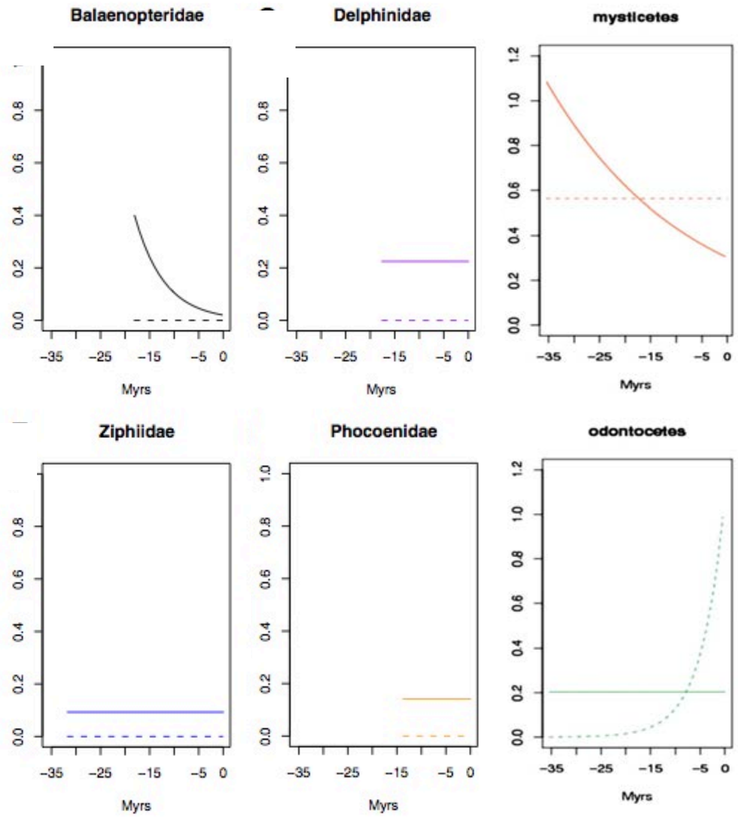


difference in species richness due to difference in speciation rates

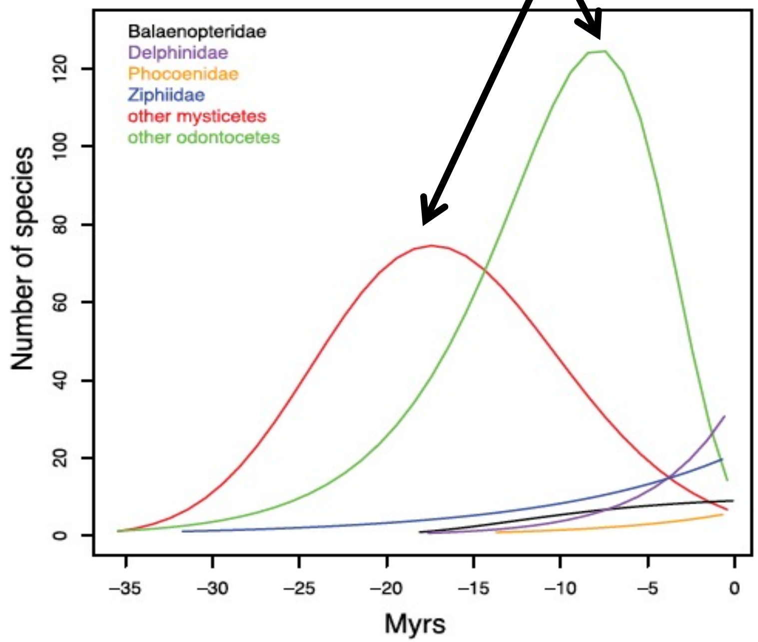
Morlon *et al. PNAS* 2011



Current levels of species richness result from the balance of speciation and extinction events



extinction events play a major role in explaining present-day levels of species richness / species poor groups that are the remnants of a once diverse past



Morlon *et al. PNAS* 2011

Levels of species richness result from the balance of speciation and extinction events: reconstructing paleodiversity curves while accounting for uncertainties

Olivier Billaud

Dan Moen

Todd Parsons

probability there were m species at time t

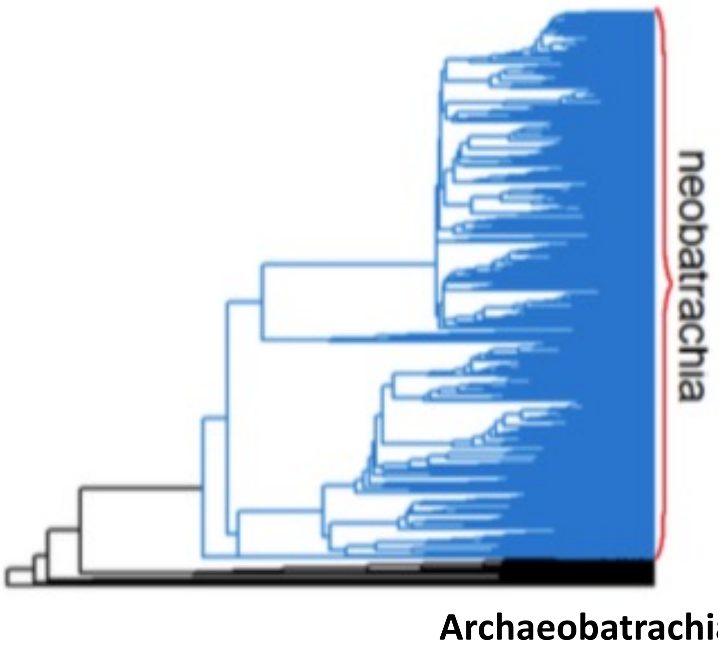
given there were x species at time s

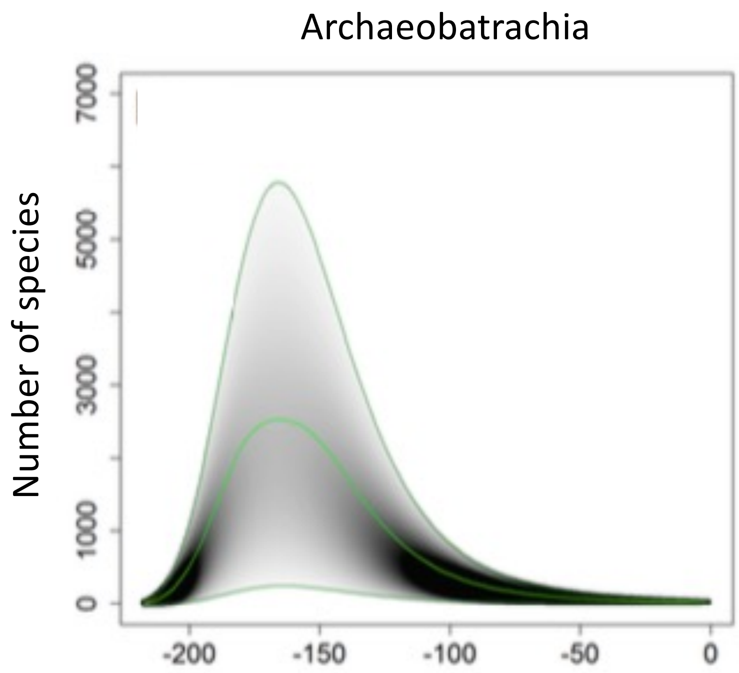
and there are n species today

$$\mathbb{P}(N(t) = m \mid N(s) = x, N(T_{pres}) = n)$$

Billaud *et al. Syst Bio* 2019

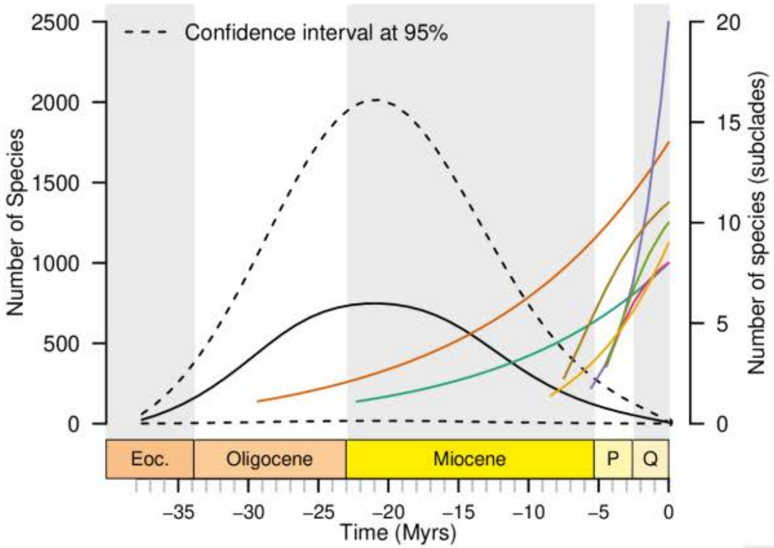
Old and poor frog families are the remnant of a diverse past





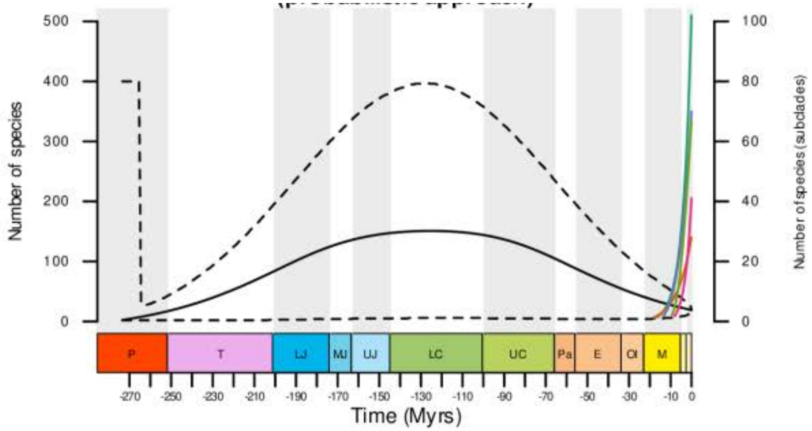
Billaud *et al. Syst Bio* 2019

Other examples of old and poor groups that are the remnant of a diverse past

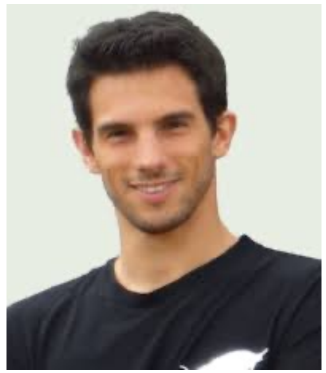


Nathan Mazet

Pierre-Henri Fabre

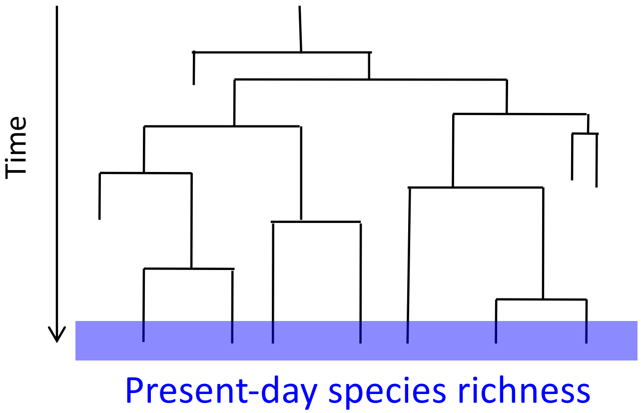


Fabien Condamine



Mazet *et al.* in prep.

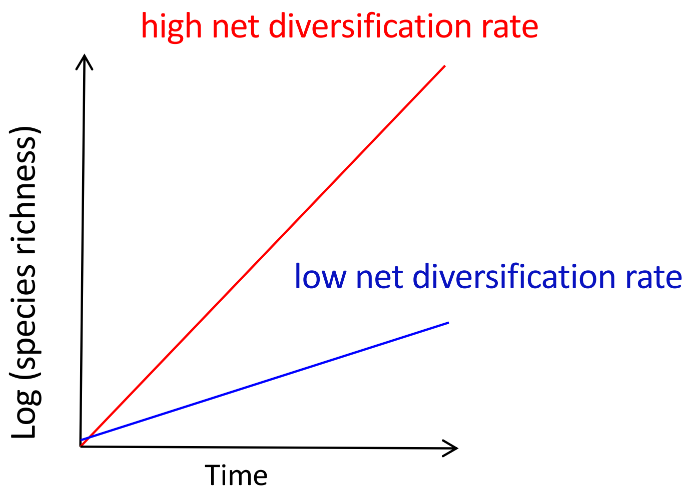
Current levels of species richness result from the balance of speciation and extinction events



Speciation rate
average number of speciation events per Myr per lineage

Extinction rate
average number of extinction events per Myr per lineage

Net diversification rate
speciation rate – extinction rate



What are the factors that modulate speciation & extinction rates?

The Court Jester

The Red Queen

EXTRINSIC

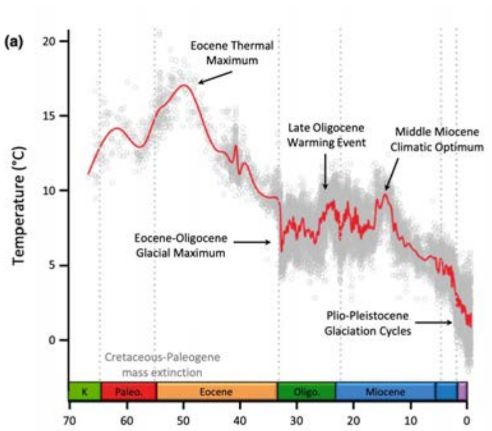
INTRINSIC

Abiotic factors
climatic variation
geological context

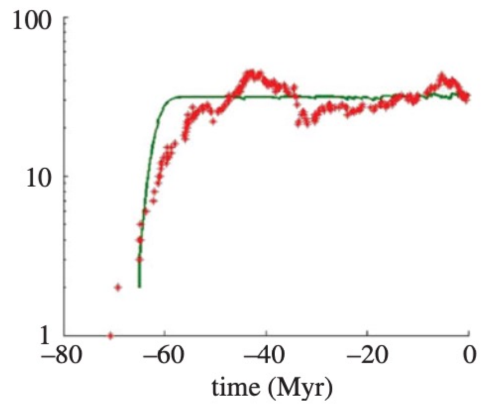
Biotic factors
competition
mutualistic and antagonistic interactions

Species-specific traits
reproduction mode
life-history traits
dispersal capacity

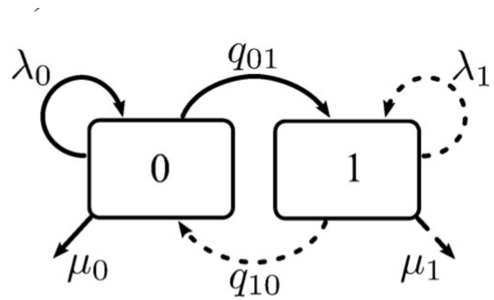
From the 90’s to today:
a battery of new models to quantify why diversification rates vary through time and across lineages



Condamine *et al.* Eco Lett 2013, Cantalapiedra *et al.* PRSB 2012, etc…



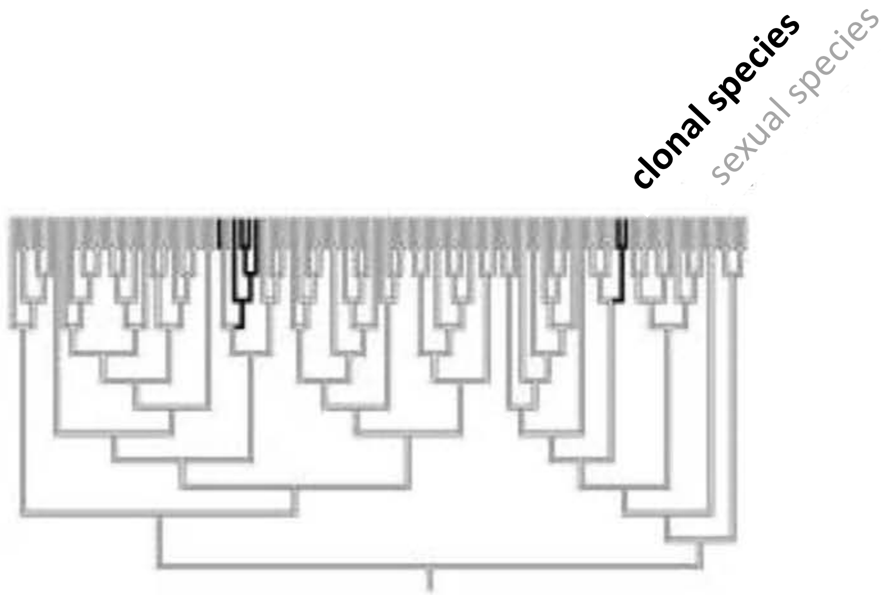
Etienne *et al.* PRSB 2012



Maddison *et al.* Syst Bio 2004,
Fitzjohn *et al.* Syst Bio 2010,
Goldberg *et al.* Syst Bio 2011,
etc…

Species-specific traits can influence speciation and extinction rates

Transitions to clonality happen frequently, but clonal species have higher extinction rates

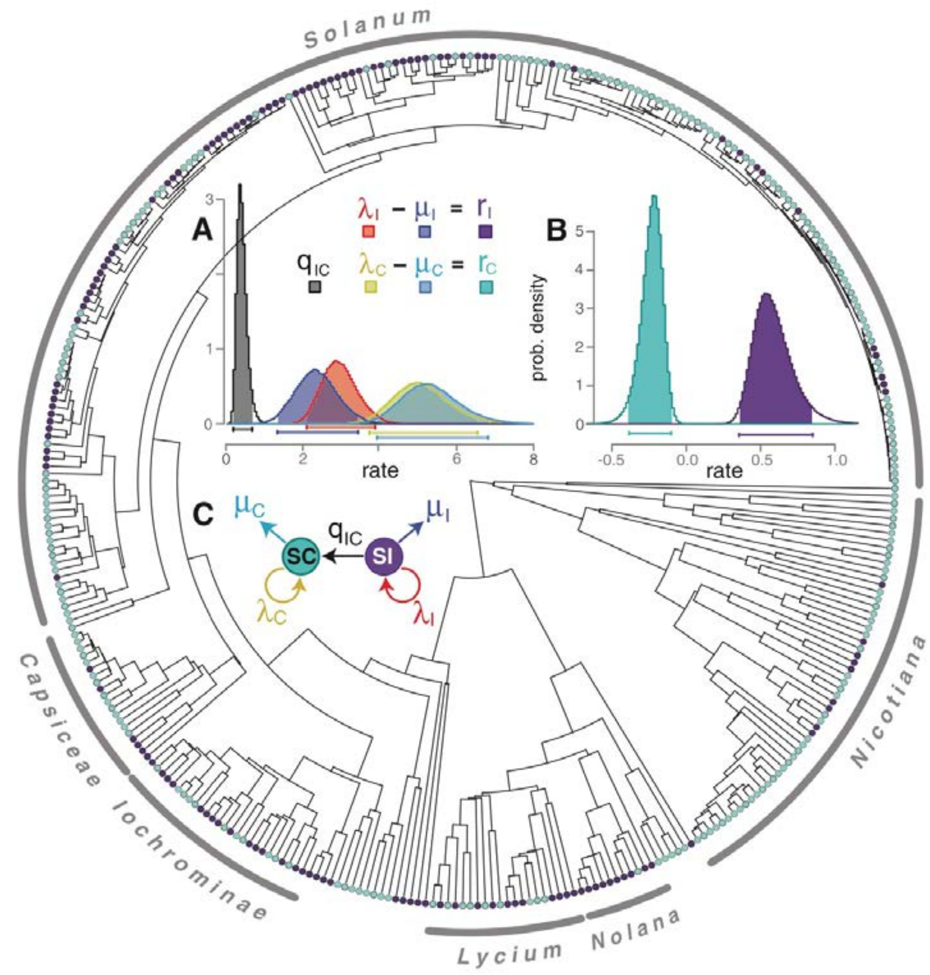


de Vienne et al. 2013 PLoS One

Gouyon & Giraud 2009 Aux origines de la sexualité. Fayard

Species-specific traits can influence speciation and extinction rates

Transitions to asexuality happen frequently, but sexual species have higher net diversification rates



