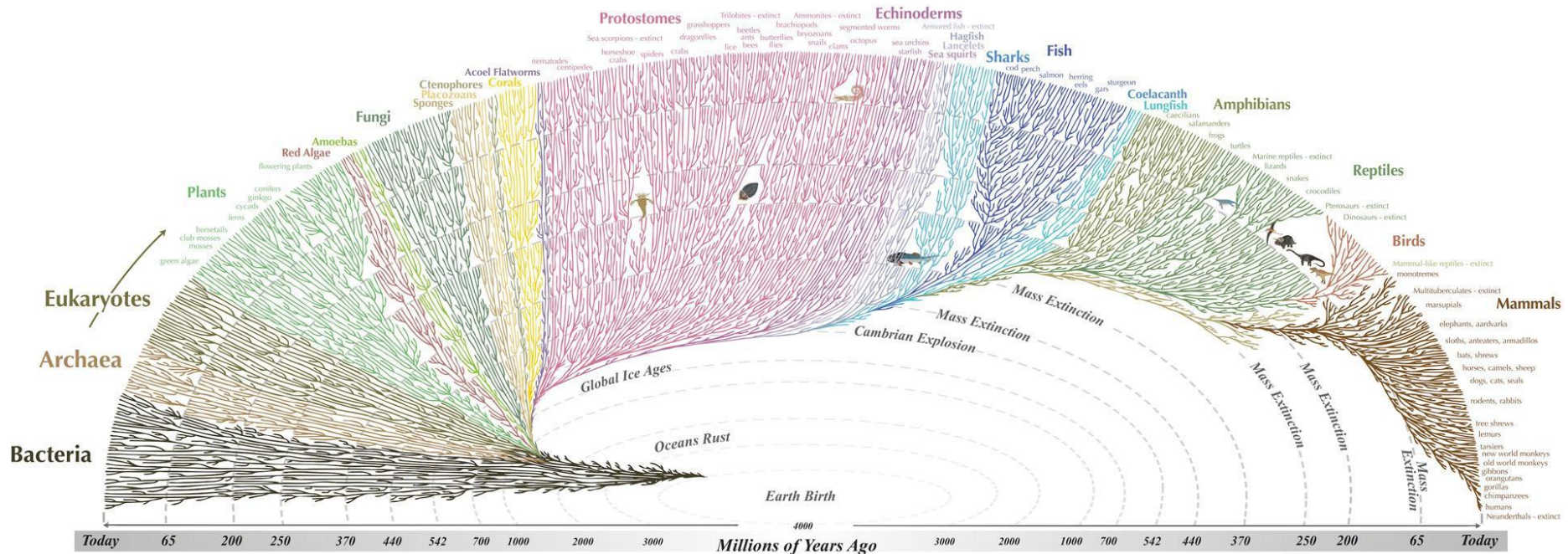
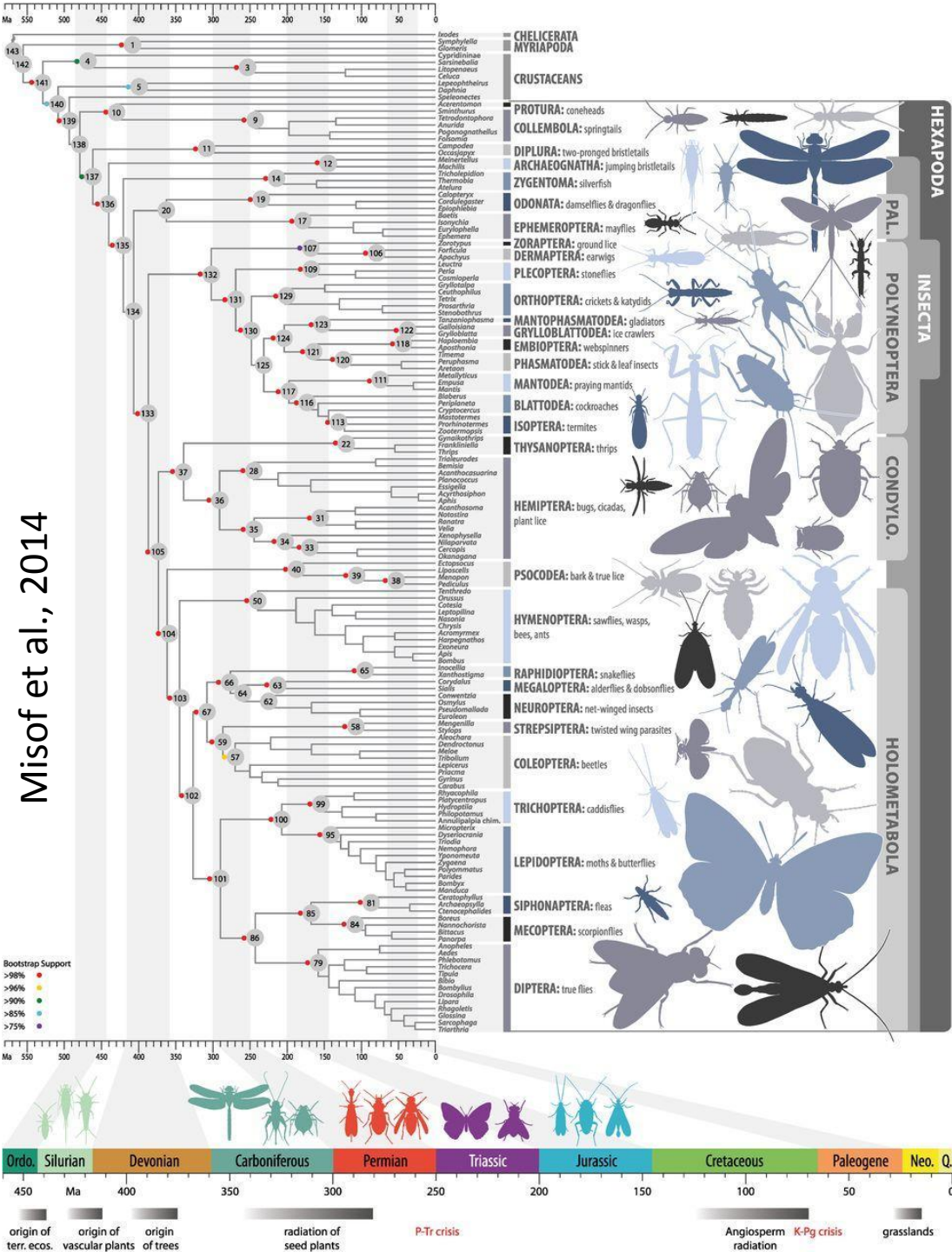
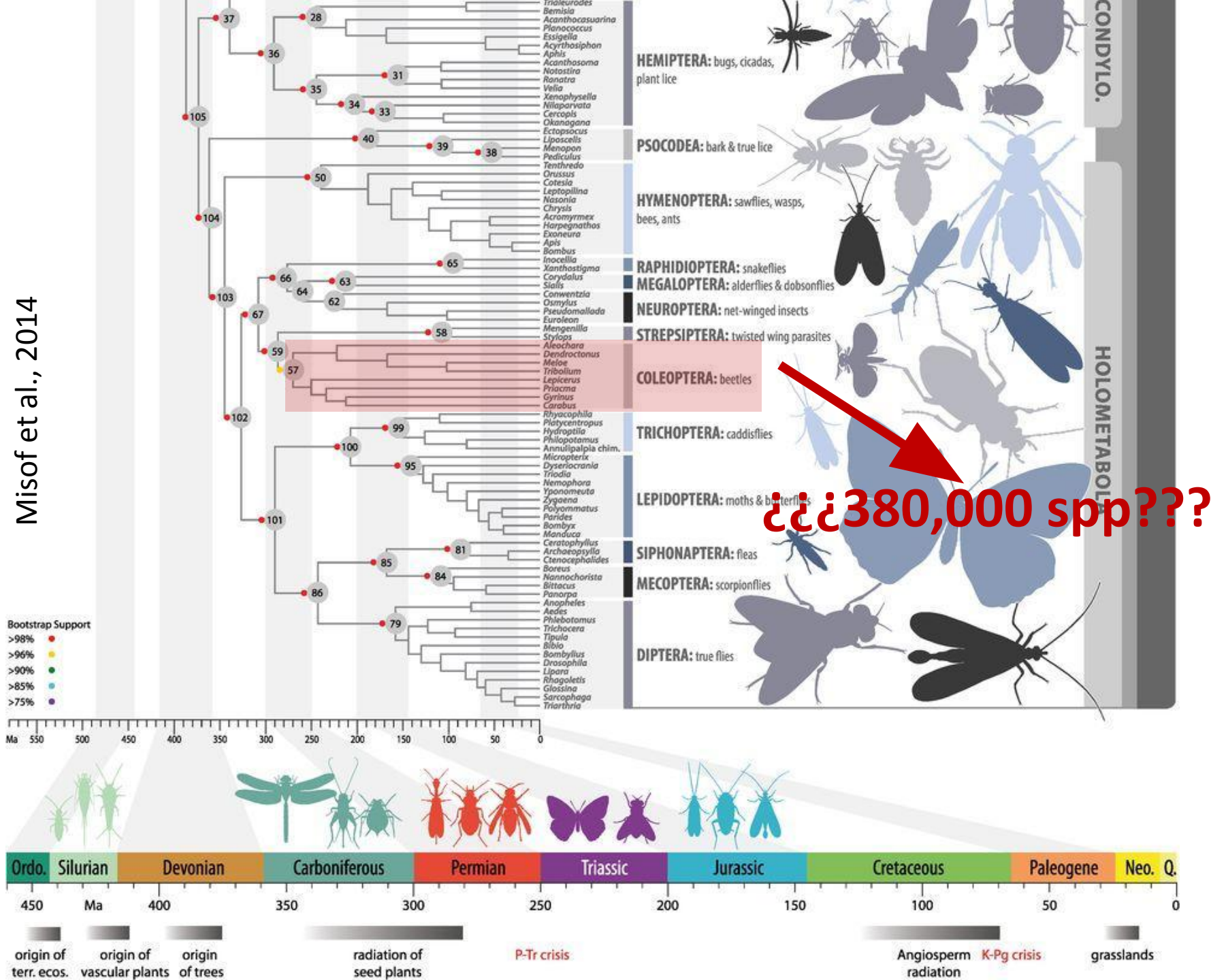