Goldberg *et al. Science* 2010

Species-specific traits can influence speciation and extinction rates

PROCEEDINGS OF THE ROYAL SOCIETY B

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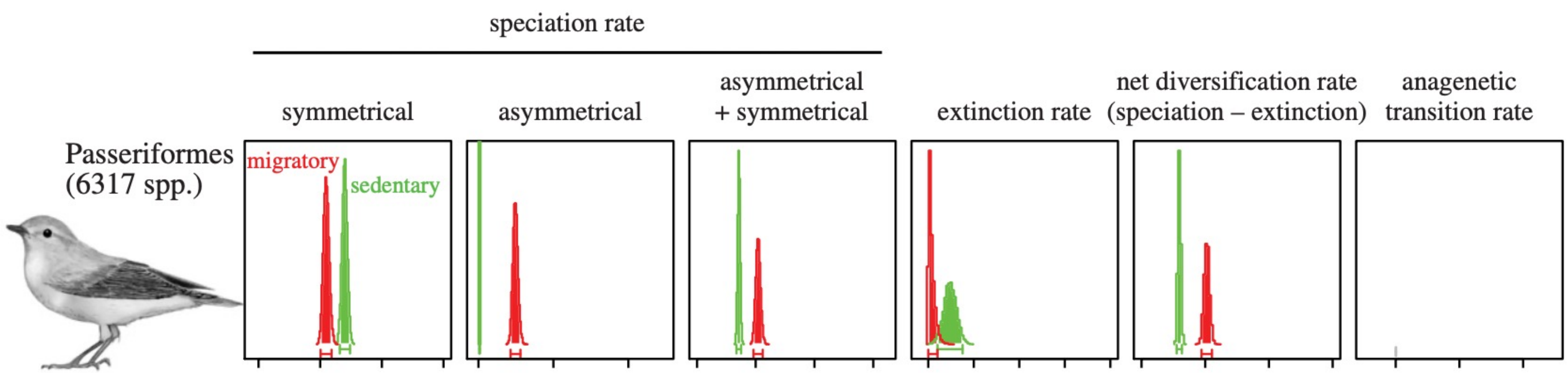
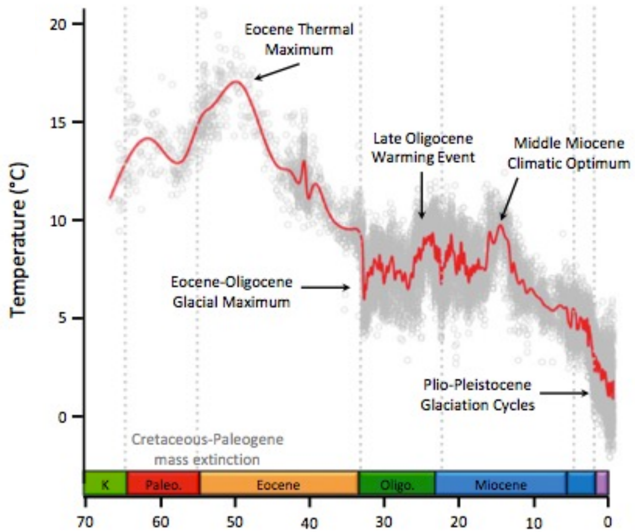
Settling down of seasonal migrants promotes bird diversification

Jonathan Rolland[1,2,3], Frédéric Jiguet[2], Knud Andreas Jønsson[4,5], Fabien L. Condamine[1] and Hélène Morlon[1,3]



The Court Jester

Abiotic factors, such as climatic changes, can influence speciation and extinction rates



Condamine *et al.* Eco Lett 2013

Temperature affects major aspects of biology through its effect on metabolic rates, body-size, and productivity

Kleiber's law

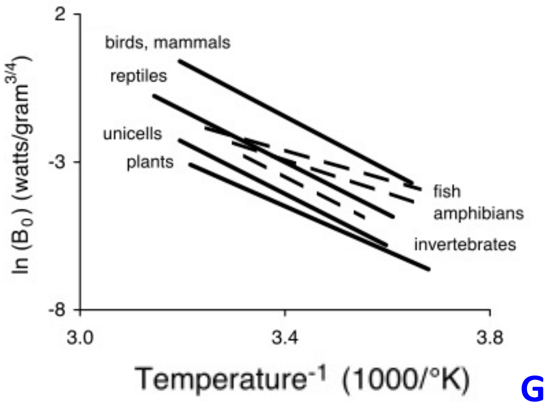
$$B \sim M^{3/4} e^{-E_i/kT}$$

metabolic rate (B)

body-size (M)

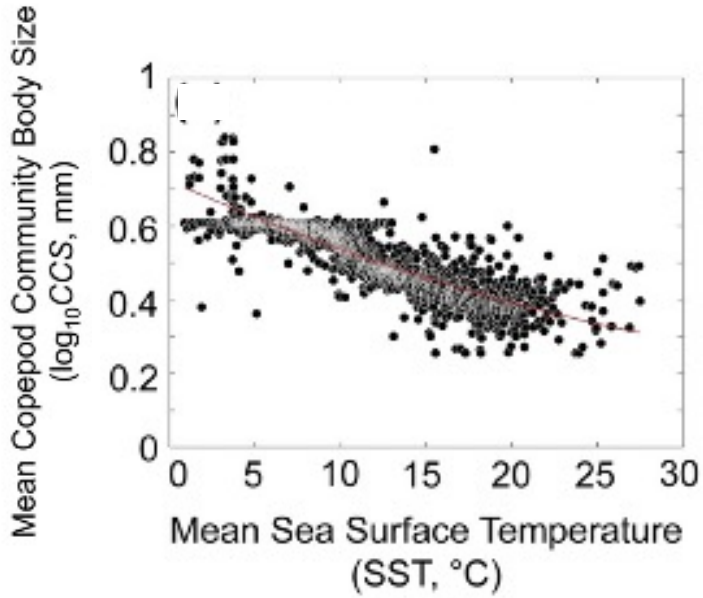
activation energy (E_i)

Boltzmann's constant (k)



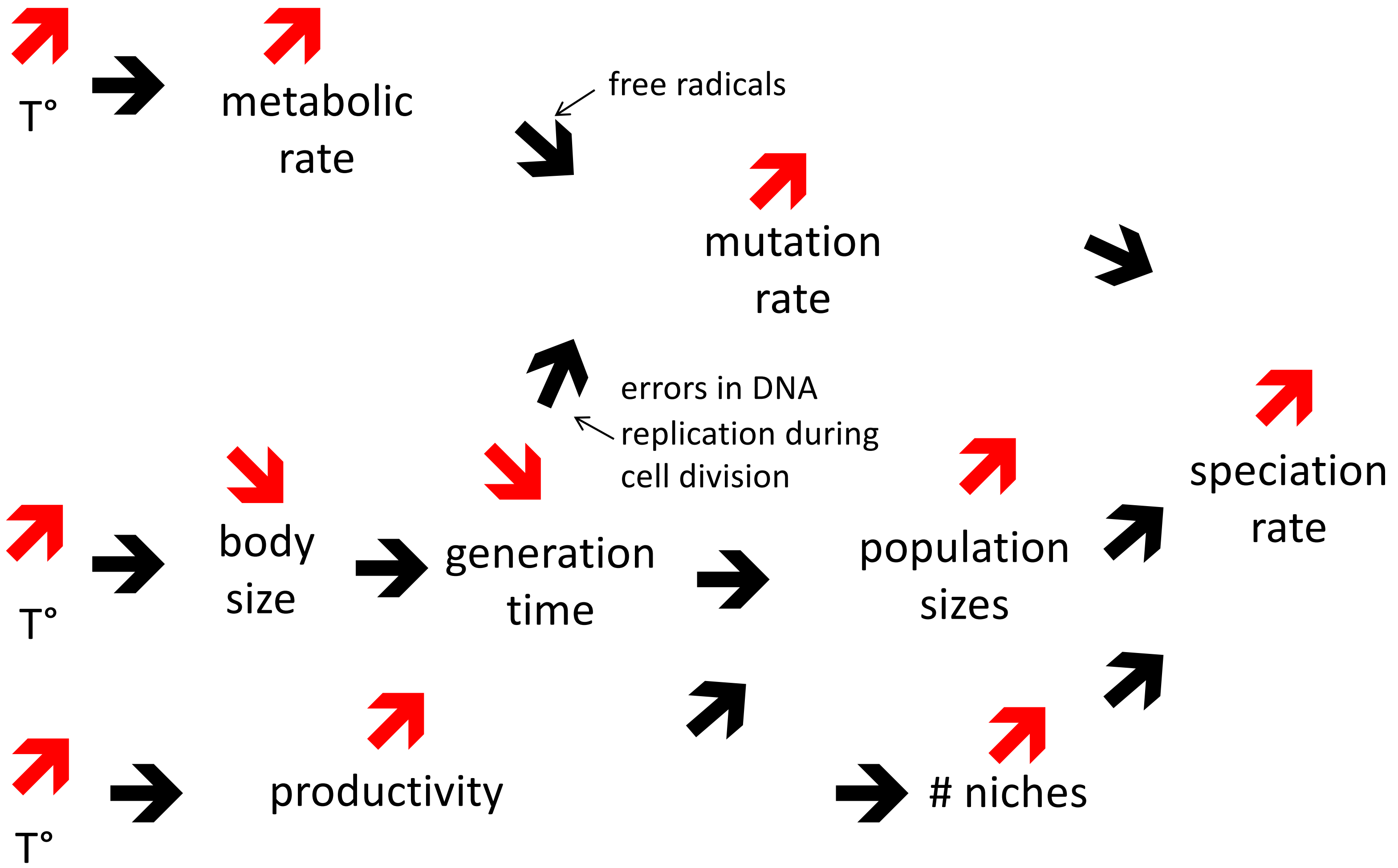
Gillooly *et al. Science* 2001

Bergmann's rule

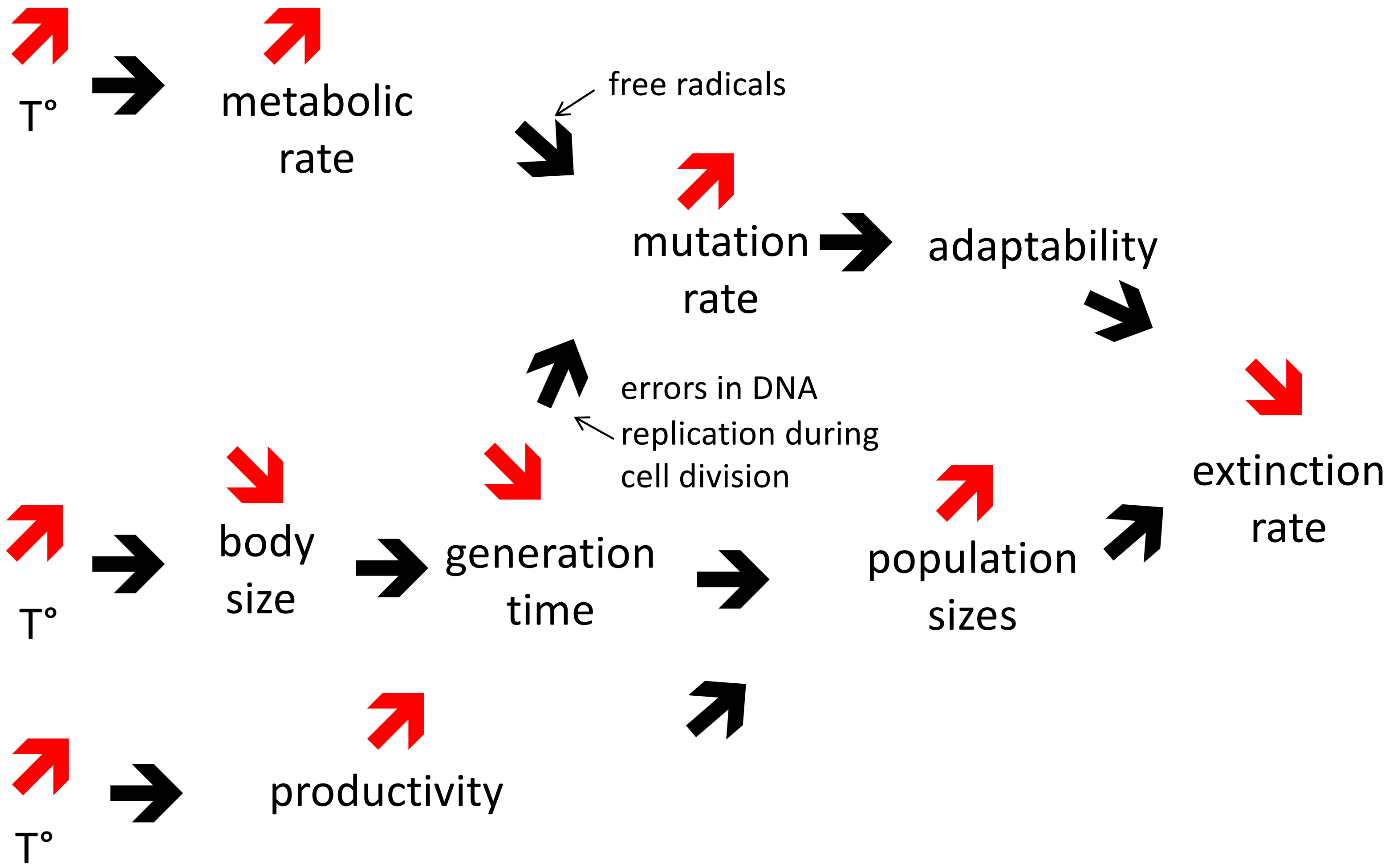


Evans *et al. Ecography* 2019

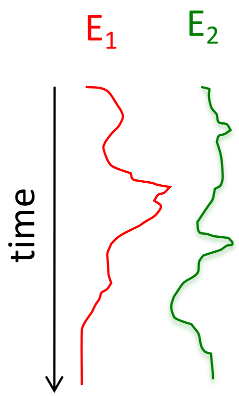
Based on the metabolic, body-size and productivity hypotheses, temperature should (positively) affect speciation rates



Based on the metabolic, body-size and productivity hypotheses, temperature should (negatively) affect extinction rates



Models of diversification with rates that depend on measured (a)biotic variables



$$\tilde{\lambda}(t) = \lambda(t, E_1(t), E_2(t), \ldots, E_k(t))$$

$$\tilde{\mu}(t) = \mu(t, E_1(t), E_2(t), \ldots, E_k(t))$$

Condamine et al. Eco Lett 2013
Lewitus et al. Syst Bio 2017

A meta-analysis of the effect of environmental changes on diversification

212 phylogenies across tetrapods

Comparison of 21 models including constant rate diversification models, models with time-varying rates, diversity-dependent models, and temperature-dependent models

Temperature-dependent models:

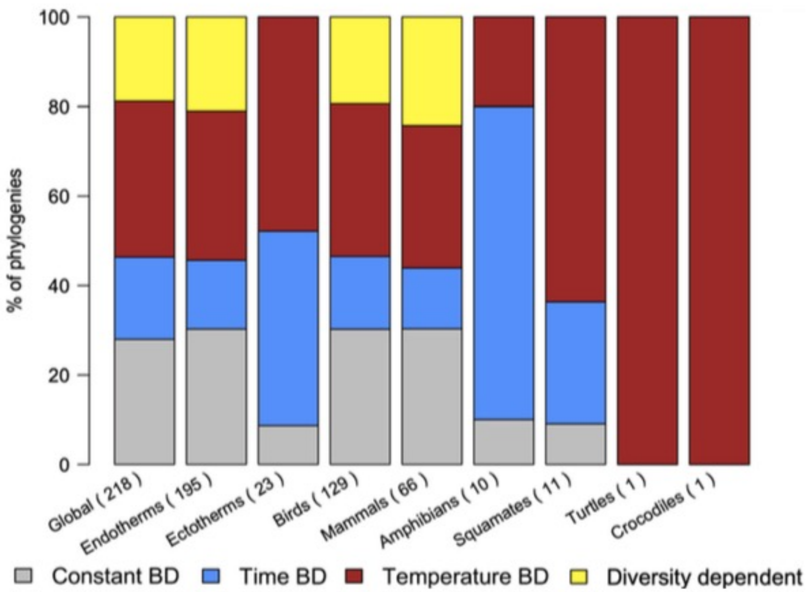
exponential dependence: $\tilde{\lambda}(t) = \lambda_0 \times e^{\alpha T(t)}$

linear dependence: $\tilde{\lambda}(t) = \lambda_0 + \alpha T_{(t)}$

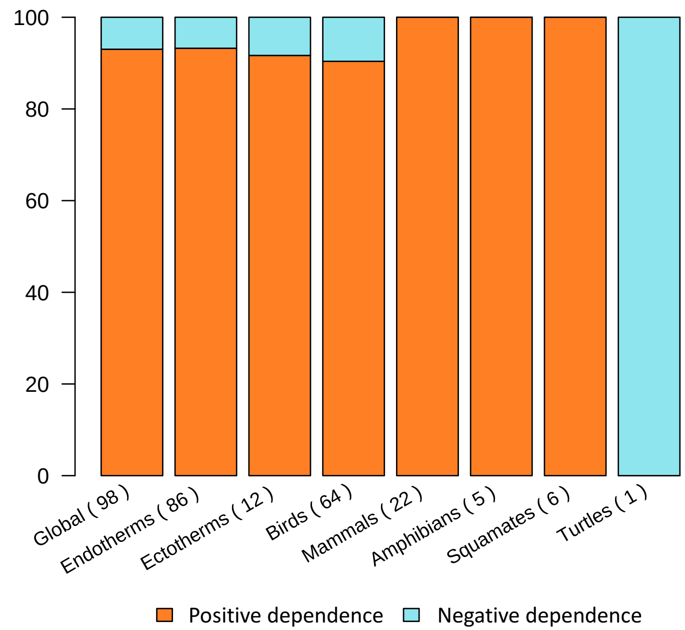
metabolic predictions : $\tilde{\lambda}(t) = \lambda_0 \times e^{\frac{\alpha}{T(t)}}$