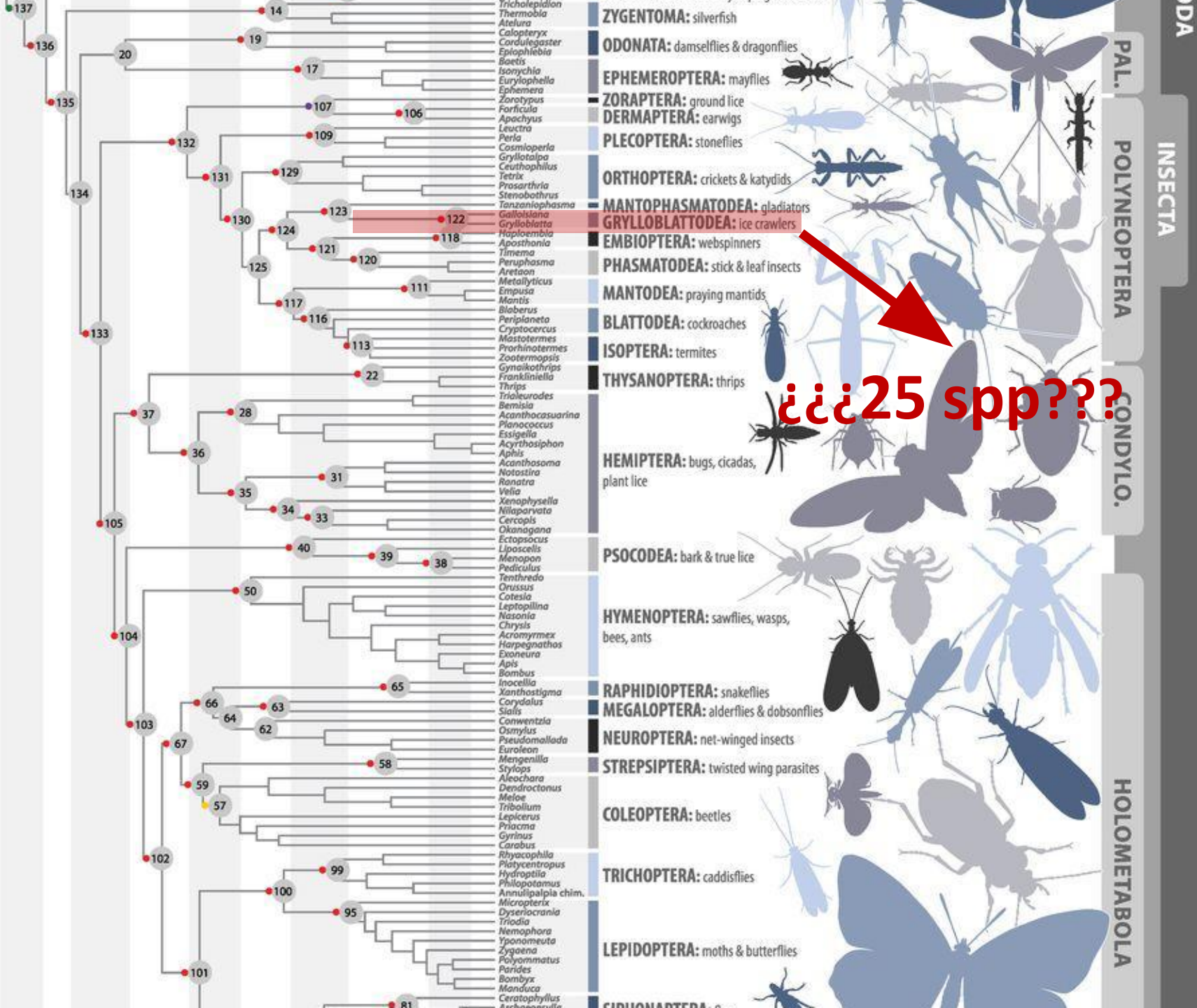
Introducción al estudio de las dinámicas de diversificación



All the major and many of the minor living branches of life are shown on this diagram, but only a few of those that have gone extinct are shown. Example: Dinosaurs - extinct

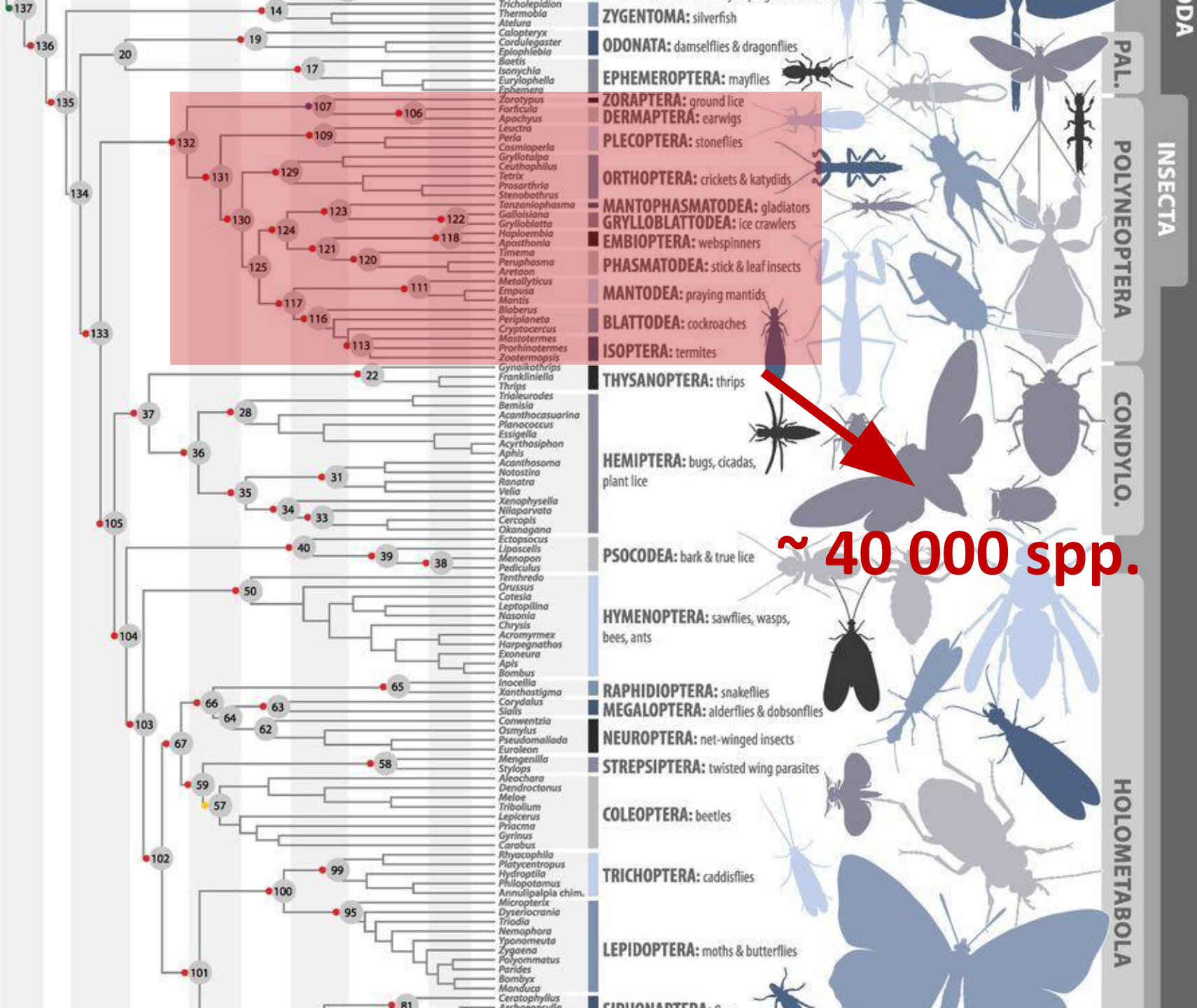


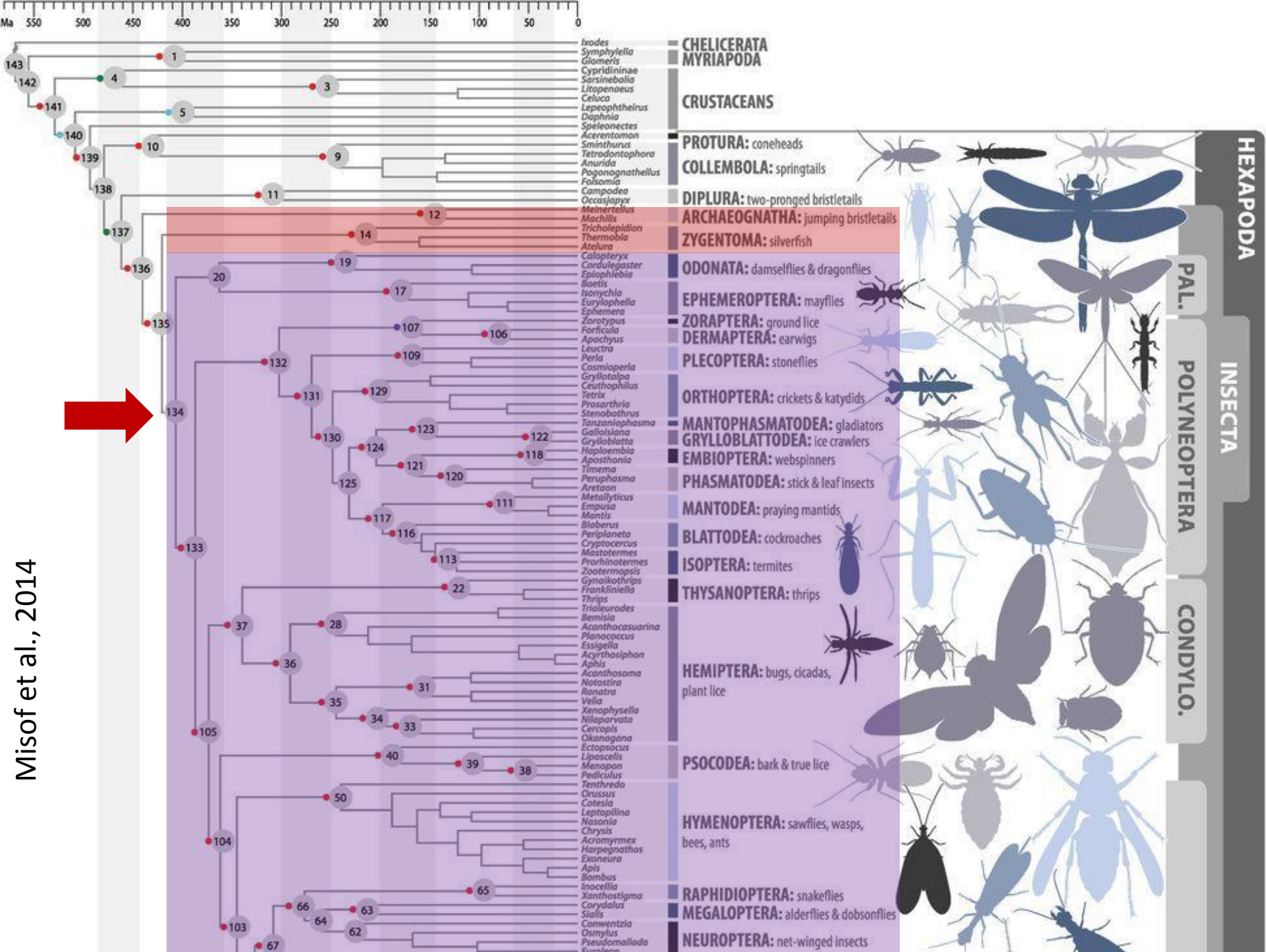


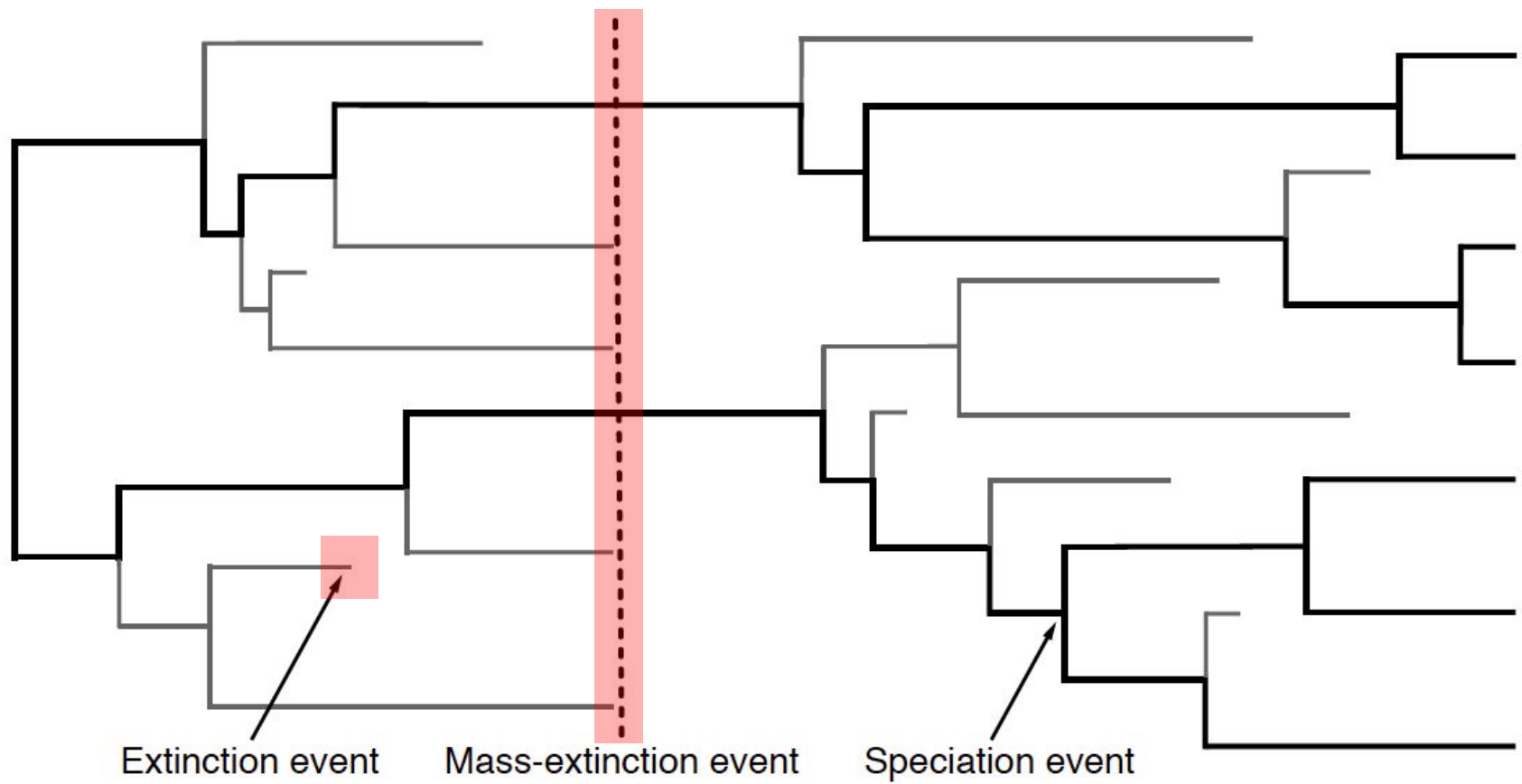


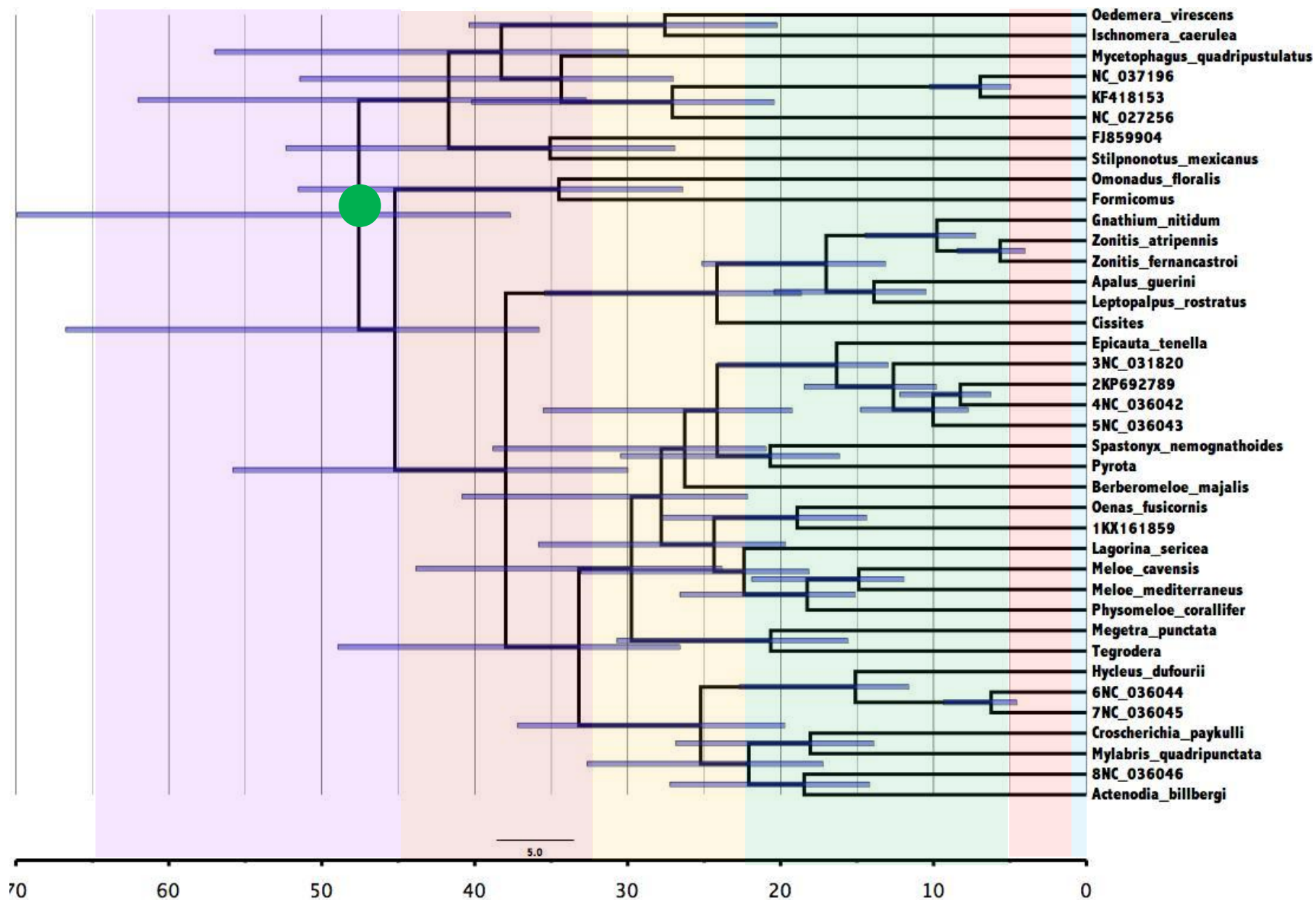


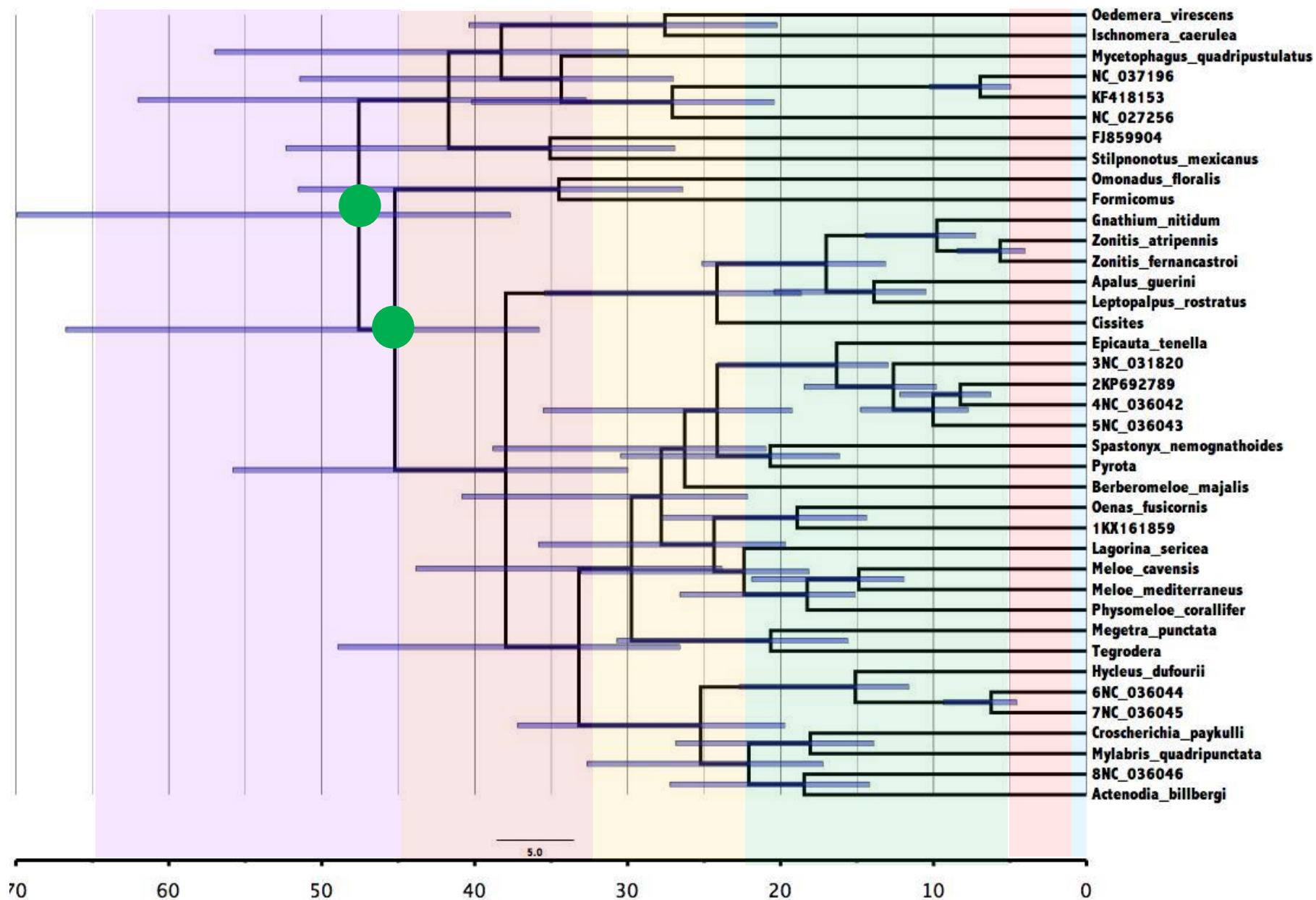
Misof et al., 2014

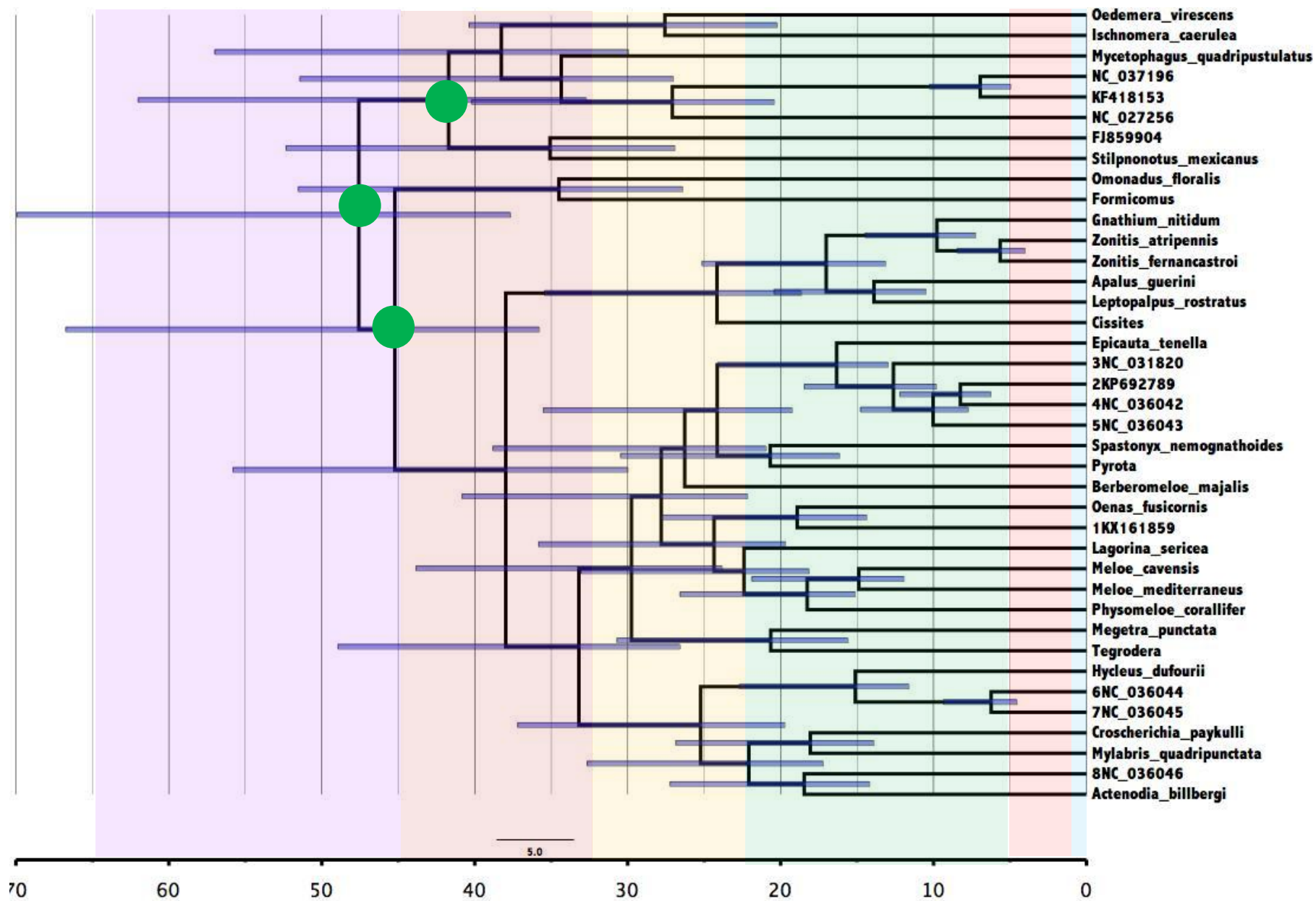