Condamine et al. Eco Lett 2019

Speciation rates often vary with temperature

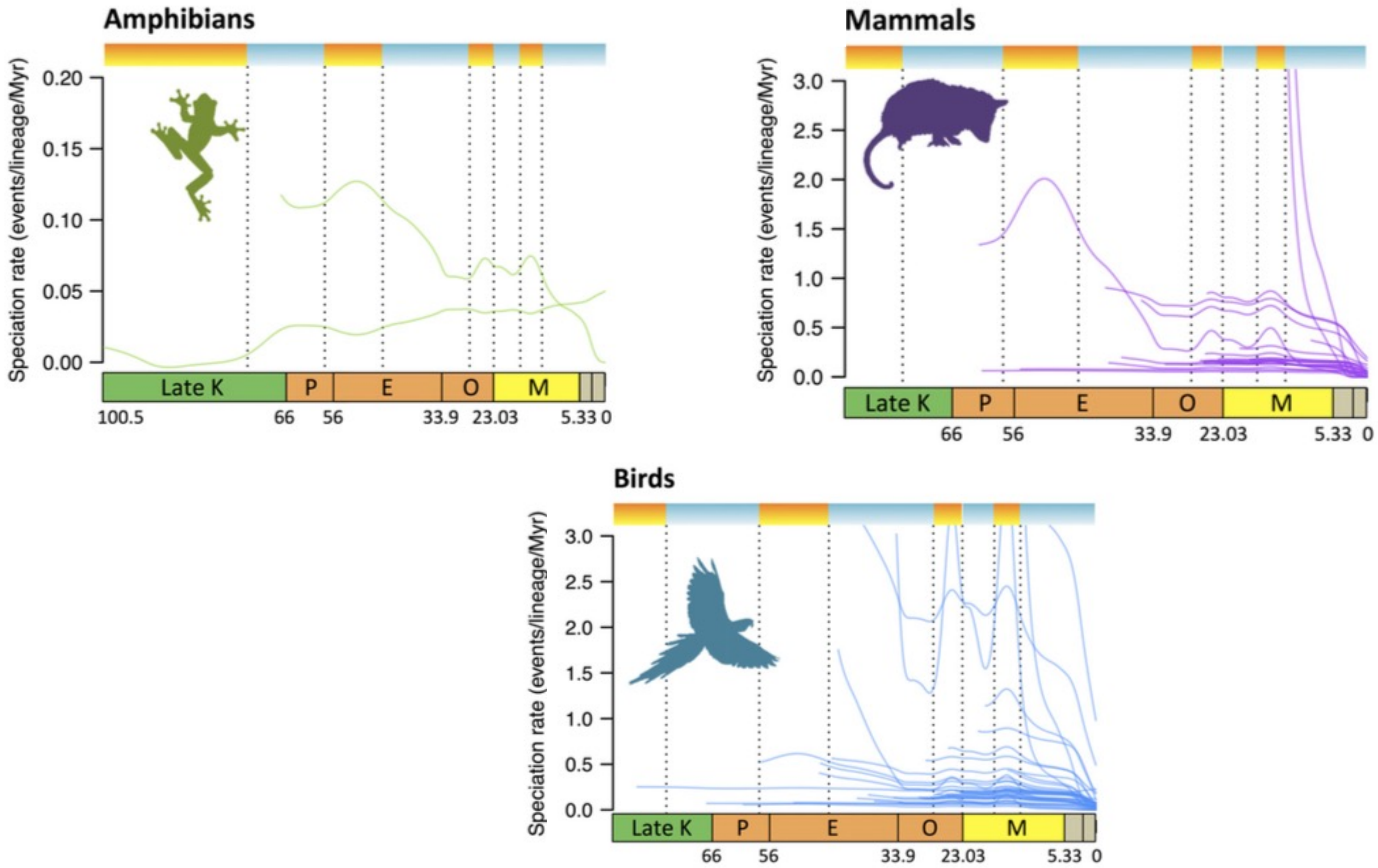


Speciation rates are higher during warm geological periods



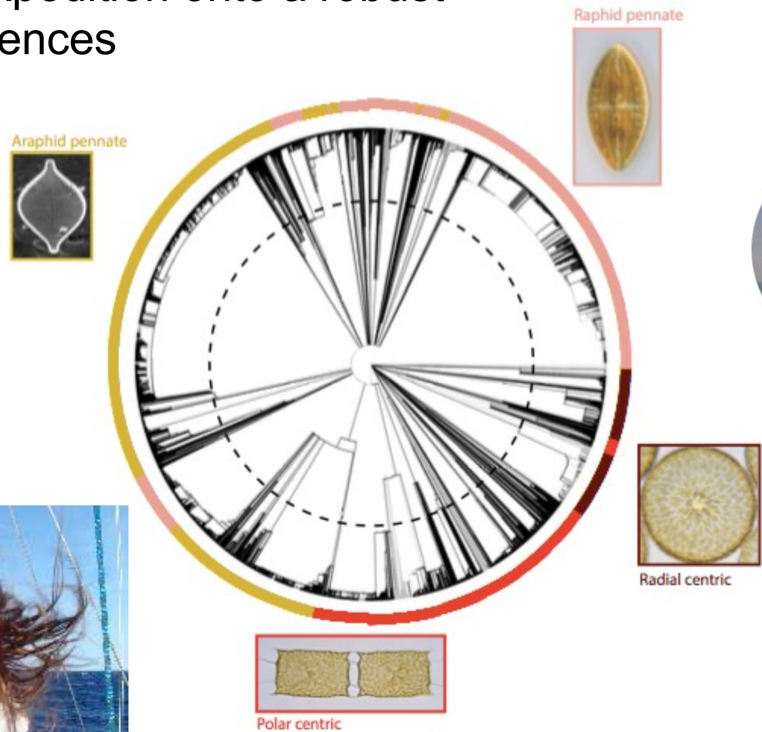
Condamine et al. Eco Lett 2019

Climate cooling during the Cenozoic results in a slowdown in diversification



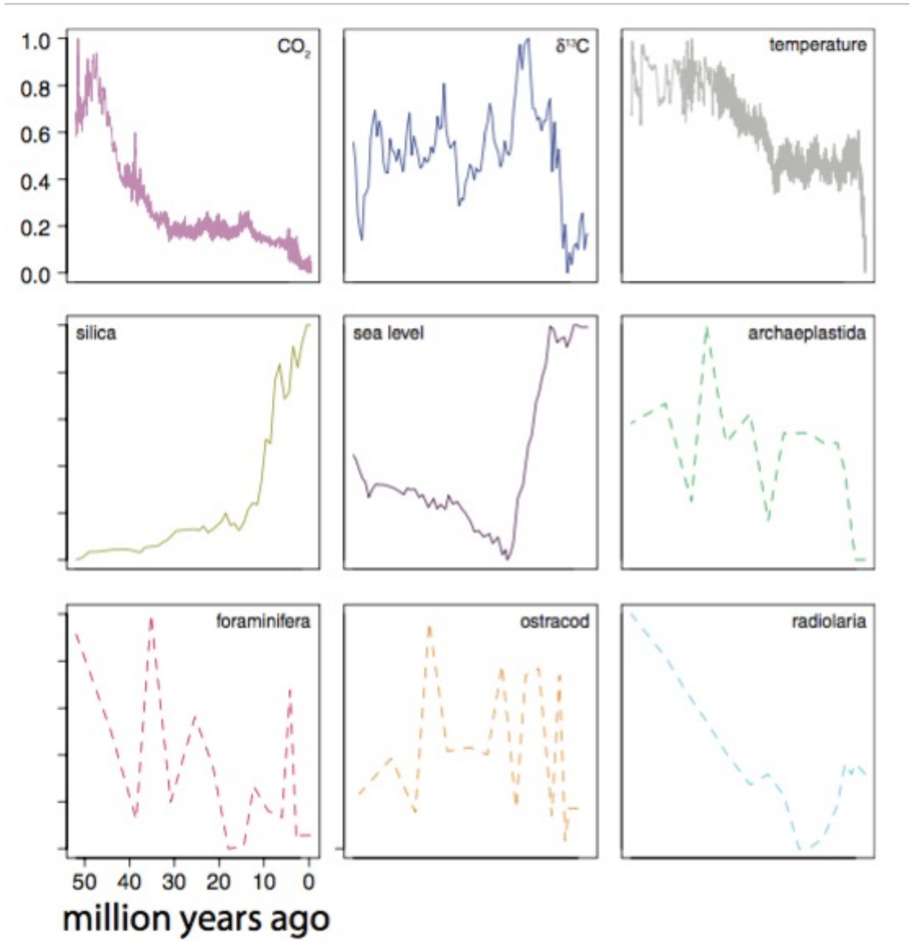
What are the environmental factors that shaped the diversification of diatoms?

« Thoroughly » sampled phylogeny of diatoms (~20,000 OTUs) obtained by grafting metabarcoding data from the *Tara* oceans expedition onto a robust phylogeny of reference sequences



Lewitus *et al.* Nature Ecol Evol 2018

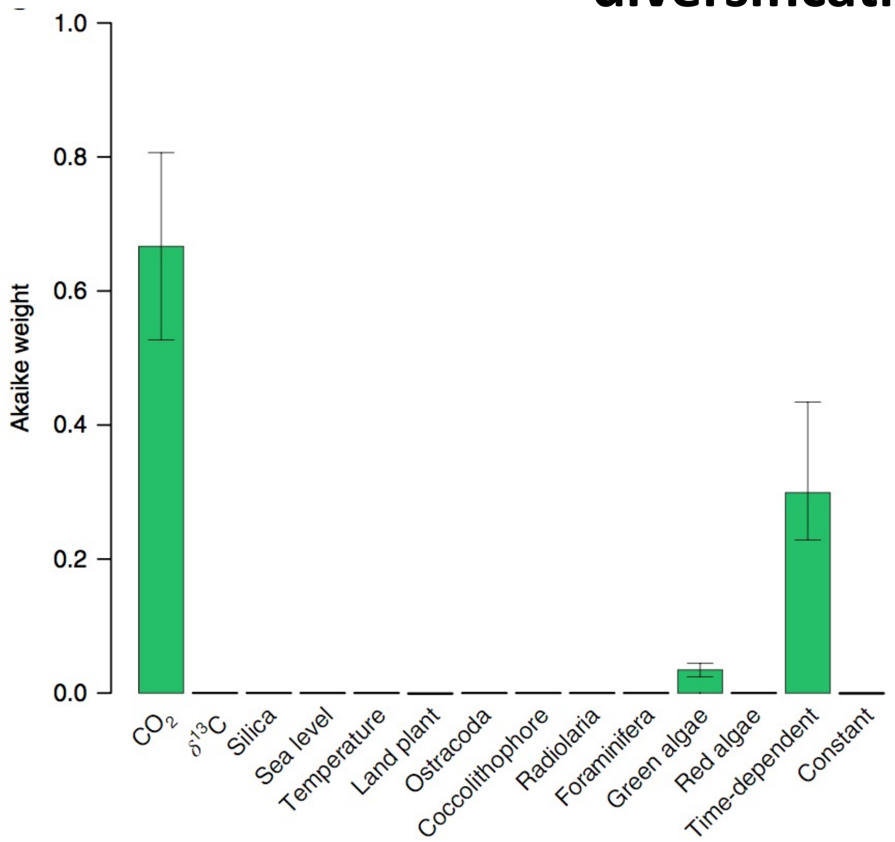
How did past environmental conditions shape the diversification of diatoms?

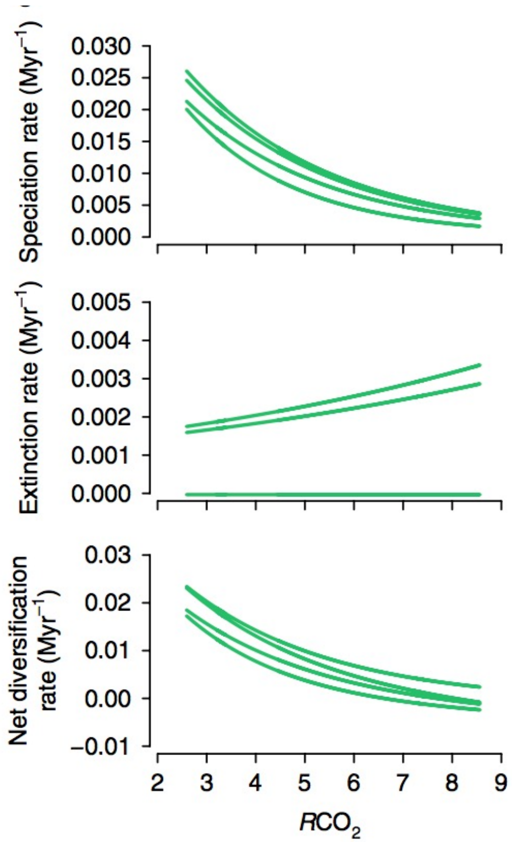


5 abiotic and 4 biotic variables

Lewitus *et al.* Nature Ecol Evol 2018

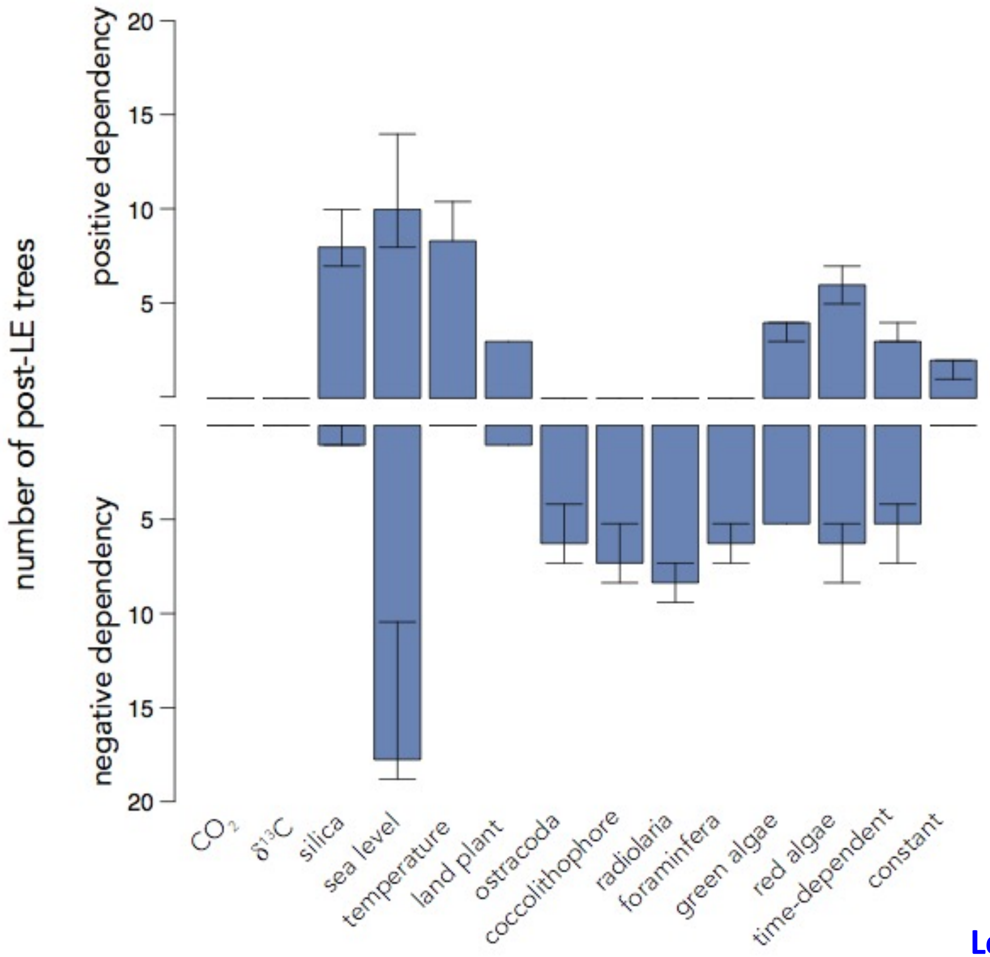
Pre-LE, pCO_2 is the most important driver, with a positive relationship between decreasing CO_2 and diatoms diversification





Lewitus *et al.* Nature Ecol Evol 2018

Post-LE, distinct diatom clades are influenced by different environmental factors, and not necessarily in the same way



50% of the clades influenced primarily by biotic factors

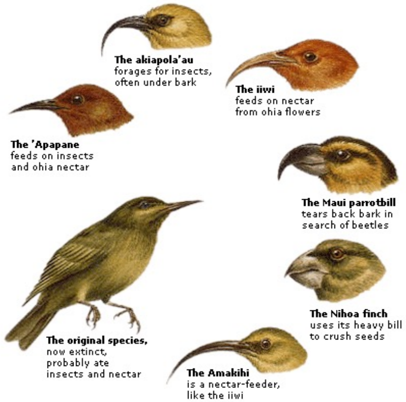
40% of the clades influenced primarily by abiotic factors

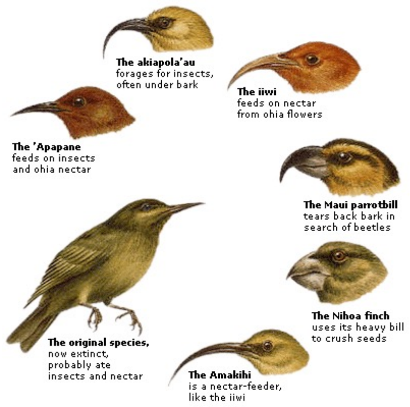
10% of the clades influenced by factors not measured here

Lewitus *et al.* Nature Ecol Evol 2018

Biotic factors, such as competition and mutualistic or antagonistic interactions, can influence speciation and extinction rates

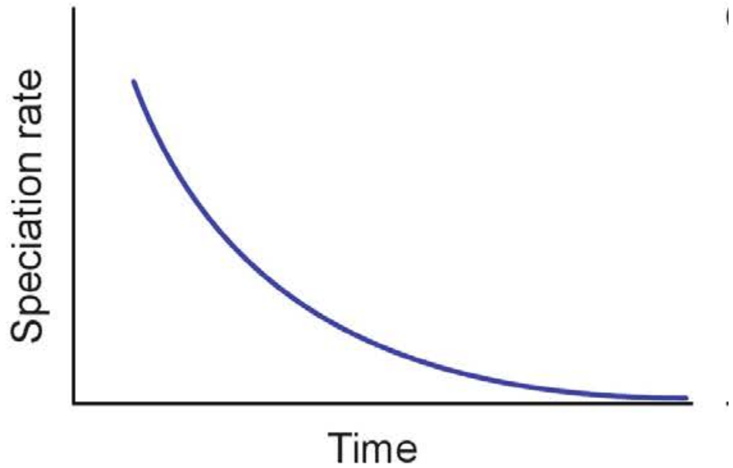
The Red Queen

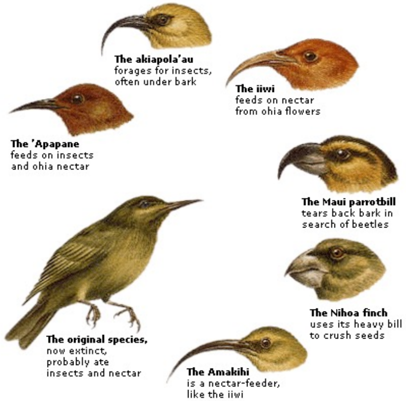




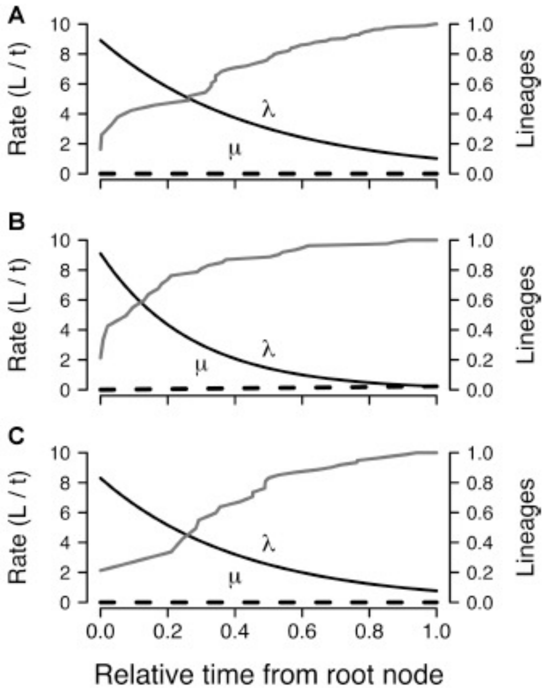
In verbal evolutionary theories, such as the theory of adaptive radiations, interspecific competition is thought to induce fast speciation followed by a diversification slowdown as species fill ecological niche space