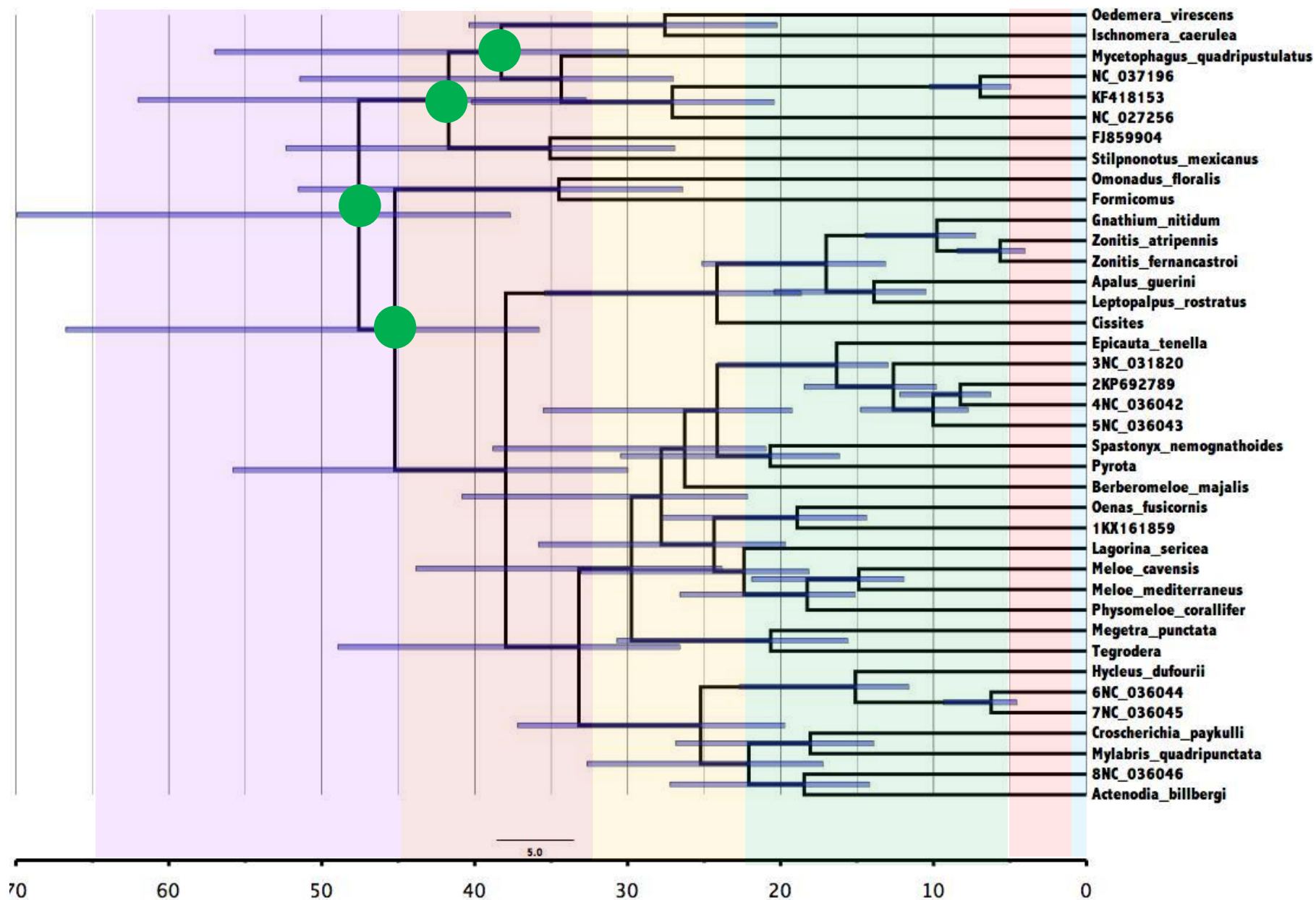






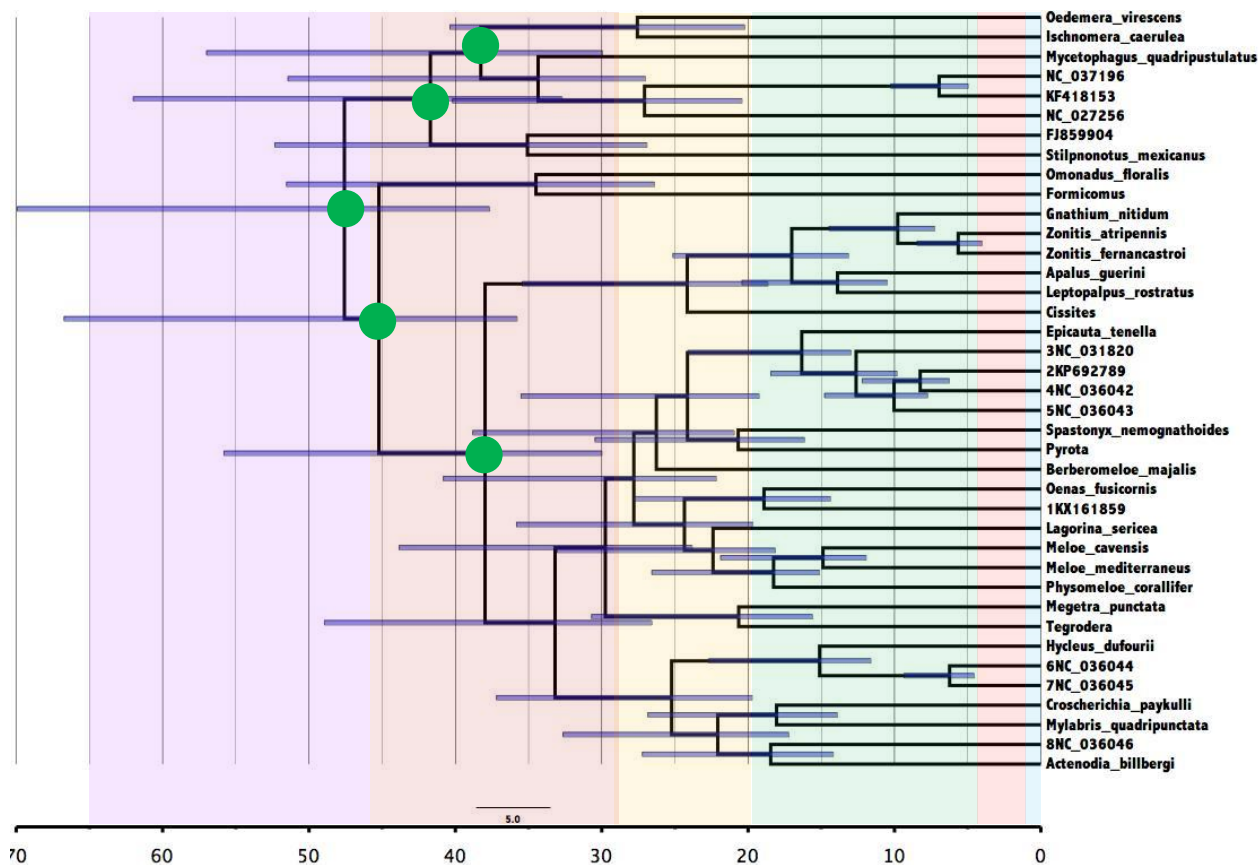






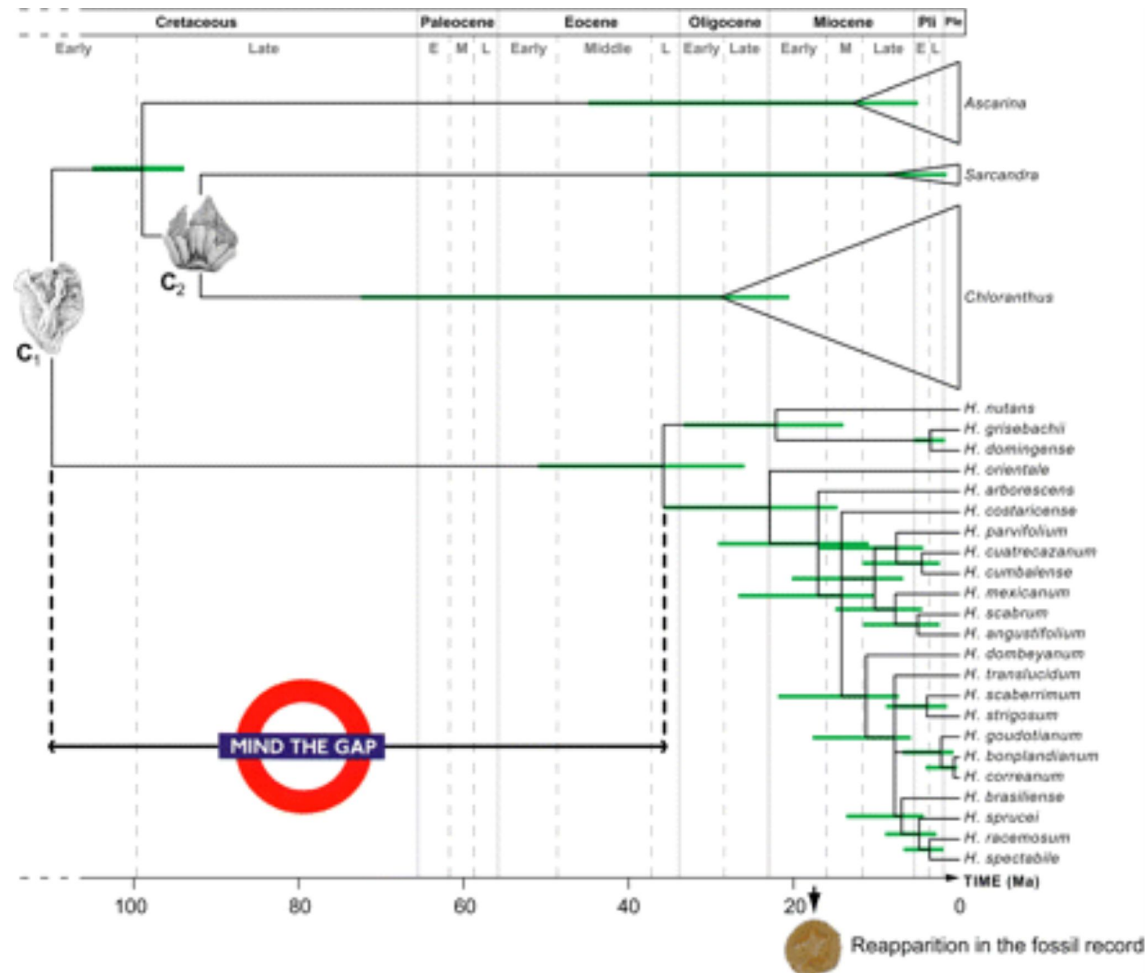
Especiación

$$\lambda = X$$



Extinción

$$\mu = y$$



Antonelli & Sanmartin, 2011



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$