Simpson 1953
Harmon et al. Science 2003

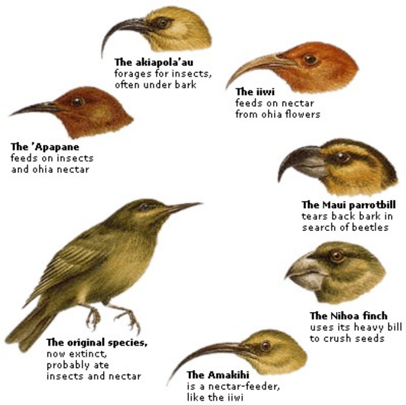




The effect of competition has been tested by testing the support for models with declining speciation rates ("early burst" models)



Rabosky & Lovette Evolution 2008



The effect of competition has also been tested by testing the support for models with diversity-dependent diversification

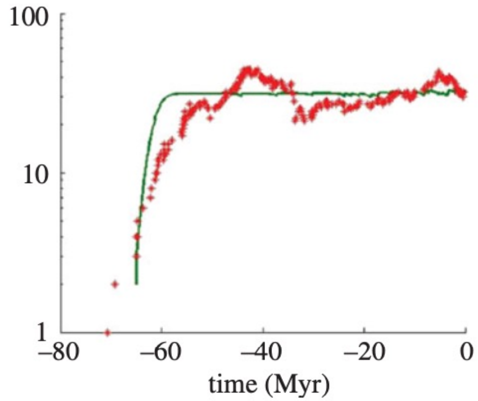
PROCEEDINGS OF THE ROYAL SOCIETY B

Proc. R. Soc. B (2012) **279**, 1300–1309
doi:10.1098/rspb.2011.1439
Published online 12 October 2011

Diversity-dependence brings molecular phylogenies closer to agreement with the fossil record

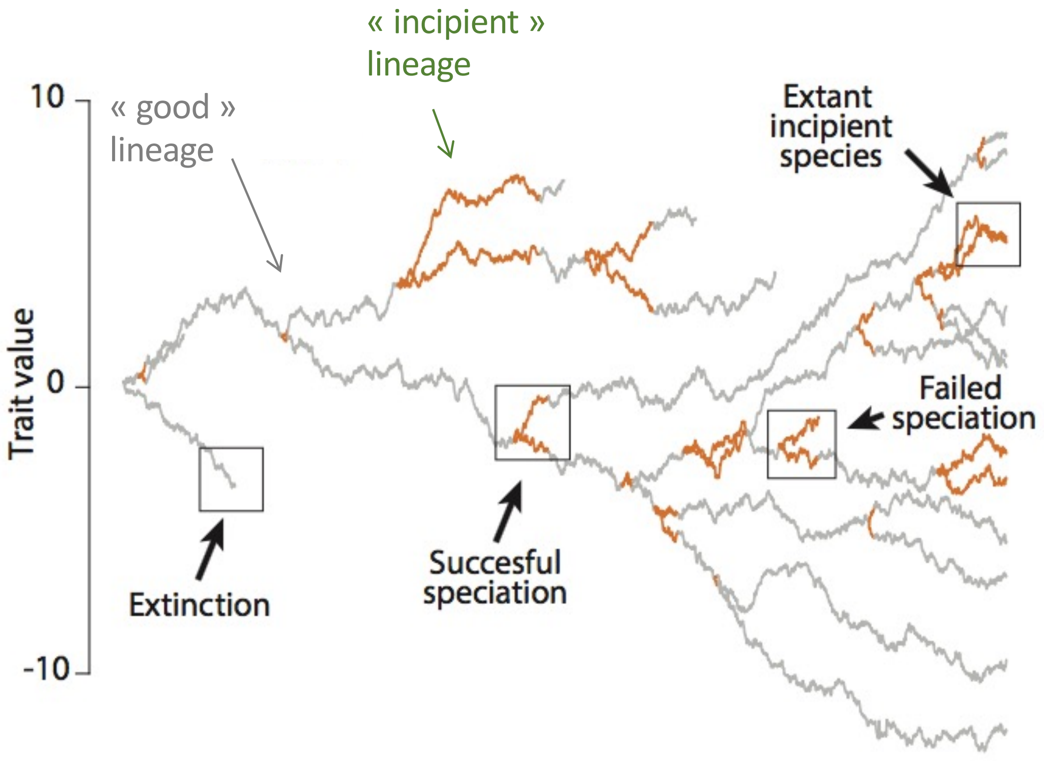
Rampal S. Etienne[1,*], Bart Haegeman[2], Tanja Stadler[3], Tracy Aze[4], Paul N. Pearson[4], Andy Purvis[5] and Albert B. Phillimore[5]

[1]*Community and Conservation Ecology, Centre for Ecological and Evolutionary Studies,*



Etienne *et al.* PRSB 2012

Beyond verbal expectations:
a simulation model to assess under which conditions we can actually expect competition to generate a slowdown in diversification rates



Aristide & Morlon Eco Lett 2019

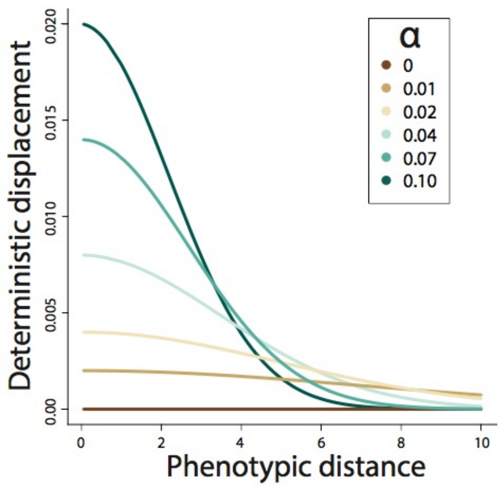
The matching competition birth-death model (MCBD)

1. Competition drives character displacement

$$x_i(t+dt) = x_i(t) + m\alpha\left[\sum_{j\neq i}^{n} sign\left(x_i(t)-x_j(t)\right)\times e^{-\alpha\left(x_i(t)-x_j(t)\right)^2}\right]dt + \delta$$

trait value lineage i

stochastic displacement



Aristide & Morlon Eco Lett 2019

The matching competition birth-death model (MCBD)

2. Character displacement speeds up speciation

Protracted speciation model **Etienne & Rosindell Syst Bio 2012**

Speciation initiation: rate $\boldsymbol{\lambda}_1$

Speciation completion: rate $\boldsymbol{\lambda}_2$

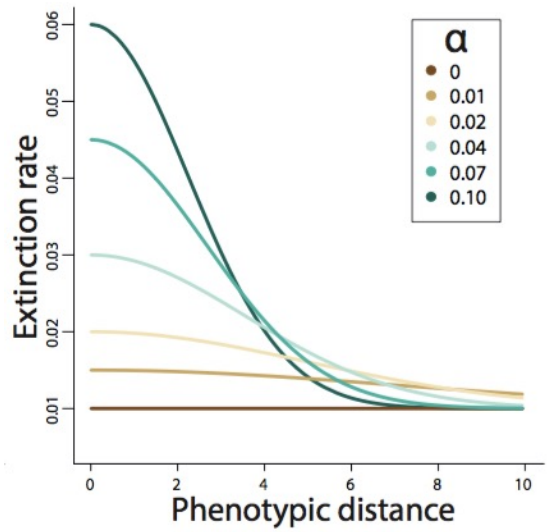
$$\lambda_{2i}(t) = \tau_0 e^{\beta\left(x_j(t) - x_k(t)\right)^2}$$

Aristide & Morlon Eco Lett 2019

The matching competition birth-death model (MCBD)

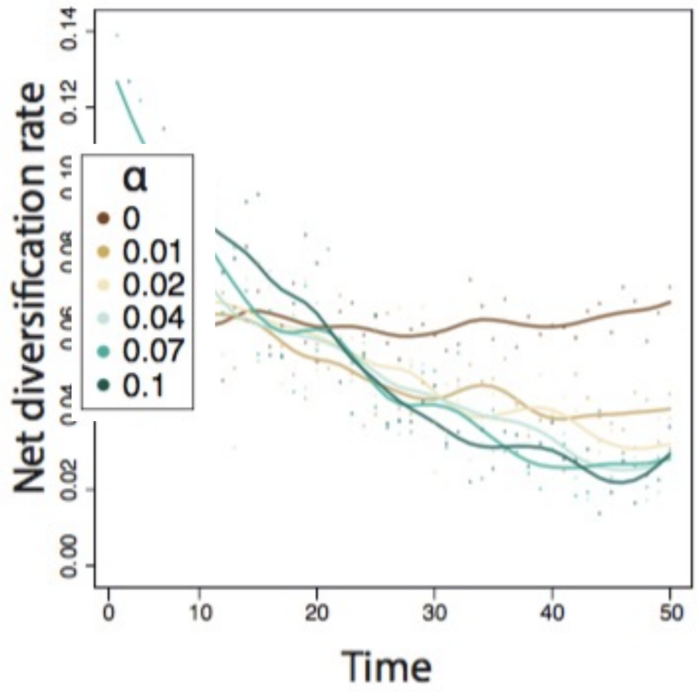
3. Phenotypically similar species experience competitive exclusion

$$\mu_i = \alpha\mu_0 e^{-\alpha(\sum_{j\neq i}(x_i(t)-x_j(t))^2)} + \mu_{bg}$$



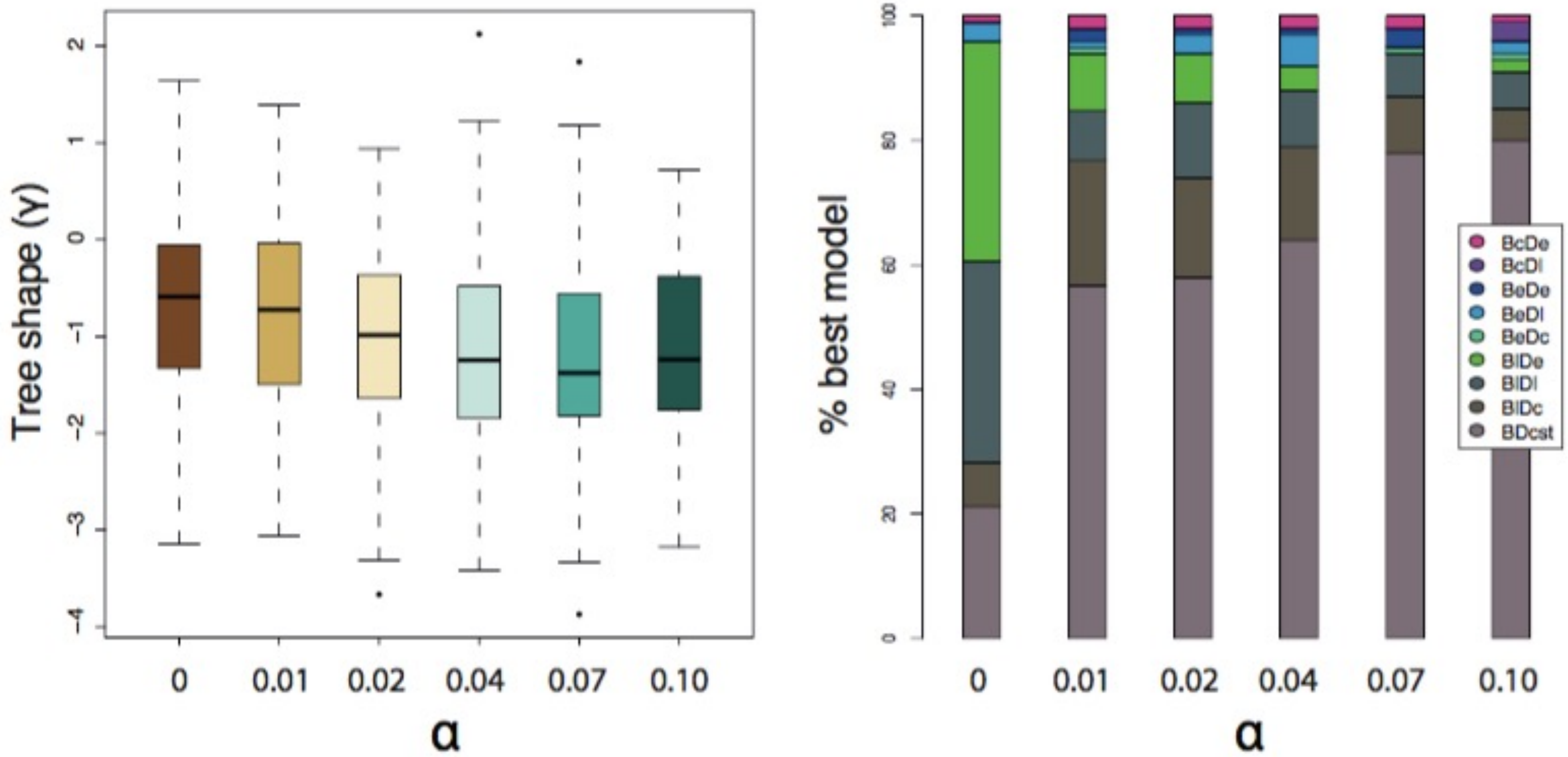
Aristide & Morlon Eco Lett 2019

Competition produces declines in diversification rates, even if trait space is unbounded



Aristide & Morlon Eco Lett 2019

Declines in diversification rates do not leave a clear signal in reconstructed phylogenetic trees, at least not as detected by currently available models



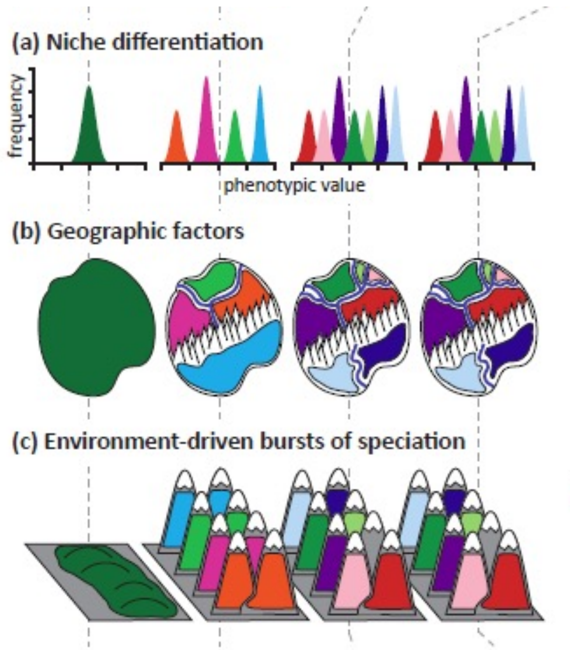
Aristide & Morlon Eco Lett 2019

Opinion

CellPress

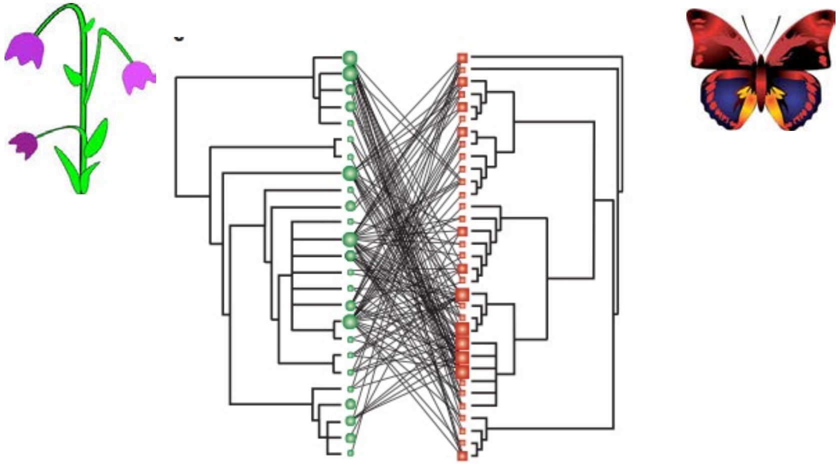
Why does diversification slow down?

Daniel Moen and Hélène Morlon



Trends Ecol Evol 2014

Verbal evolutionary theories on the effect of mutualistic and antagonistic interactions on diversification rates remain poorly tested



Robustly testing such theories would require modeling the eco-evolutionary emergence of interaction networks and building associated inference tools to fit them to empirical data

REVIEW

Journal of Evolutionary Biology WILEY

Detecting the macroevolutionary signal of species interactions

Luke J. Harmon[1,2] | Cecilia S. Andreazzi[3] | Florence Débarre[4] | Jonathan Drury[5] | Emma E. Goldberg[6] | Ayana B. Martins[1,7] | Carlos J. Melián[1] | Anita Narwani[8] | Scott L. Nuismer[2] | Matthew W. Pennell[9] | Seth M. Rudman[10] | Ole Seehausen[1,11] | Daniele Silvestro[12] | Marjorie Weber[13] | Blake Matthews[1,14]

JEB 2018

Annual Review of Ecology, Evolution, and Systematics

Ecological Interactions and Macroevolution: A New Field with Old Roots

David H. Hembry[1,2] and Marjorie G. Weber[3]

Review

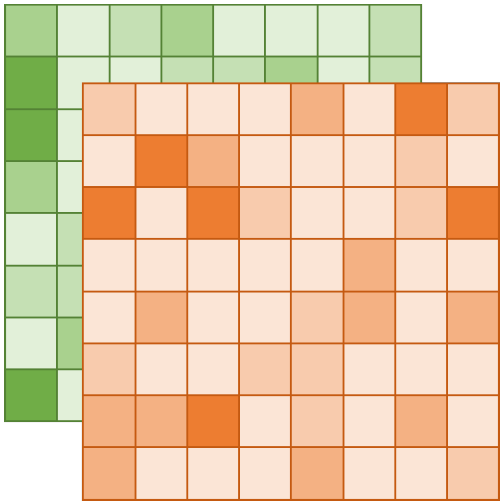
TREE 2017

Evolution in a Community Context: On Integrating Ecological Interactions and Macroevolution

Marjorie G. Weber,[1,*] Catherine E. Wagner,[2]
Rebecca J. Best,[3,4] Luke J. Harmon,[3,5] and Blake Matthews[3]

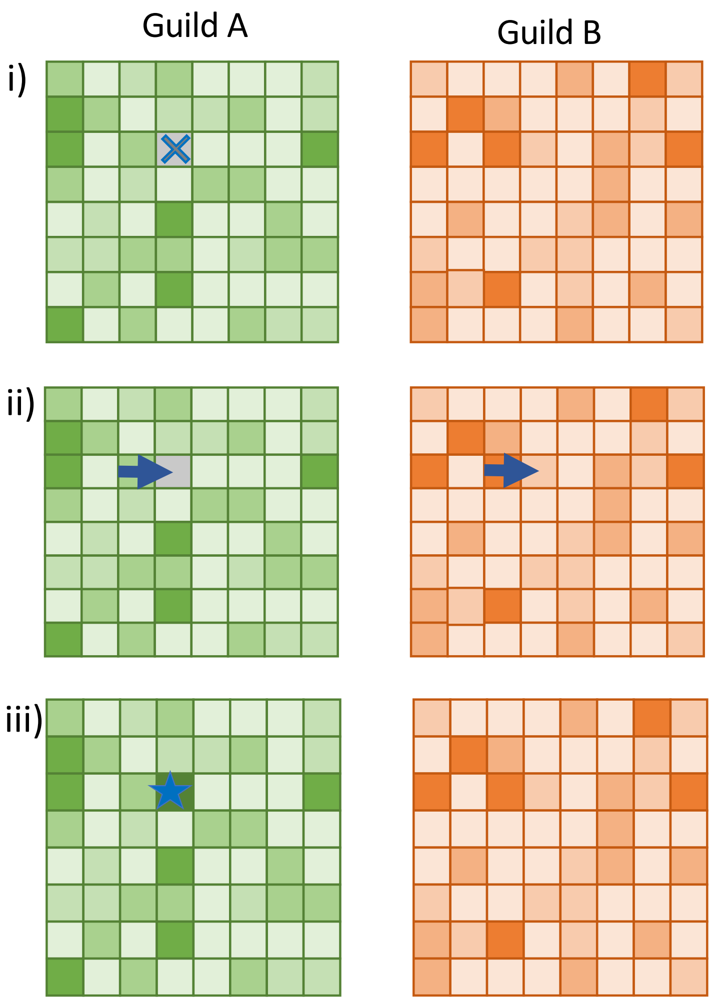
BipartiteEvol: An individual based model for the eco-evolutionary emergence of bipartite interaction networks

Individuals from 2 guilds A and B and characterized by a 3-dimensional trait evolve on a fixed grid



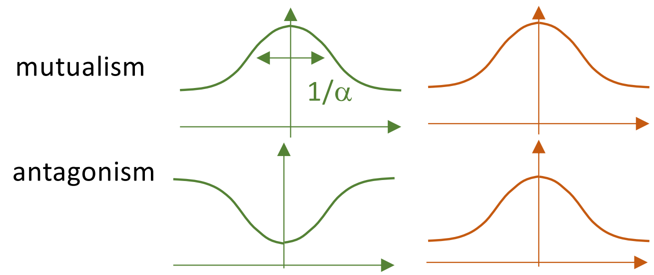
Maliet et al. *Ecology Letters* 2020

An individual based model for the eco-evolutionary emergence of bipartite interaction networks



1 individual in guild A die at random

the replacing individual is the child from a parent drawn in A according to its fitness, which depends on its trait value and that of the interacting individual from B (trait matching)

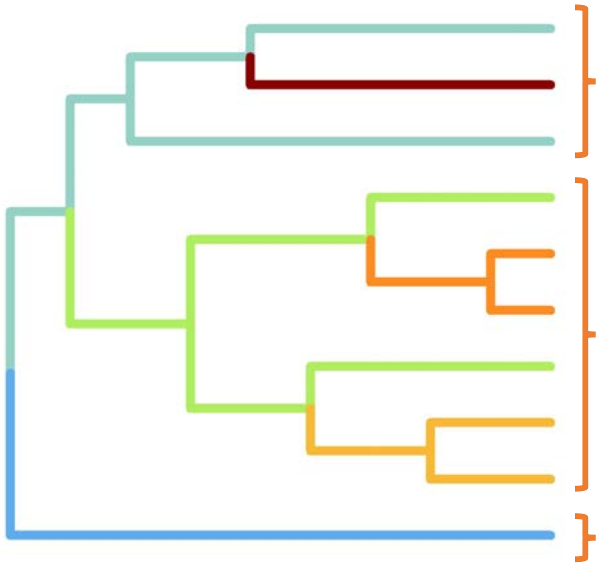


the child can experience a mutation that generates a gaussian trait variation

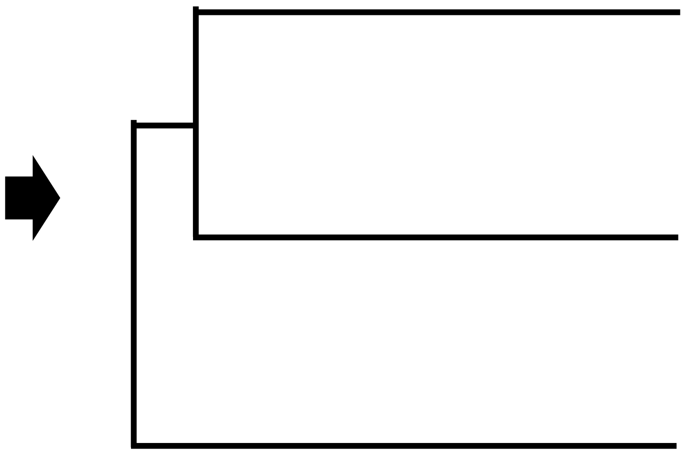
REPEAT WITH GUILD B, AND REPEAT FOR MANY GENERATIONS

An individual based model for the eco-evolutionary emergence of bipartite interaction networks

We define species as "the smallest monophyletic group of individuals such that two individuals from different species are separated by at least s mutations"



Genealogy of individuals

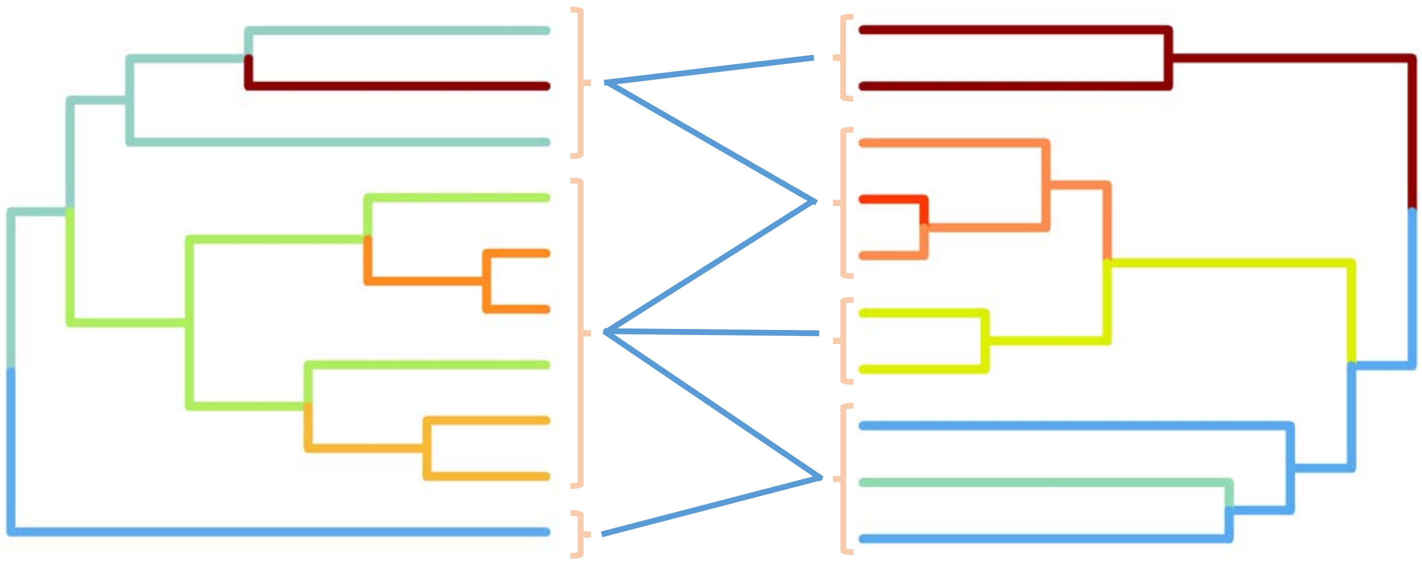


Species phylogeny

Manceau et al. Eco Lett 2015
Rosindell et al. Eco Lett 2015

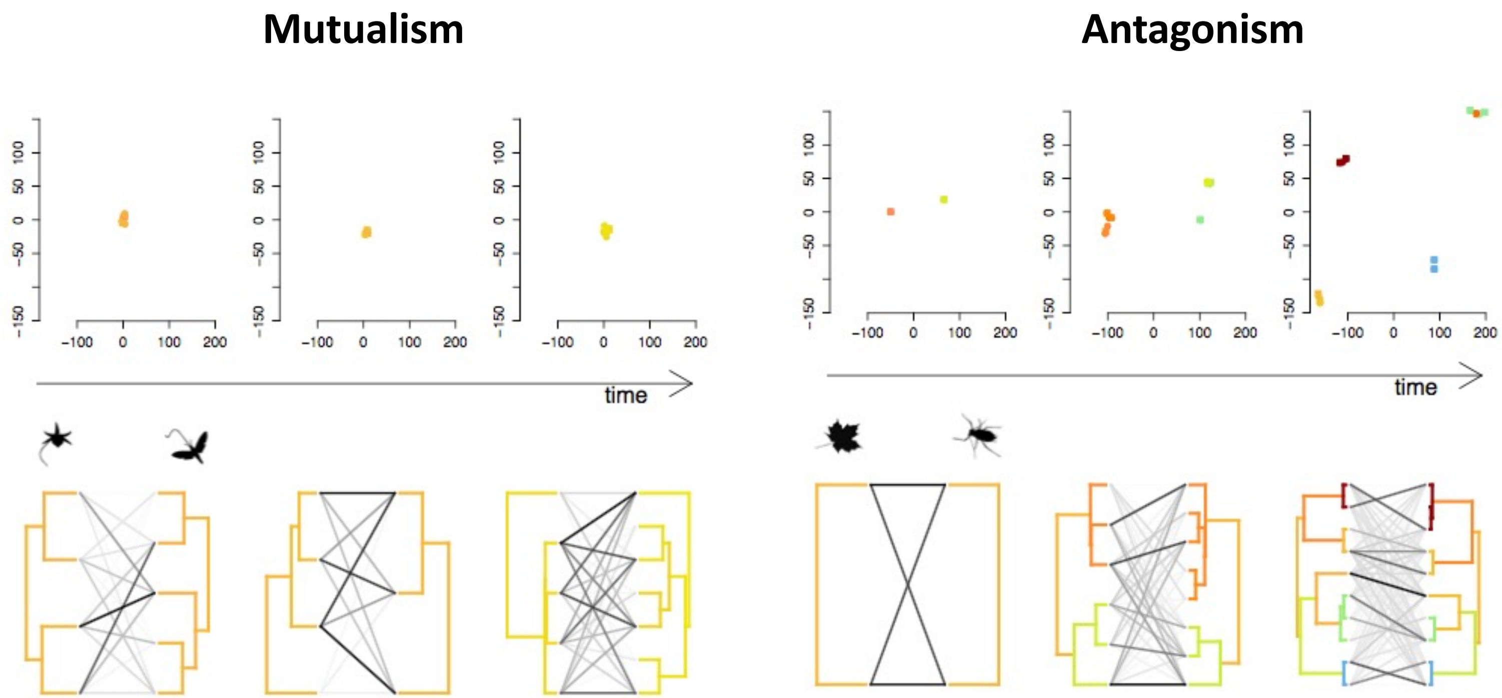
An individual based model for the eco-evolutionary emergence of bipartite interaction networks

Two individuals interact if they are on the same grid cell
Two species interact if at least one individual from each species interact



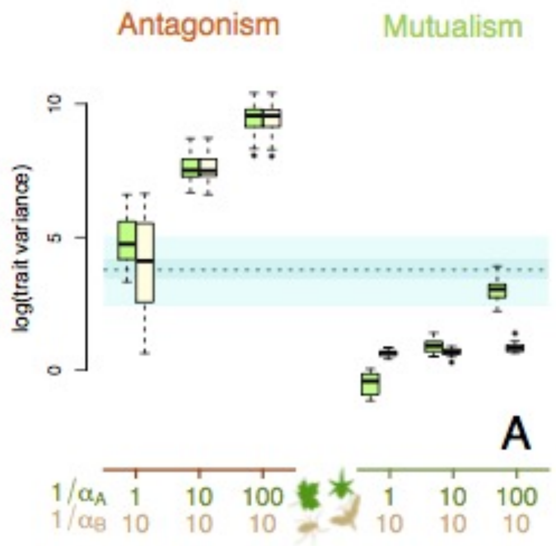
Maliet et al. *Ecology Letters* 2020

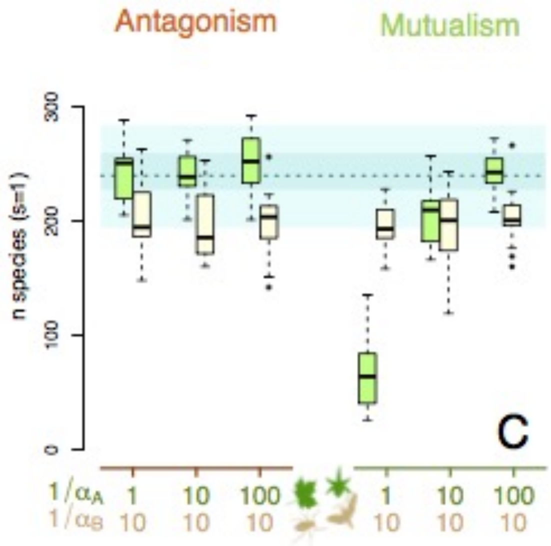
Mutualist and antagonist interactions lead to very different eco-evolutionary dynamics



Maliet et al. *Ecology Letters* 2020

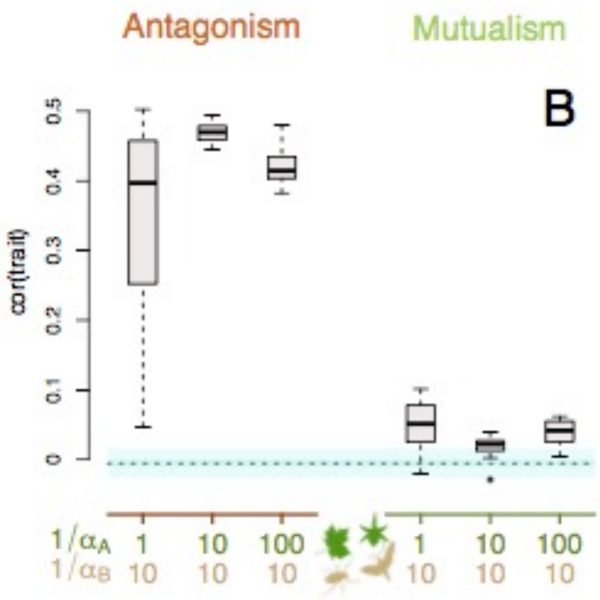
Antagonism fosters, while mutualism impedes, trait and species diversity





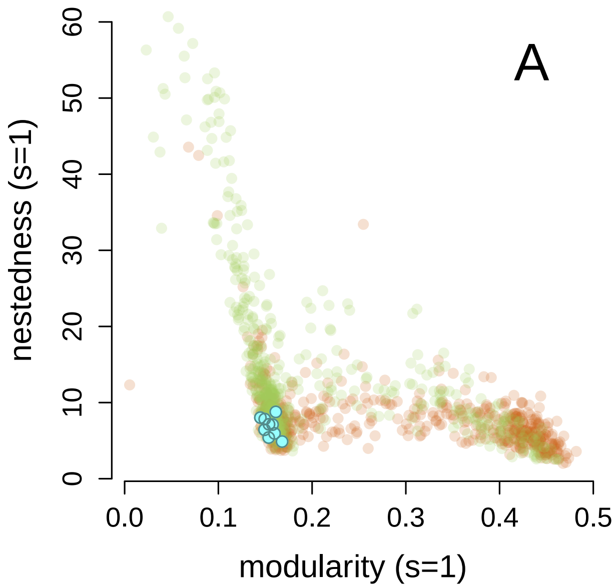
Maliet et al. *Ecology Letters* 2020

Co-evolution occurs in antagonistic, but not mutualistic networks

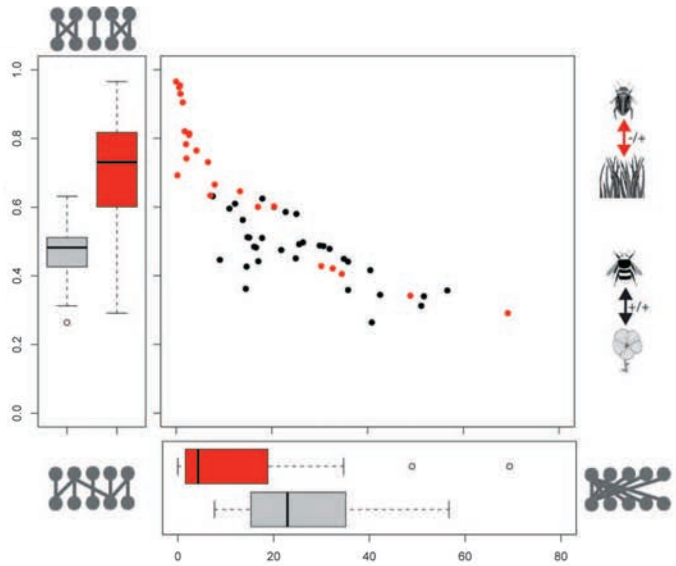


Maliet et al. *Ecology Letters* 2020

Mutualistic networks are nested, while antagonistic networks are modular, as observed in empirical communities



Maliet et al. *Ecology Letters* 2020



Thébault and Fontaine Science 2010

We did not yet develop the statistical tools to fit BipartiteEvol to empirical data

What are the factors that modulate speciation & extinction rates?

The Court Jester

The Red Queen

EXTRINSIC

INTRINSIC

Abiotic factors
climatic variation
geological context

Biotic factors
competition
mutualistic and antagonistic interactions

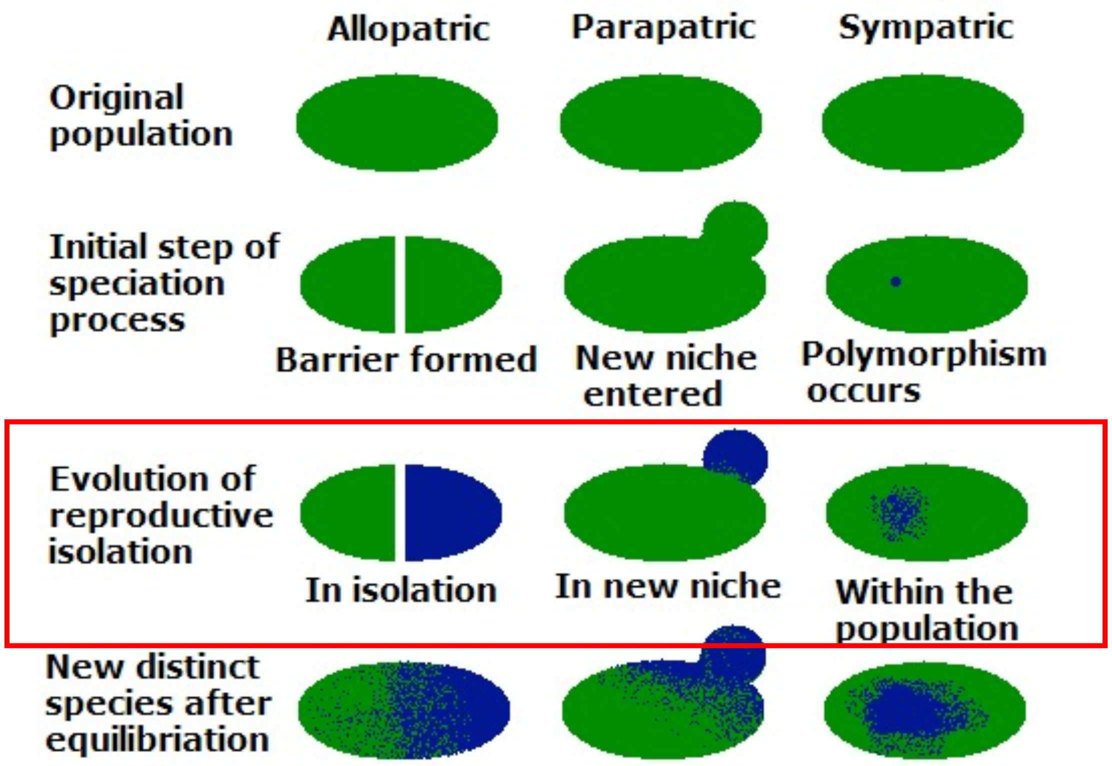
Species-specific traits
reproduction mode
life-history traits
dispersal capacity

By which processes do various factors modulate speciation and extinction rates?