Diversificación

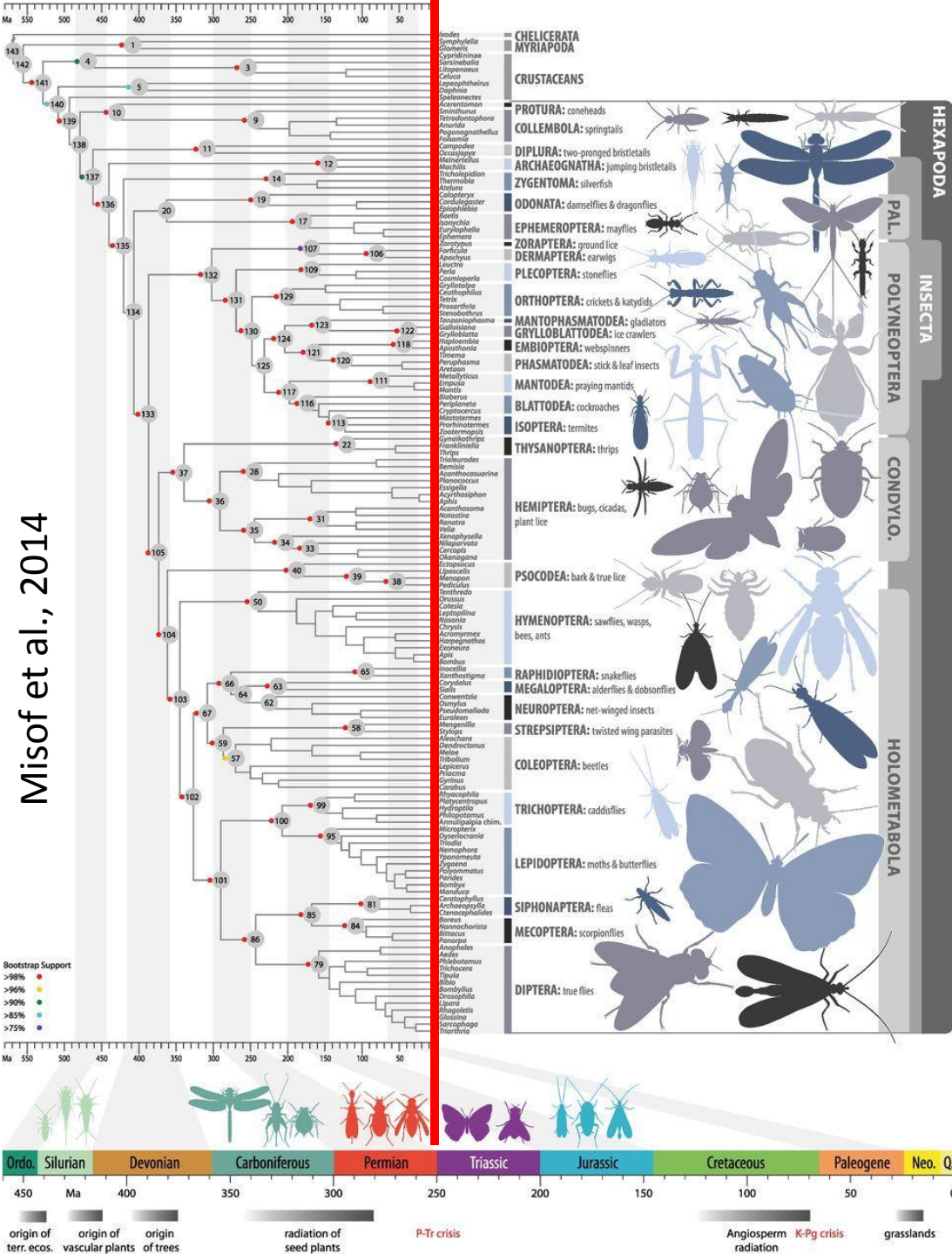
$$r = (\lambda - \mu)$$



Diversificación

$$r = (\lambda - \mu)$$

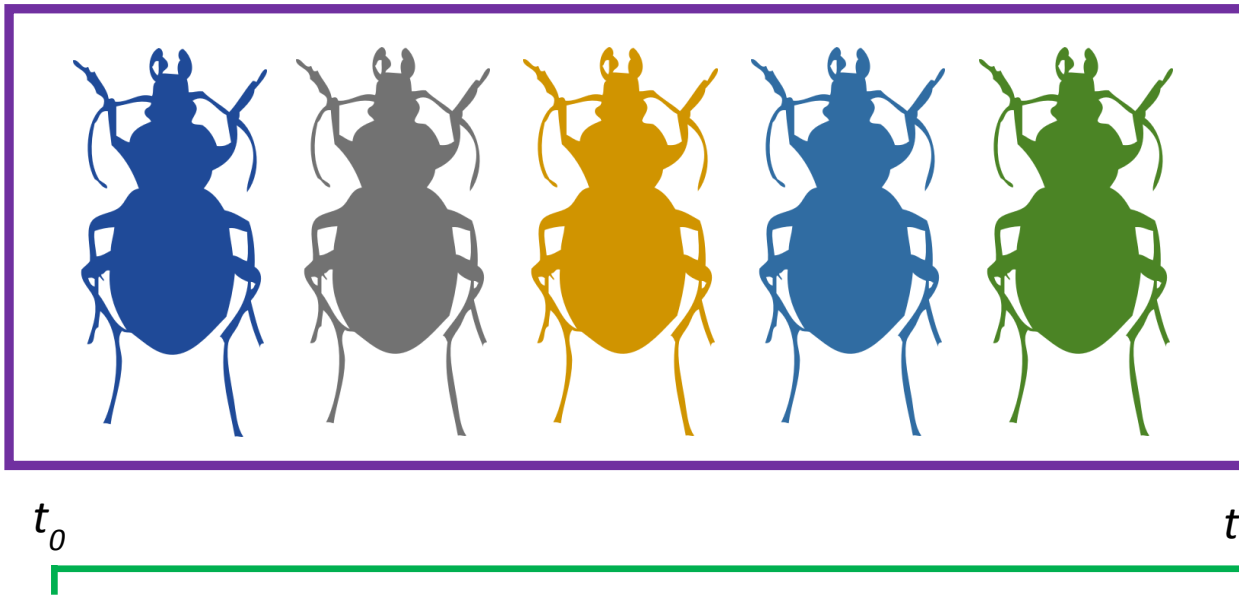




¿Qué es lo que vemos hoy?

Extinción relativa Recambio (*turnover*)