Abiotic and biotic factors, in combination with species-specific traits, influence extinction rates by their effects on demography

By which processes do various factors modulate speciation and extinction rates?

Abiotic and biotic factors, in combination with species-specific traits, must influence speciation rates by somehow influencing the speciation process



Mixed support for an association between reproductive isolation and speciation rates

Macroevolutionary speciation rates are decoupled from the evolution of intrinsic reproductive isolation in *Drosophila* and birds

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

updates

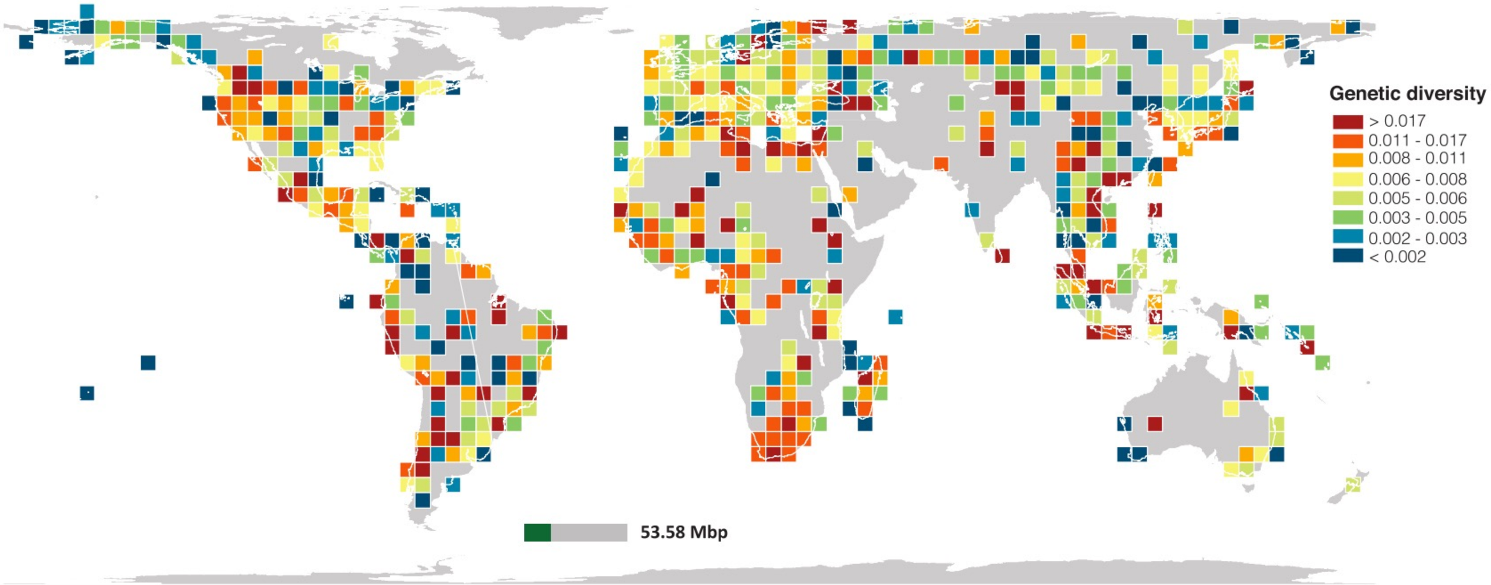
Positive association between population genetic differentiation and speciation rates in New World birds

Michael G. Harvey[a,b,c,d,1], Glenn F. Seeholzer[a,b], Brian Tilston Smith[a,b,e], Daniel L. Rabosky[c,d], Andrés M. Cuervo[a,b,f], and Robb T. Brumfield[a,b]

No link between population isolation and speciation rate in squamate reptiles

Sonal Singhal[a,1], Guarino R. Colli[b], Maggie R. Grundler[c,d], Gabriel C. Costa[e], Ivan Prates[f,g], and Daniel L. Rabosky[f,g,1]

Are genetic diversity and speciation rates coupled in mammals?



Silva et al. in prep.

Are genetic diversity and diversification rates coupled?

Supply of genetic variation

Reproductive isolation

Geographic structure

Genetic diversity → **Speciation**

Under geographic and ecological models of speciation, we expect a positive association between genetic diversity and speciation rate

Testing the impact of effective population size on speciation rates – a negative correlation or lack thereof in lichenized fungi

Jen-Pan Huang[1], Steven D. Leavitt[2] & H. Thorsten Lumbsch[1]

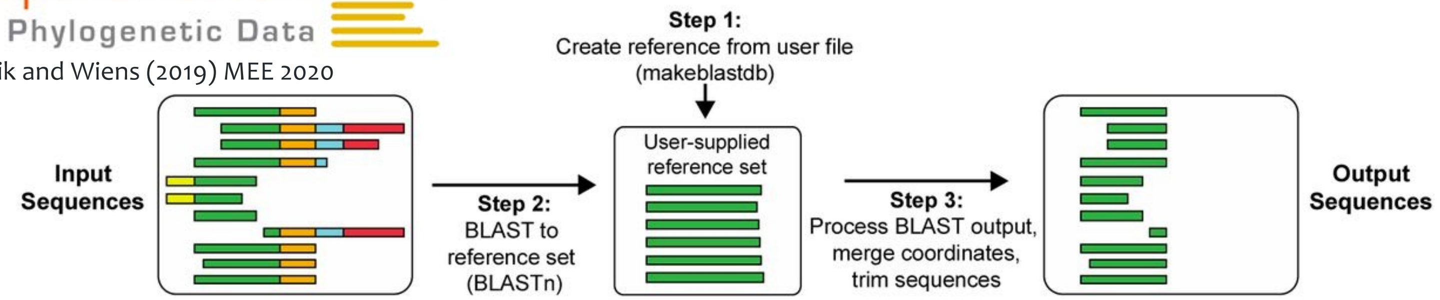
Estimating intraspecific genetic diversity

GenBank "Mammalia"[Organism] AND CYTB NOT "Homo sapiens"[Organism]

124,289 sequences of mammals Cytochrome b

Split into 138 families for better alignments

SuperCRUNCH
For Phylogenetic Data
Portik and Wiens (2019) MEE 2020

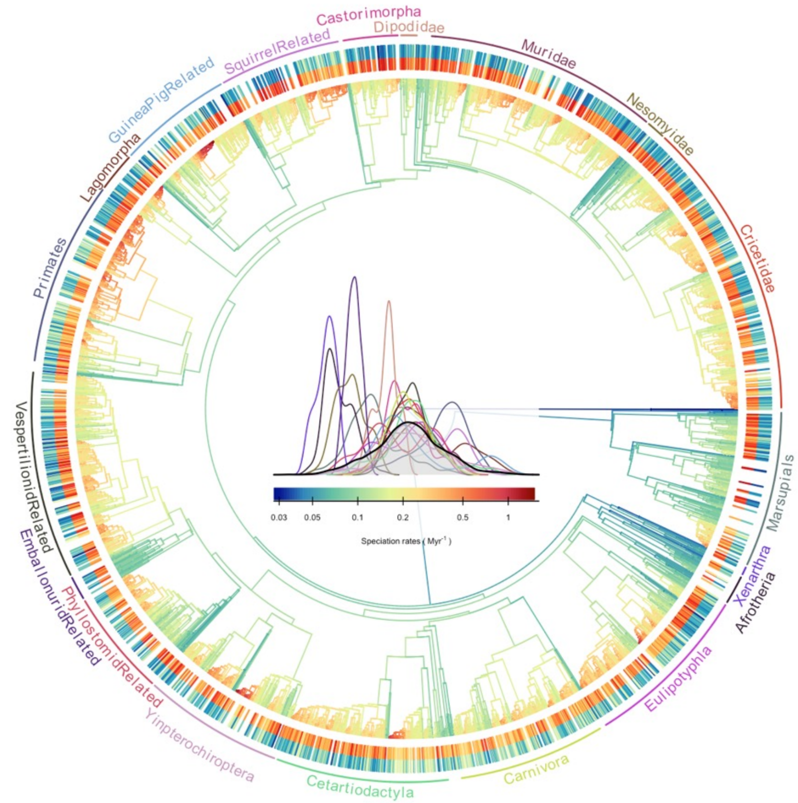


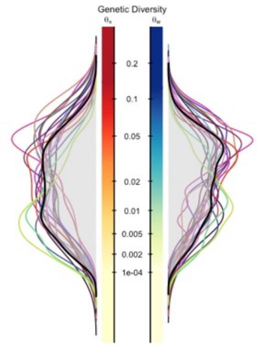
3899 species → 2004 species with at least 5 individuals → genetic diversity

Silva et al. in prep.

Estimating branch-specific speciation rates

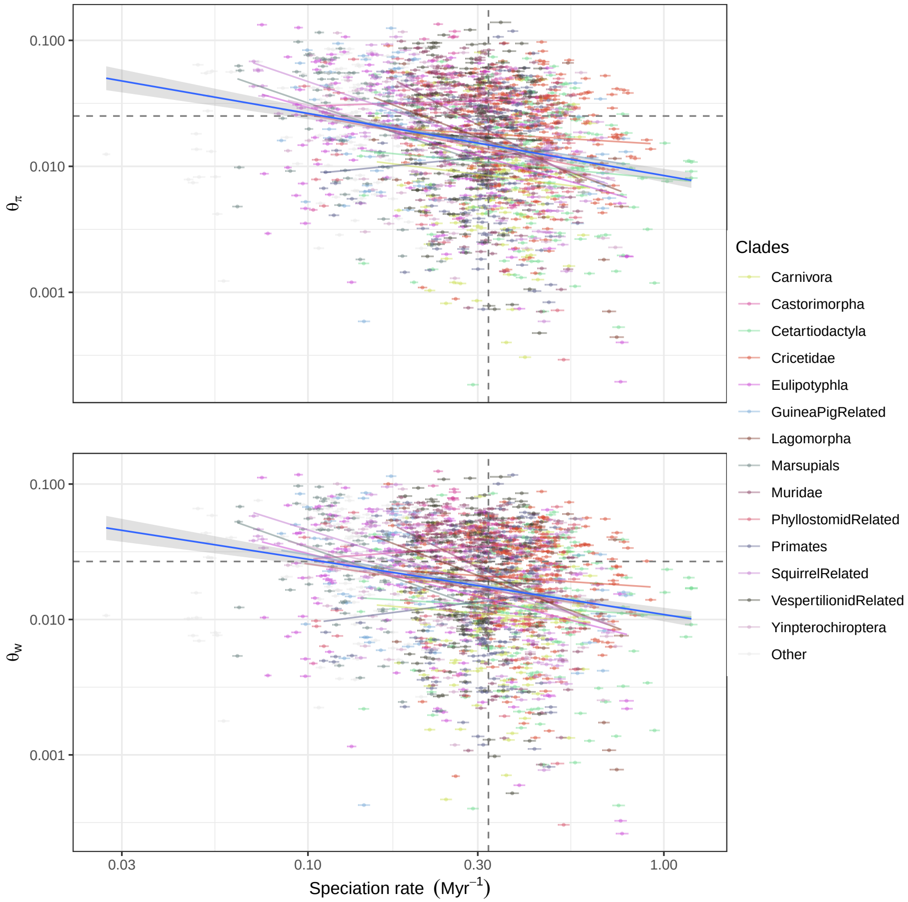
- ClaDS estimates on Upham's PLoS Biology 2019 mammals phylogeny

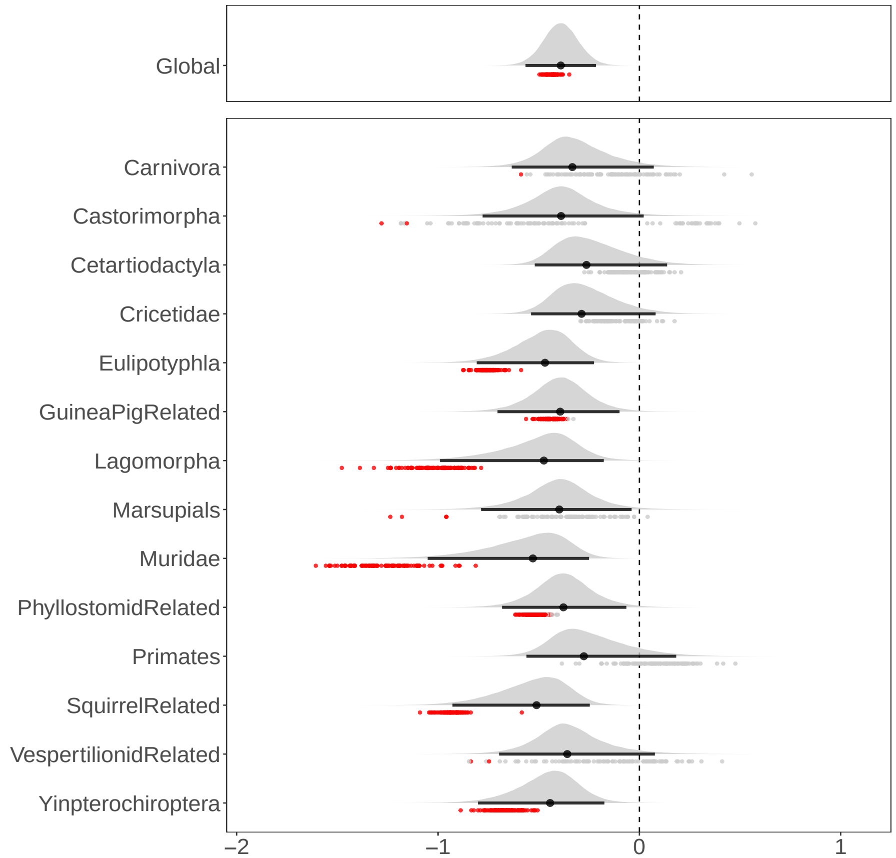




Silva et al. in prep.

Negative correlation between genetic diversity and speciation rates





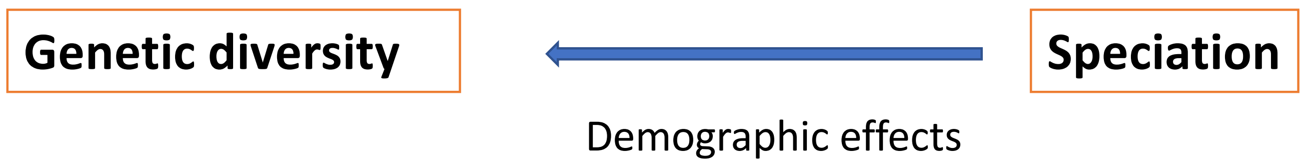
Silva et al. in prep.

The negative correlation between genetic diversity and speciation rates is not linked to an indirect effect of life history traits

	θ_π ~ Traits				λ ~ Traits				θ_π ~ λ + Traits			
	PGLS		BLML		PGLS		BLML		PGLS		BLML	
Term	Estimate	SE	Estimate	95% CI	Estimate	SE	Estimate	95% CI	Estimate	SE	Estimate	95% CI
λ									**-0.264**	0.077	-0.266	[-0.408; -0.107]
Body Mass	**-0.145**	0.026	-0.147	[-0.202; -0.095]	0.007	0.010	0.007	[-0.012; 0.025]	**-0.139**	0.025	-0.143	[-0.198; -0.09]
Range area	**0.137**	0.014	0.137	[0.109; 0.166]	-0.005	0.003	-0.005	[-0.011; 0]	**0.131**	0.015	0.131	[0.103; 0.159]
Range mean temperature	**0.330**	0.087	0.329	[0.167; 0.501]	-0.021	0.018	-0.021	[-0.057; 0.014]	**0.307**	0.087	0.307	[0.125; 0.475]
Litter size	**-0.420**	0.091	-0.420	[-0.609; -0.231]	0.051	0.028	0.050	[-0.004; 0.105]	**-0.400**	0.089	-0.406	[-0.581; -0.234]
Generation length	-0.074	0.105	-0.072	[-0.266; 0.139]	-0.008	0.030	-0.010	[-0.067; 0.049]	-0.084	0.102	-0.082	[-0.283; 0.129]

Silva et al. in prep.

What might explain the negative association between genetic diversity speciation rate?



Hypothesis 1: Speciation exerts a limit on species genetic diversity rather than the other way round

Rapid speciation limits the accumulation of genetic diversity

What might explain the negative association between genetic diversity and speciation rate?

Geographic structure

Reproductive isolation

Genetic diversity → **Speciation**

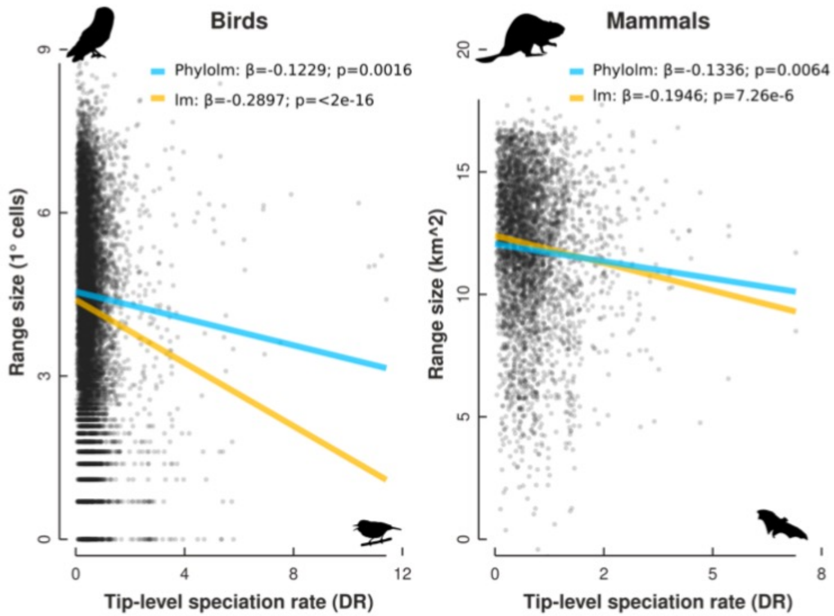
Hypothesis 2: Species that are highly geographically structured and with reproductively isolated populations indeed experience more frequent speciation events, but genetic diversity is inversely rather than positively correlated to geographic structure (Withlock 2004)

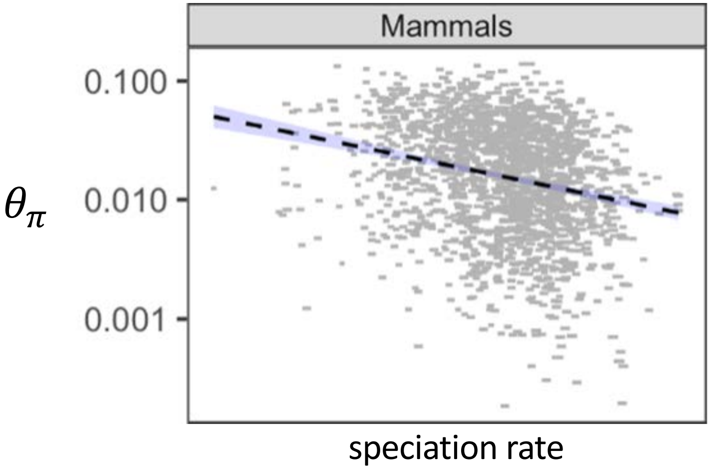
What might explain the negative association between genetic diversity and speciation rate?