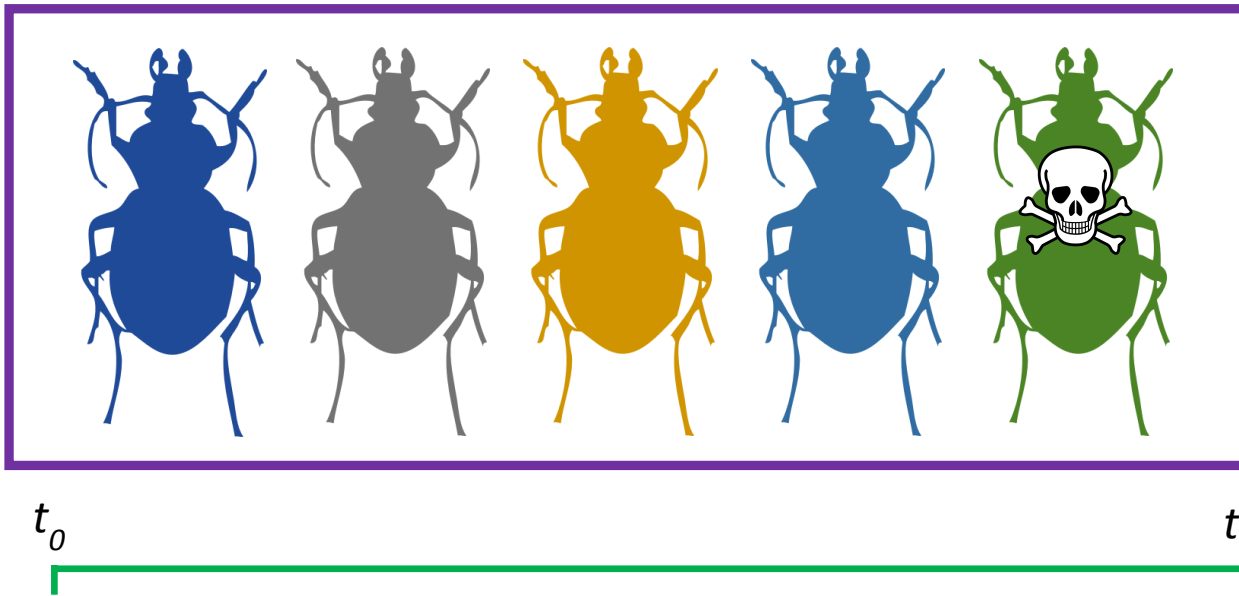
$$\varepsilon = (\mu/\lambda)$$



Extinción relativa

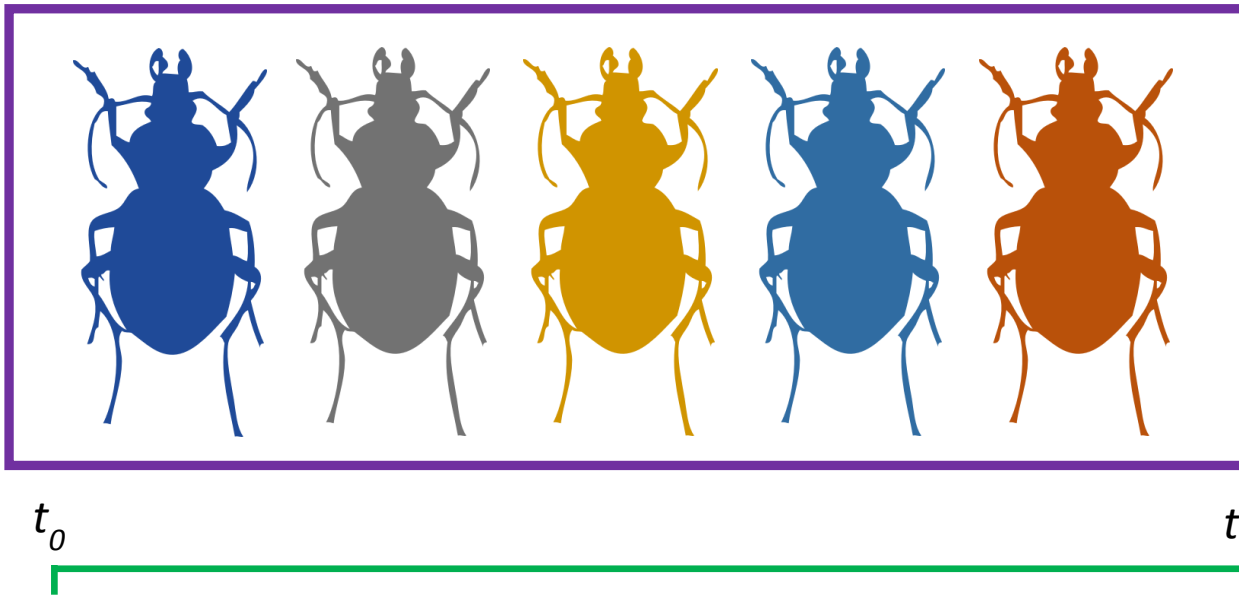
Recambio (*turnover*)

$$\varepsilon = (\mu/\lambda)$$

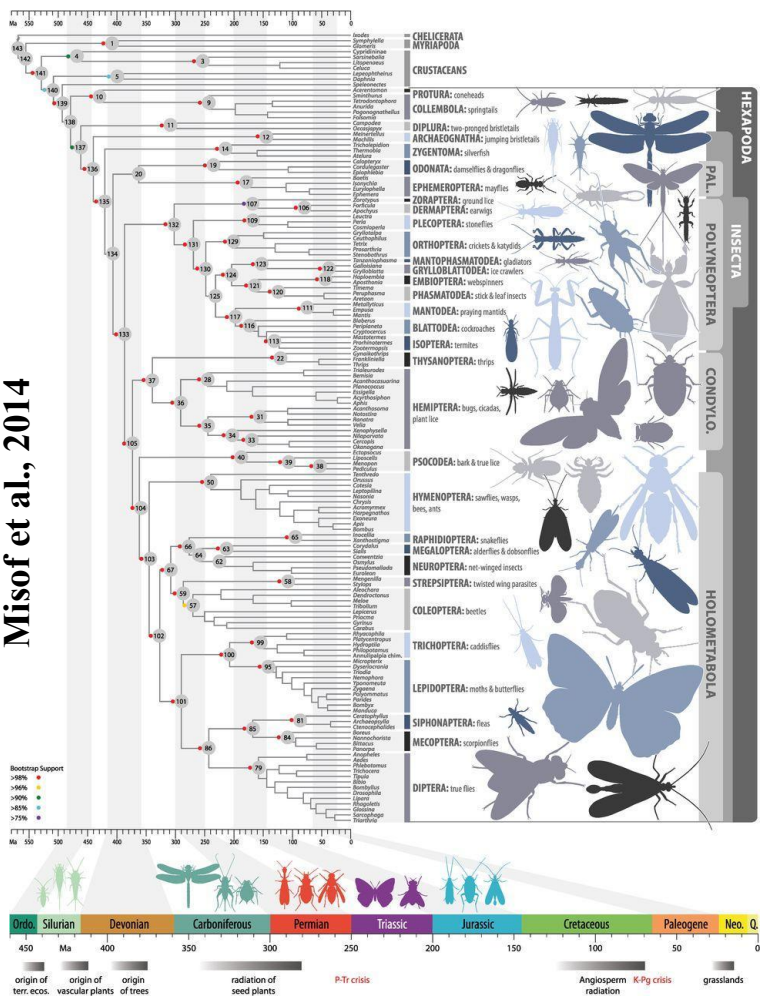


Extinción relativa Recambio (*turnover*)

$$\varepsilon = (\mu/\lambda)$$

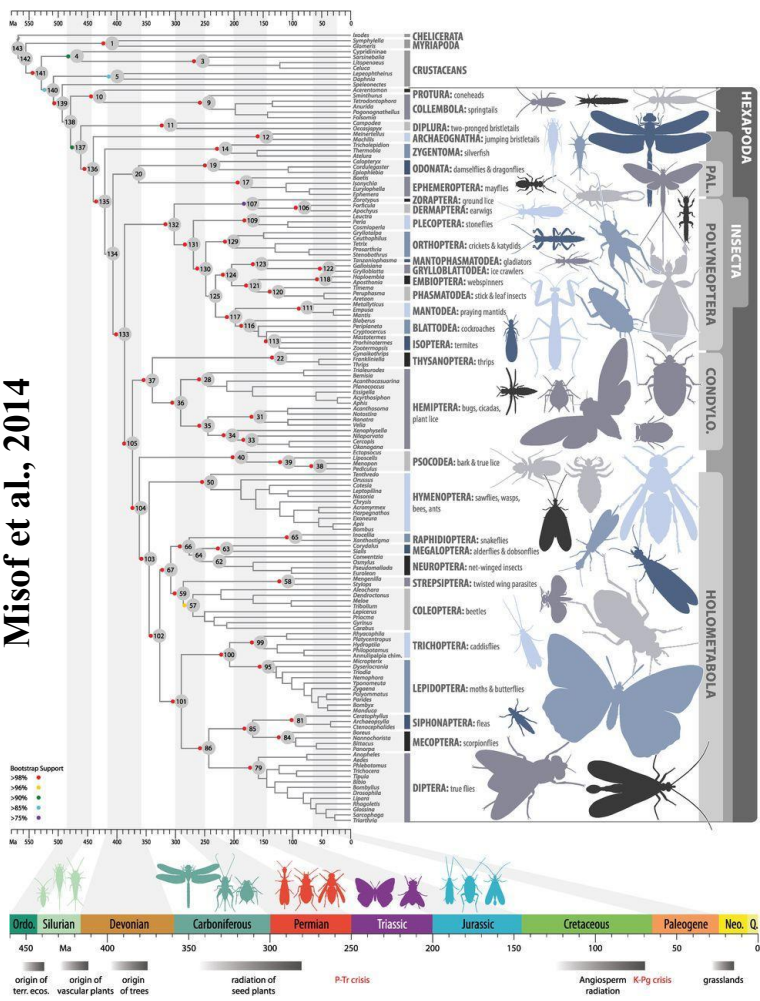


Misof et al., 2014



¿Por qué hay tantos insectos?

Misof et al., 2014

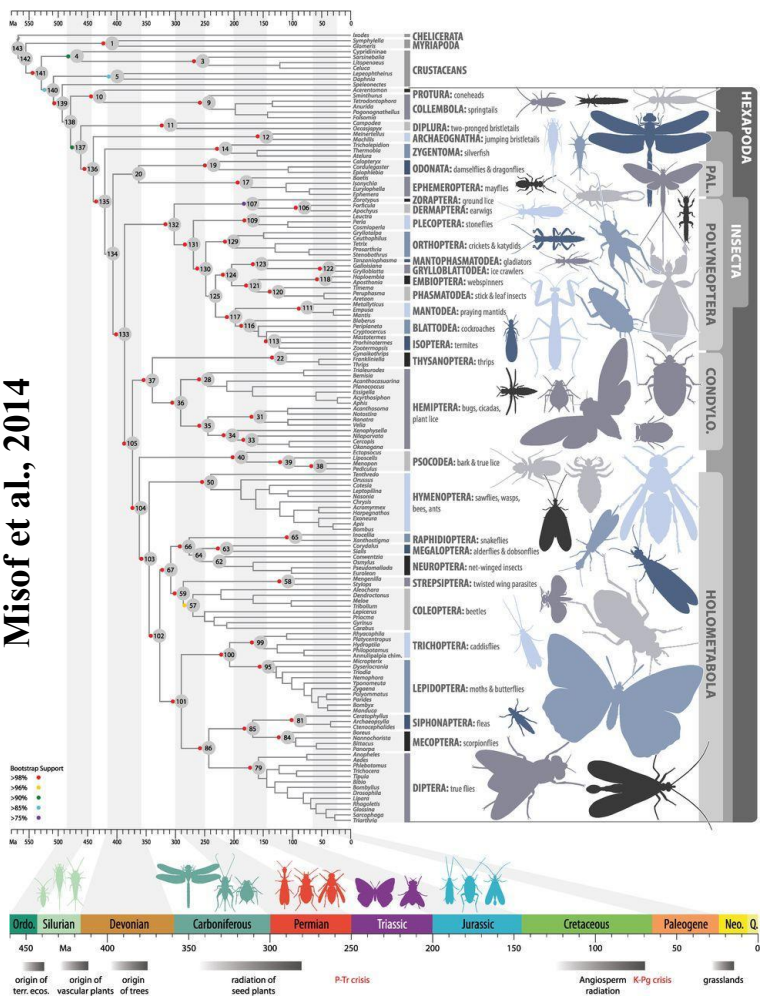


¿A qué ritmo se lleva a cabo el proceso de especiación en insectos?

$$\lambda_{(\text{Insectos})} = ??$$

DivBayes/SubT Ryberg et al., 2011

Misof et al., 2014



¿A qué ritmo se extinguen las especies de insectos?

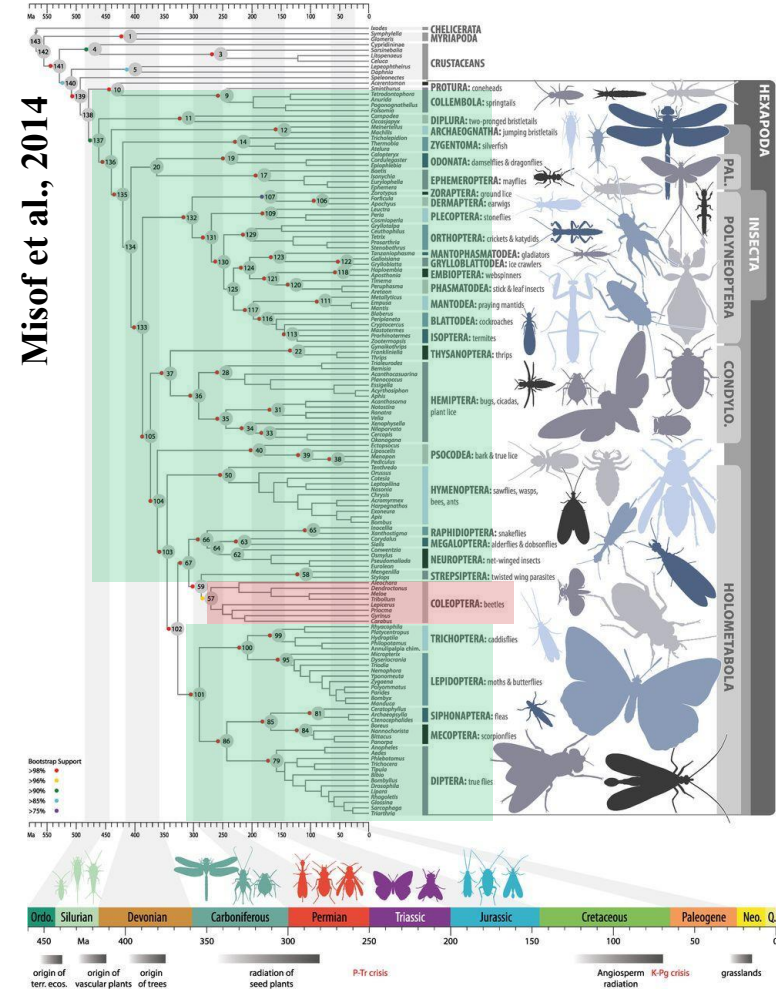
$$\mu_{(\text{Insectos})} = ??$$

¿La especiación en coleópteros es mucho más alta que en el resto de los insectos ?

$$\lambda_{(\text{Insectos})} < \lambda_{(\text{Coleoptera})}$$

¿El resto de los insectos se extingue más que los coleópteros?

$$\mu_{(\text{Insectos})} > \mu_{(\text{Coleoptera})}$$



Rabosky, 2014

Application | [Free Access](#)

RPANDA: an R package for macroevolutionary analyses on phylogenetic trees

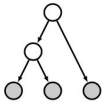
Hélène Morlon , Eric Lewitus, Fabien L. Condamine, Marc Manceau, Julien Clavel, Jonathan Drury

First published: 15 December 2015 | <https://doi.org/10.1111/2041-210X.12526> | Cited by: 49

Morlon et al., 2015



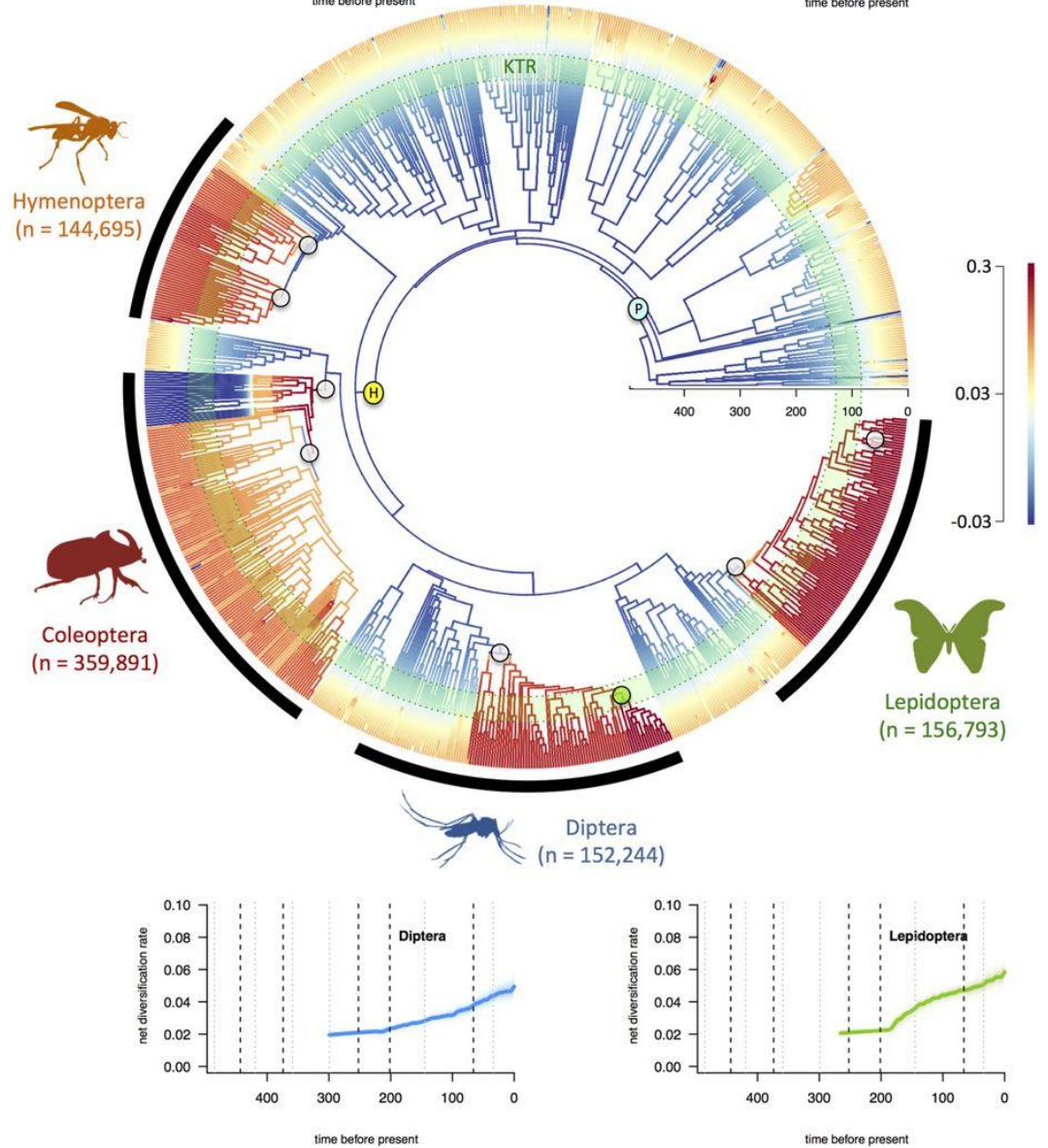
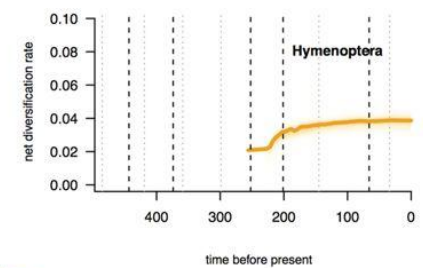
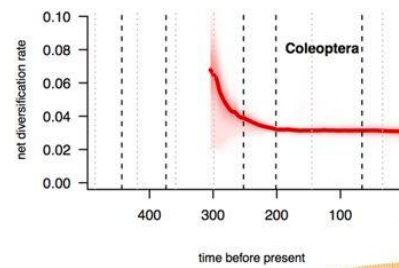
Software | Tutorials | Workshops | Jobs | Developer



RevBayes

Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language

Höhna et al., 2016

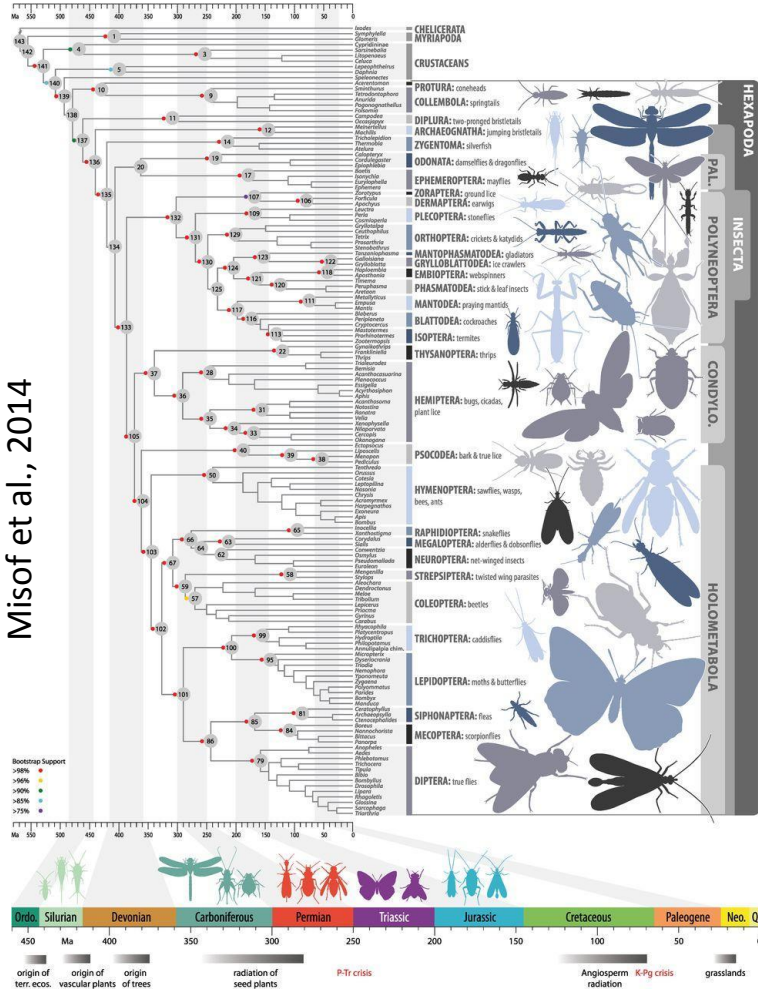


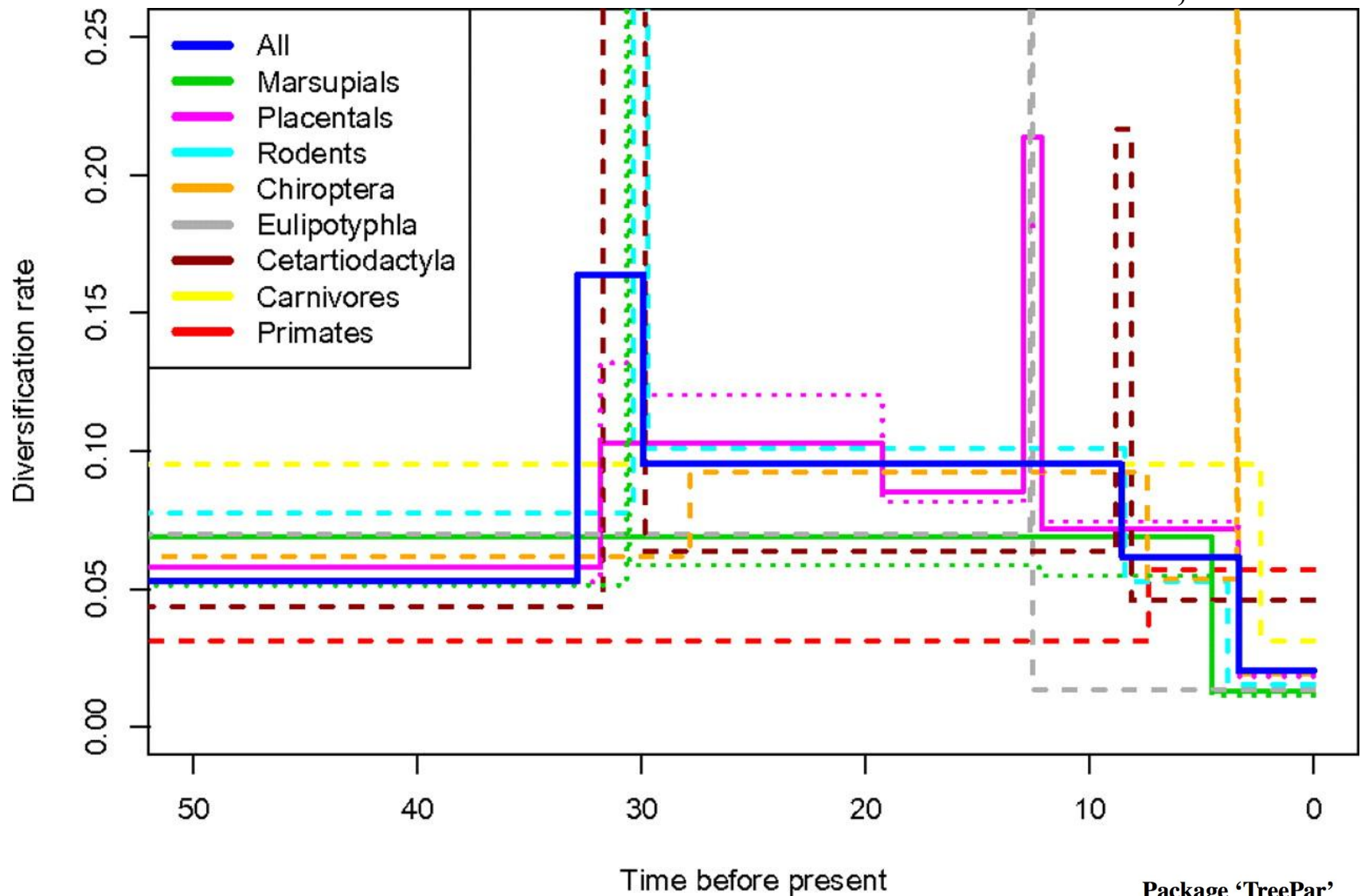
Condamine et al., 2016

¿Ha habido cambios
significativos en la tasa de
diversificación de los insectos a
lo largo del tiempo?