Demographic effects

Genetic diversity → **Speciation**

Hypothesis 3: Under the demographic model of speciation, species with small rather than large effective population sizes accumulate reproductive incompatibilities faster because of a reduced efficiency of purifying selection (Maya-Lastra & Eaton 2021)





What might explain the negative association between genetic diversity and speciation rate?

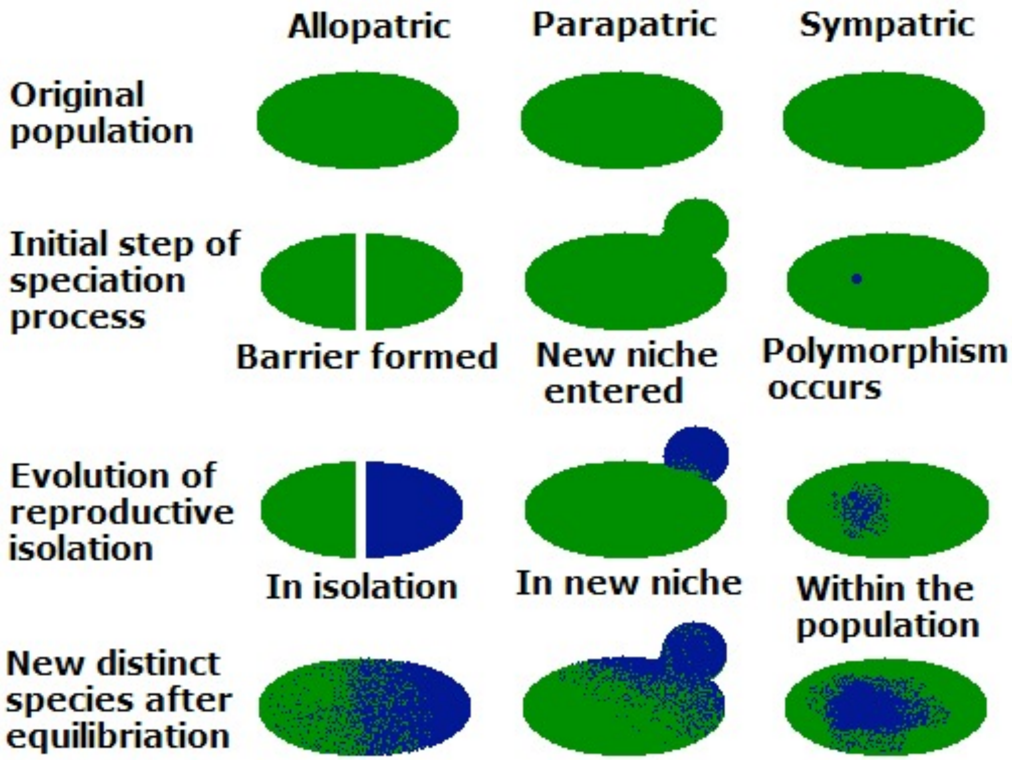
Hypothesis 1: Speciation exerts a limit on species genetic diversity rather than the other way round

Hypothesis 2: Genetic diversity is inversely rather than positively correlated to population isolation

Hypothesis 3: Species with small rather than large effective population sizes accumulate reproductive incompatibilities faster

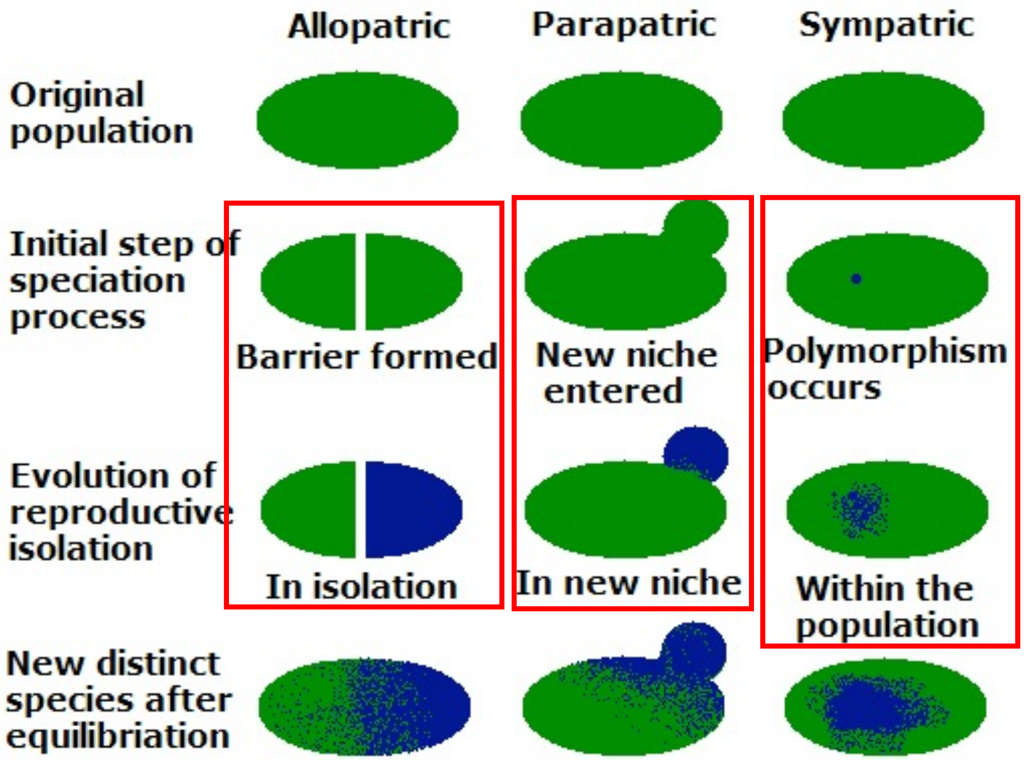
Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

At which stage of the speciation cycle are we measuring genetic diversity (or genetic differentiation, or population isolation)?



Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

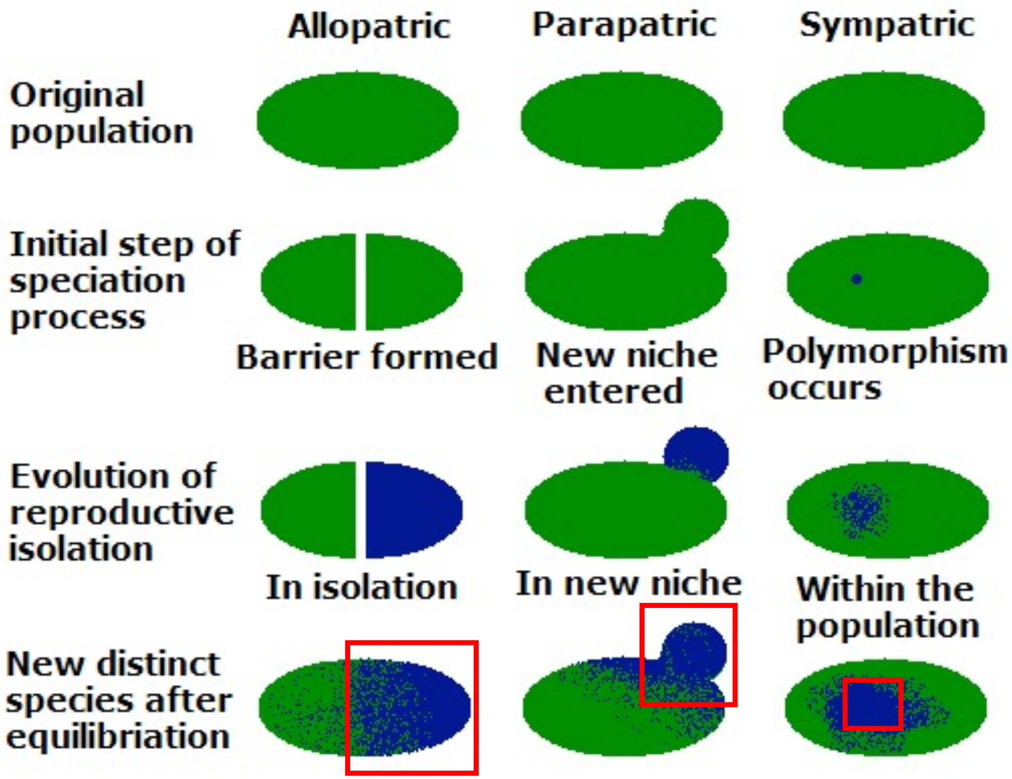
At which stage of the speciation cycle are we measuring genetic diversity (or genetic differentiation, or population isolation)?



High genetic diversity in the initial steps of speciation

Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

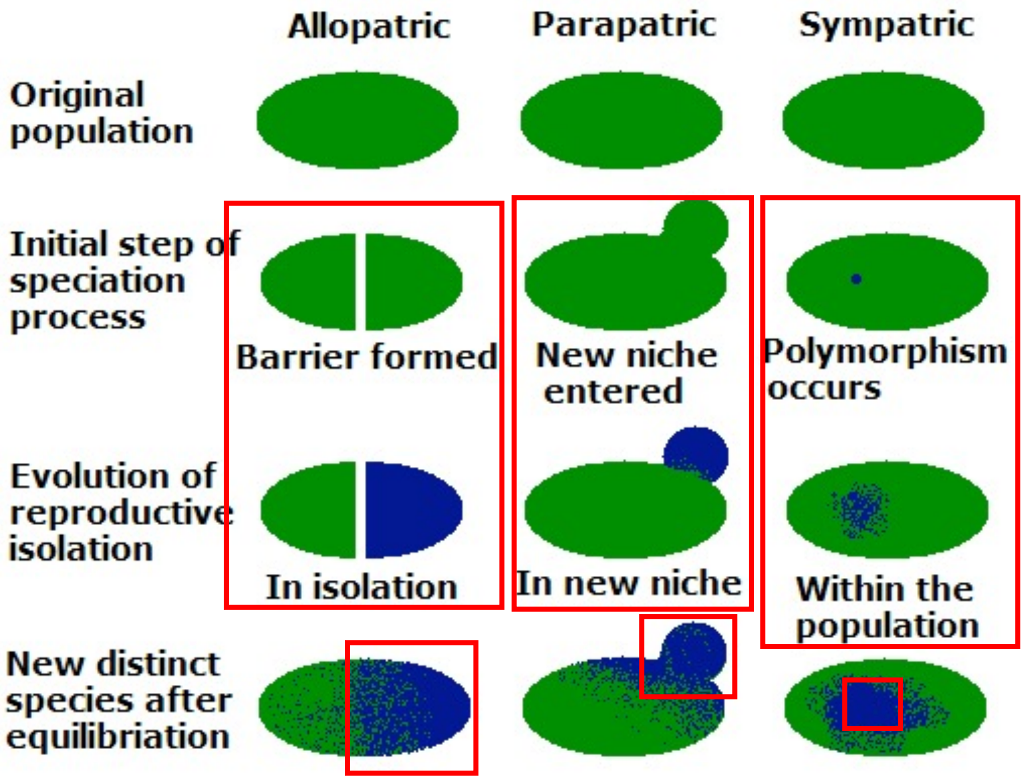
At which stage of the speciation cycle are we measuring genetic diversity (or genetic differentiation, or population isolation)?



Low genetic diversity in newly formed species

Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

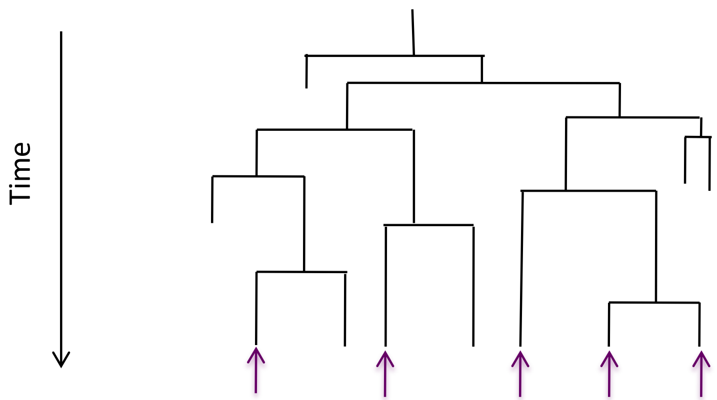
The reciprocal effect of speciation on microevolutionary (intraspecific) measures of differentiation complicates the interpretation of correlations



Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

What are we actually measuring when we measure speciation rate using comparative methods?

Stochastic birth-death process
speciation rate λ
extinction rate μ



Speciation is considered to be an instantaneous event by which two populations of the same ancestral species give rise to two distinct descendant species

Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

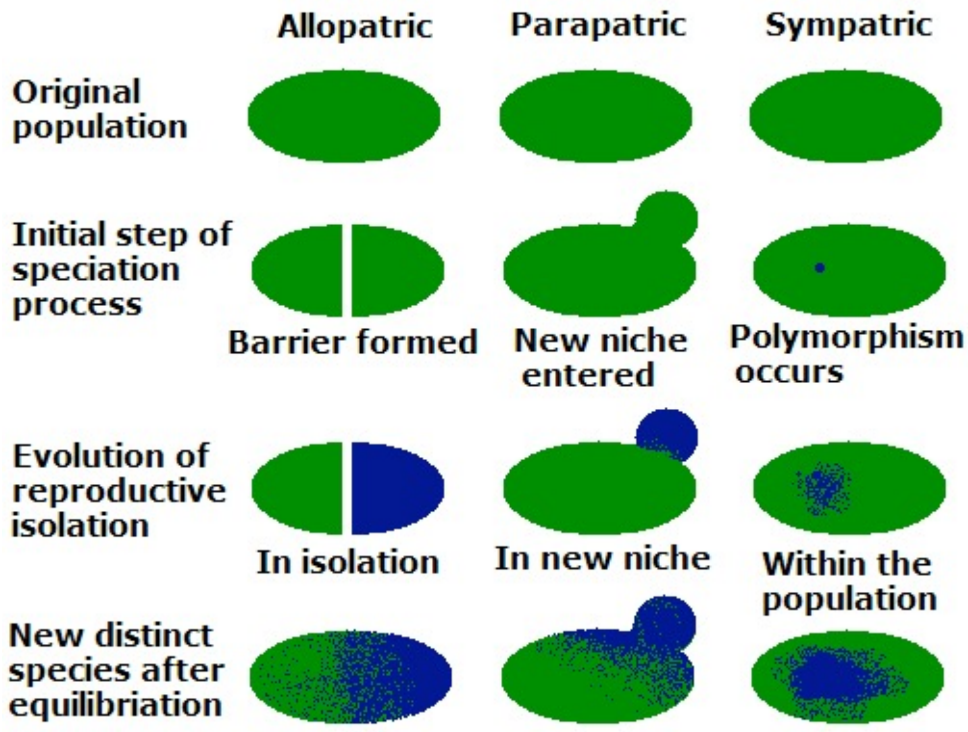
What are we actually measuring when we measure speciation rate using comparative methods?

speciation event =

speciation initiation

+ evolution of reproductive isolation

+ survival of incipient species until speciation completion



Difficulties in testing which microevolutionary process act as a rate limiting step in speciation using correlative approaches

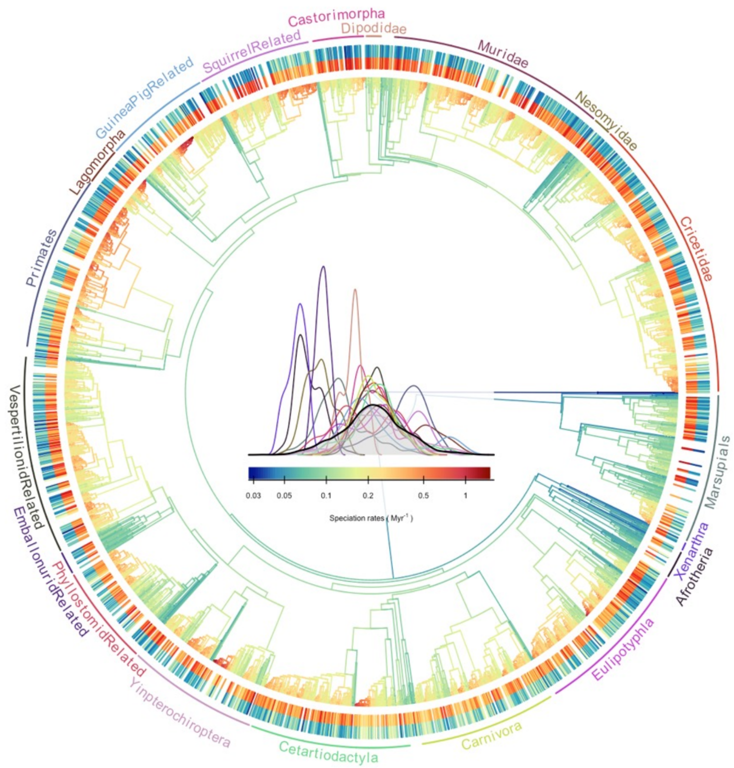
speciation event =

speciation initiation

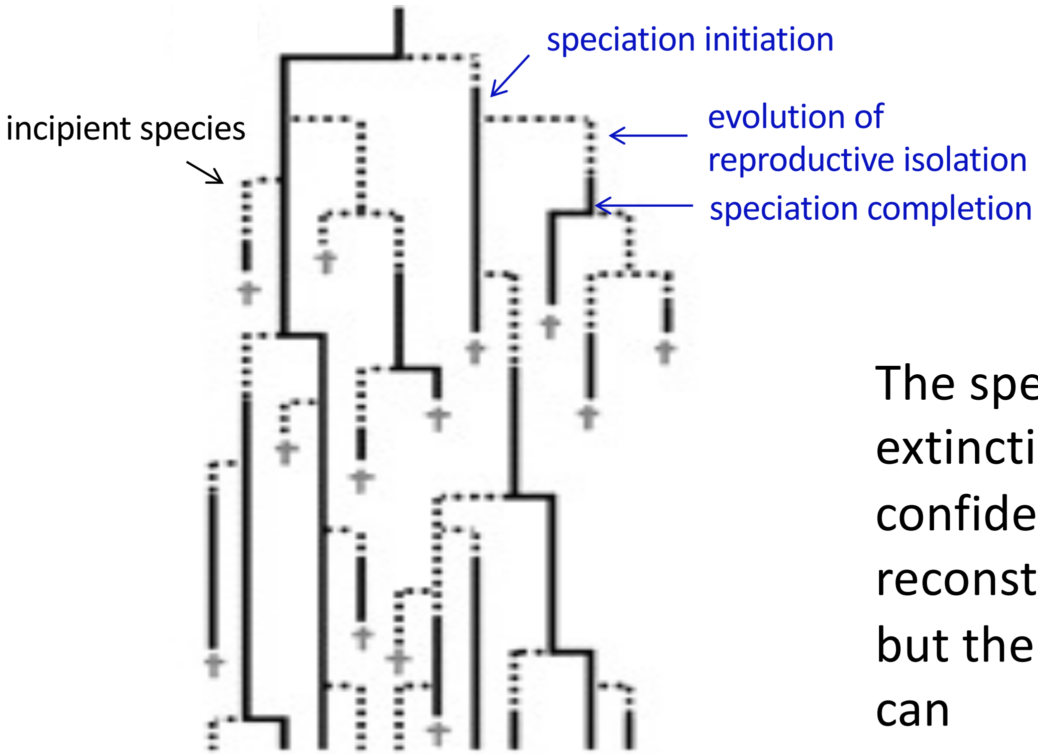
+ evolution of reproductive isolation

+ survival of incipient species until speciation completion

which of these 3 major aspects of speciation drive variation in speciation rates?



The protracted speciation model as a way to bridge micro and macroevolutionary speciation research?



Etienne & Rosindell Syst Bio 2012

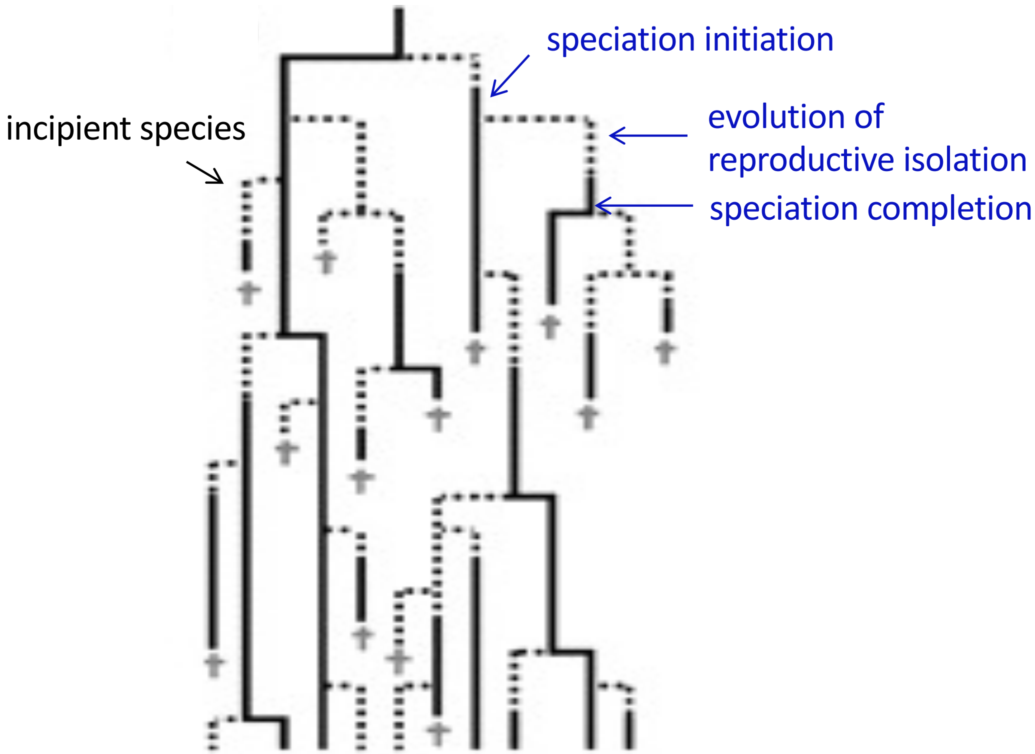
The speciation-initiation and extinction rates cannot be confidently estimated from reconstructed phylogenies, but the duration of speciation can

Etienne *et al.* Evolution 2014

Could we estimate the speciation initiation and extinction rates with intraspecific genetic data?

Could we estimate species-specific rates?

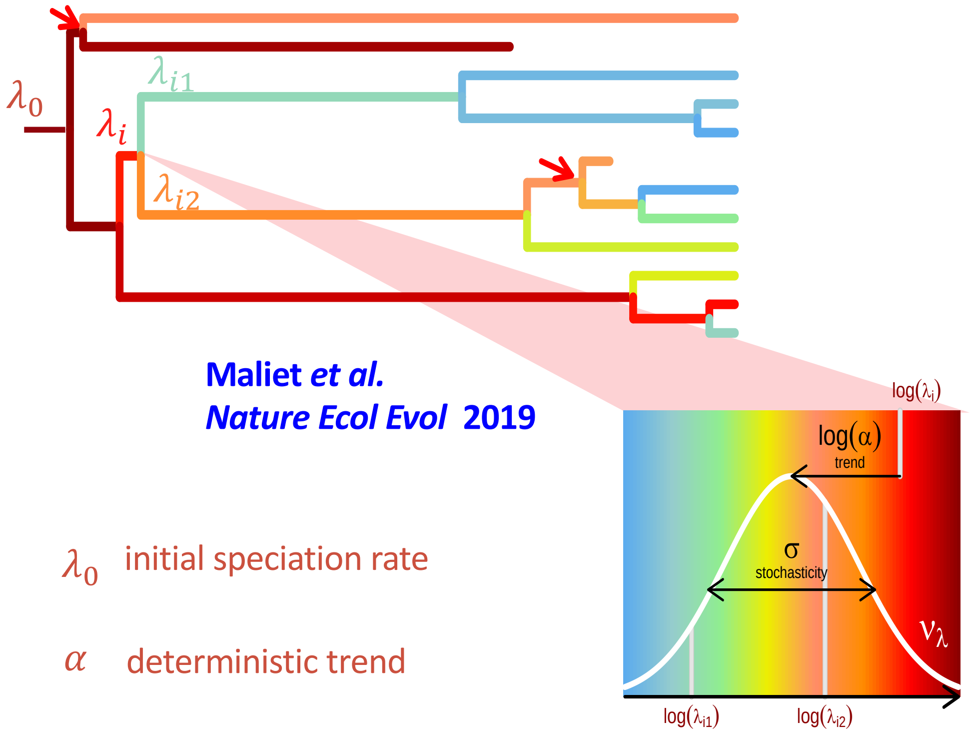
The protracted speciation model as a way to bridge micro and macroevolutionary speciation research?



Etienne & Rosindell Syst Bio 2012

The protracted speciation model remains phenomenological, with no account of the interplay between speciation and demography / intraspecific genetic differentiation

Towards macroevolutionary models accounting for the interplay between speciation and demography / intraspecific genetic differentiation



Maliet *et al.*
***Nature Ecol Evol* 2019**

λ_0 initial speciation rate

α deterministic trend

σ^2 stochastic variation

+ Demographic process

each species follows density-dependent population dynamics

Overcast et al. in prep.

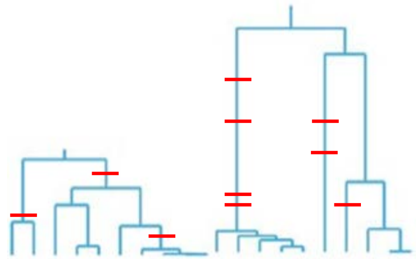
growth rate evolves as a Brownian

random split of individuals at speciation

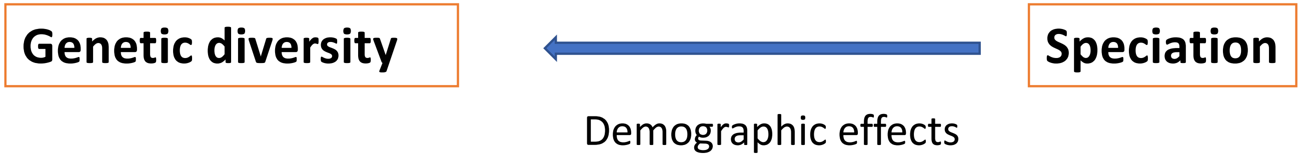
Extinction naturally proceeds from the death of all individuals in a given species

+ Population genetics

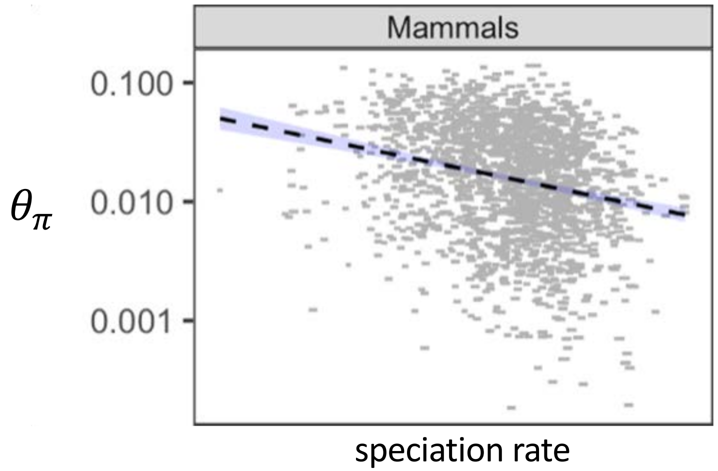
demography controls Ne



The model predicts either a positive or negative association between speciation rate and genetic diversity depending of the relative pace of speciation and accumulation of genetic diversity



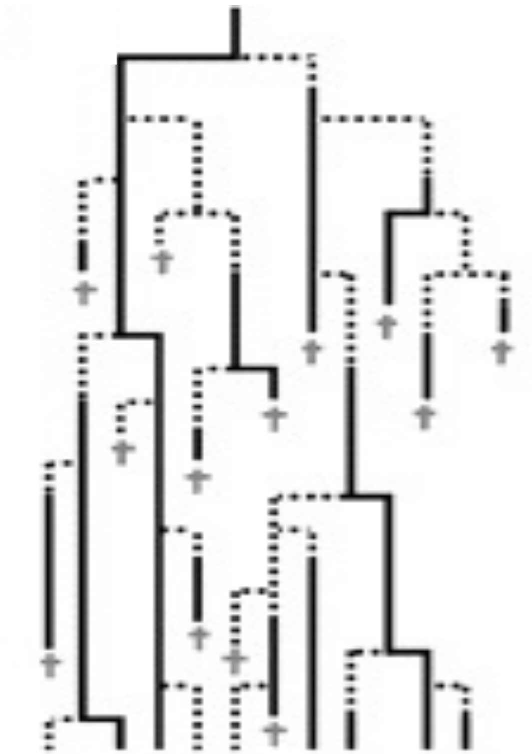
Rapid speciation can limit the accumulation of genetic diversity



The model can be fitted to data using machine learning techniques

Overcast et al. in prep.

Towards macroevolutionary models accounting for the interplay between speciation and demography / intraspecific genetic differentiation

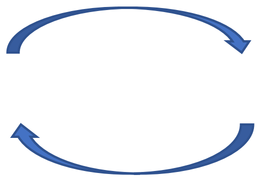


speciation event =

speciation initiation

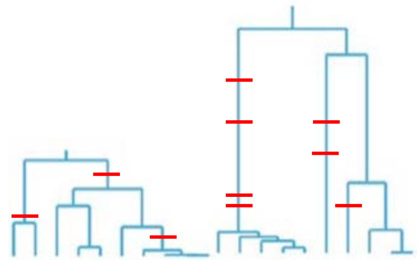
+ evolution of
reproductive isolation

+ speciation completion



Demographic process

Population genetics



Conclusions

Speciation and extinction rates vary widely across lineages, explaining why some species groups are much more species rich than others

Differences in speciation and extinction rates can be linked to species specific traits as well as abiotic and biotic factors

We have well developed models to assess the effect of species-specific traits and abiotic factors on speciation and extinction rates; testing the effect of interspecific interactions remains challenging

Understanding which microevolutionary processes act a rate-limiting step in speciation (and therefore drive present day species richness patterns) also remains a major research frontier


Ana Silva


Isaac Overcast


Odile Maliet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erc
PANDA

AGENCE NATIONALE DE LA RECHERCHE
ANR

cnrs
dépasser les frontières

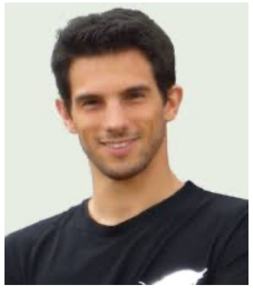

Leandro Aristide

THANKS!


Eric Lewitus

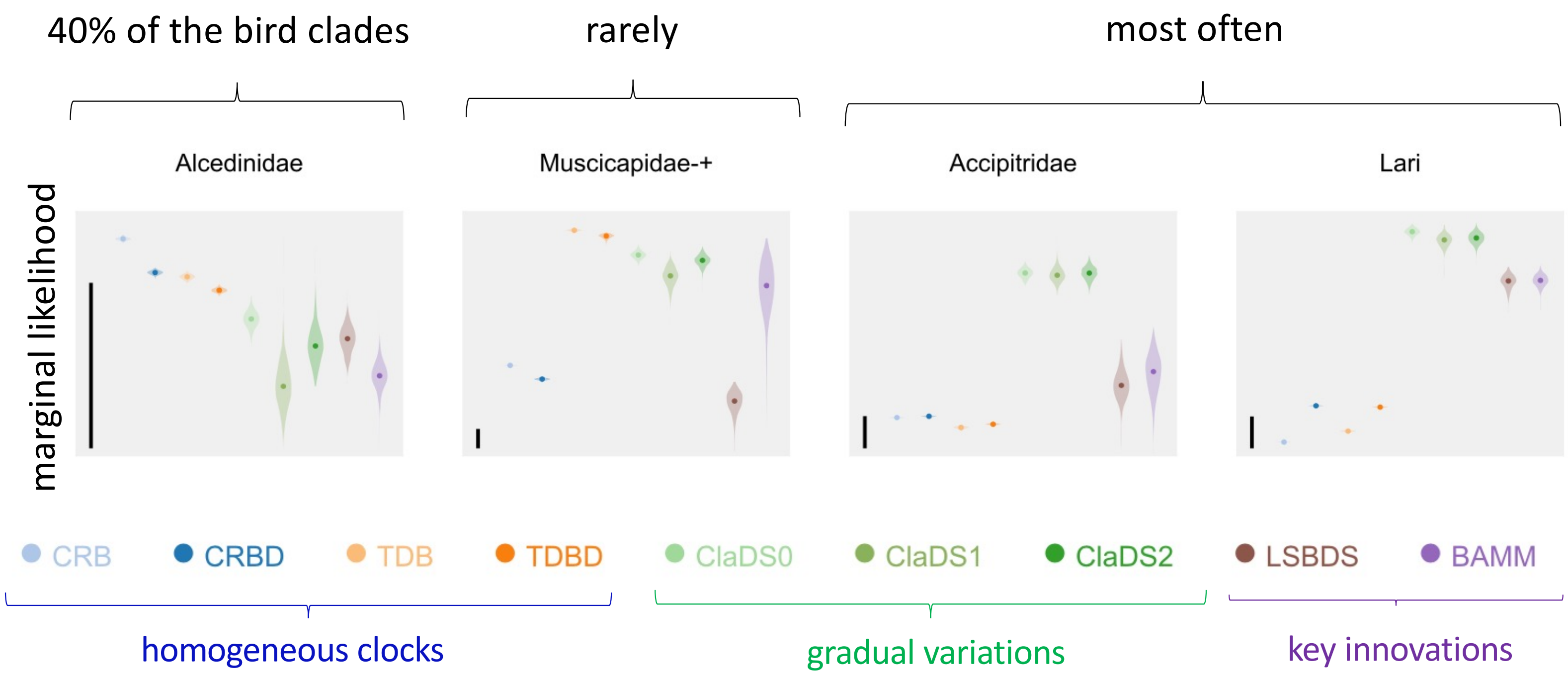
MEMO
LABEX LIFE


Nathan Mazet


Fabien Condamine

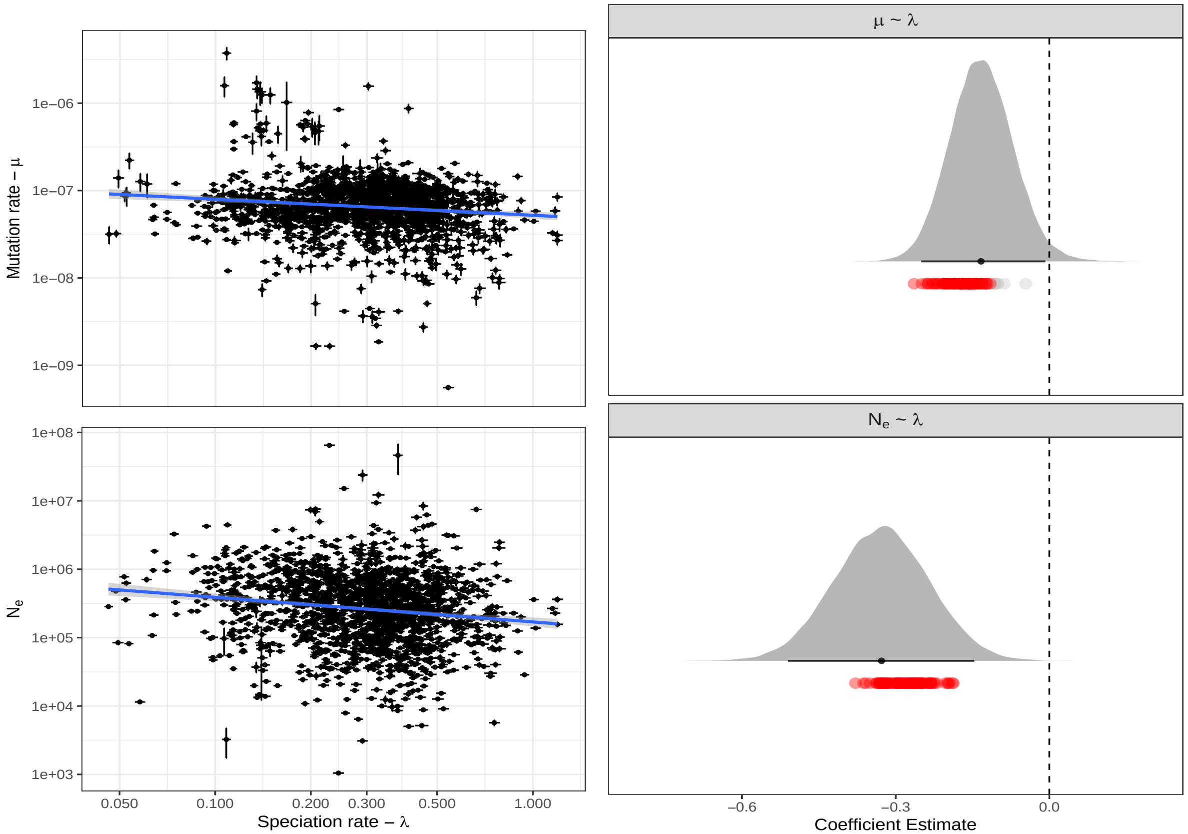
iBioGen

What is the role of key innovations in the diversification of life?



Ronquist *et al. Comm Biol* 2021

Both mutation rates and Ne are negatively correlated to speciation rates



Silva et al. in prep.