$$r_{t0} < \Delta r_{t1}$$

$$r_{t0} > \Delta r_{t1}$$





Package 'TreePar'

February 19, 2015

Type Package

Title Estimating birth and death rates based on phylogenies

Version 3.3

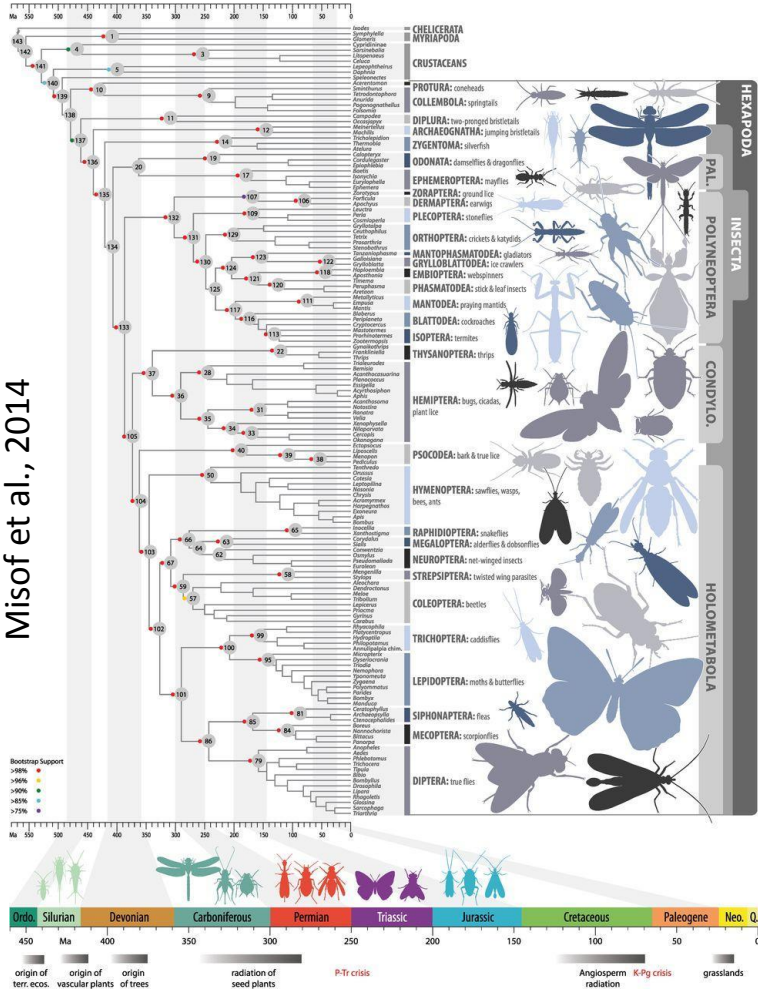
Date 2015-01-02

Author Tanja Stadler

Software Tutorials Workshops Jobs Developer

RevBayes

Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language



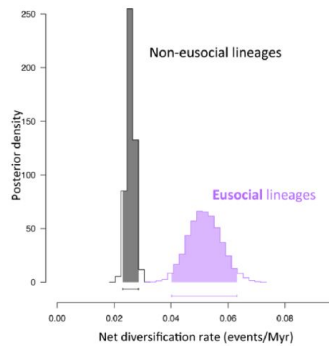
¿El aumento en la tasa de diversificación está asociado a un estado de carácter?

$$r \sim f(A)$$

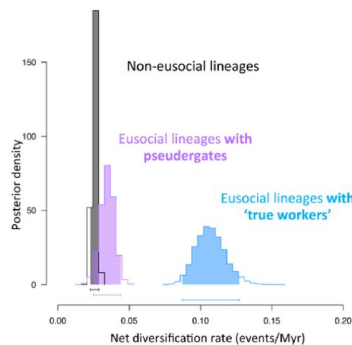
ó

$$r \sim f(B)$$

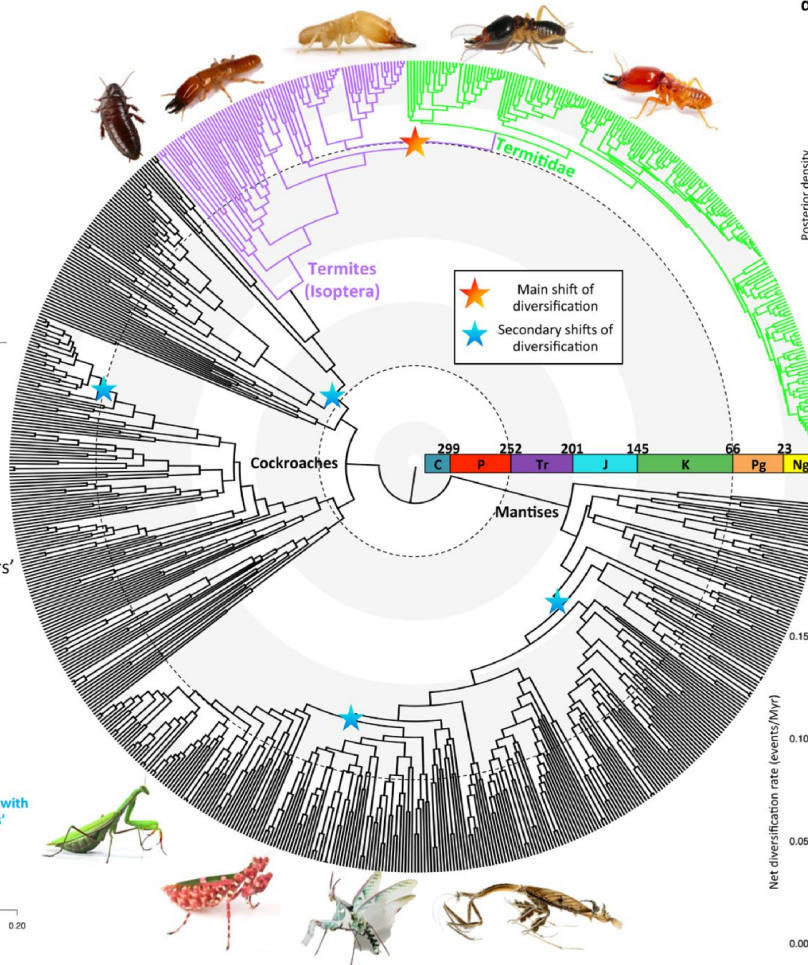
b) Eusocial lineages diversified faster



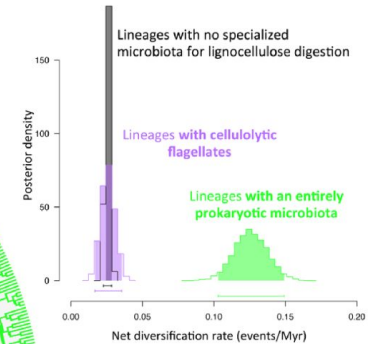
c) Eusocial lineages with 'true workers' diversified even faster



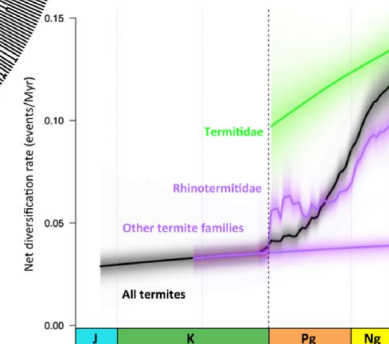
a) Evolutionary history of Dictyoptera



d) Termitidae diversified fast, perhaps due to their hindgut microbiota



e) Diversification dynamics through time for termite lineages



Package 'diversitree'

April 5, 2017

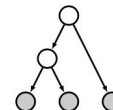
Version 0.9-10

Title Comparative 'Phylogenetic' Analyses of Diversification

Author Richard G. FitzJohn <fitzjohn@zoology.ubc.ca>, with 'GeoSSE' and 'ClaSSE' by Emma E. Goldberg <eeg@uic.edu>, and 'BiSSE-ness' by Karen Magnuson-Ford.

FitzJohn et al., 2012

Software Tutorials Workshops Jobs Developer



RevBayes

Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language

Höhna et al., 2016

RPANDA: an R package for macroevolutionary analyses on phylogenetic trees

Hélène Morlon [✉](#), Eric Lewitus, Fabien L. Condamine, Marc Manceau, Julien Clavel, Jonathan Drury

First published: 15 December 2015 | <https://doi.org/10.1111/2041-210X.12526> | Cited by: 49

A Bayesian approach for detecting the impact of mass-extinction events on molecular phylogenies when rates of lineage diversification may vary

Michael R. May, Sebastian Höhna, Brian R. Moore [✉](#)

First published: 26 March 2016 | <https://doi.org/10.1111/2041-210X.12563> | Cited by: 17

Package 'diversitree'

April 5, 2017

Version 0.9-10

Title Comparative 'Phylogenetic' Analyses of Diversification

Author Richard G. FitzJohn <fitzjohn@zoology.ubc.ca>, with 'GeoSSE' and 'ClaSSE' by Emma E. Goldberg <eeg@uic.edu>, and 'BiSSE-ness' by Karen Magnuson-Ford.



Package 'TreePar'

February 19, 2015

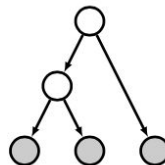
Type Package

Title Estimating birth and death rates based on phylogenies

Version 3.3

Date 2015-01-02

Author Tanja Stadler

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RevBayes

Bayesian phylogenetic inference using probabilistic graphical models and an interpreted language

$$\lambda \sim f(\text{wings}) + \lambda_{t0} < \Delta \lambda_{t1}$$

$$\lambda \sim f(\text{wingless})$$

$$+ \lambda_{(\text{Strepsiptera})} < \lambda_{(\text{Coleoptera})} + \text{MEE}$$

$$+ \lambda_{(\text{Insects})} = \text{Insect diversification dynamics}$$

Introduction to diversification methods

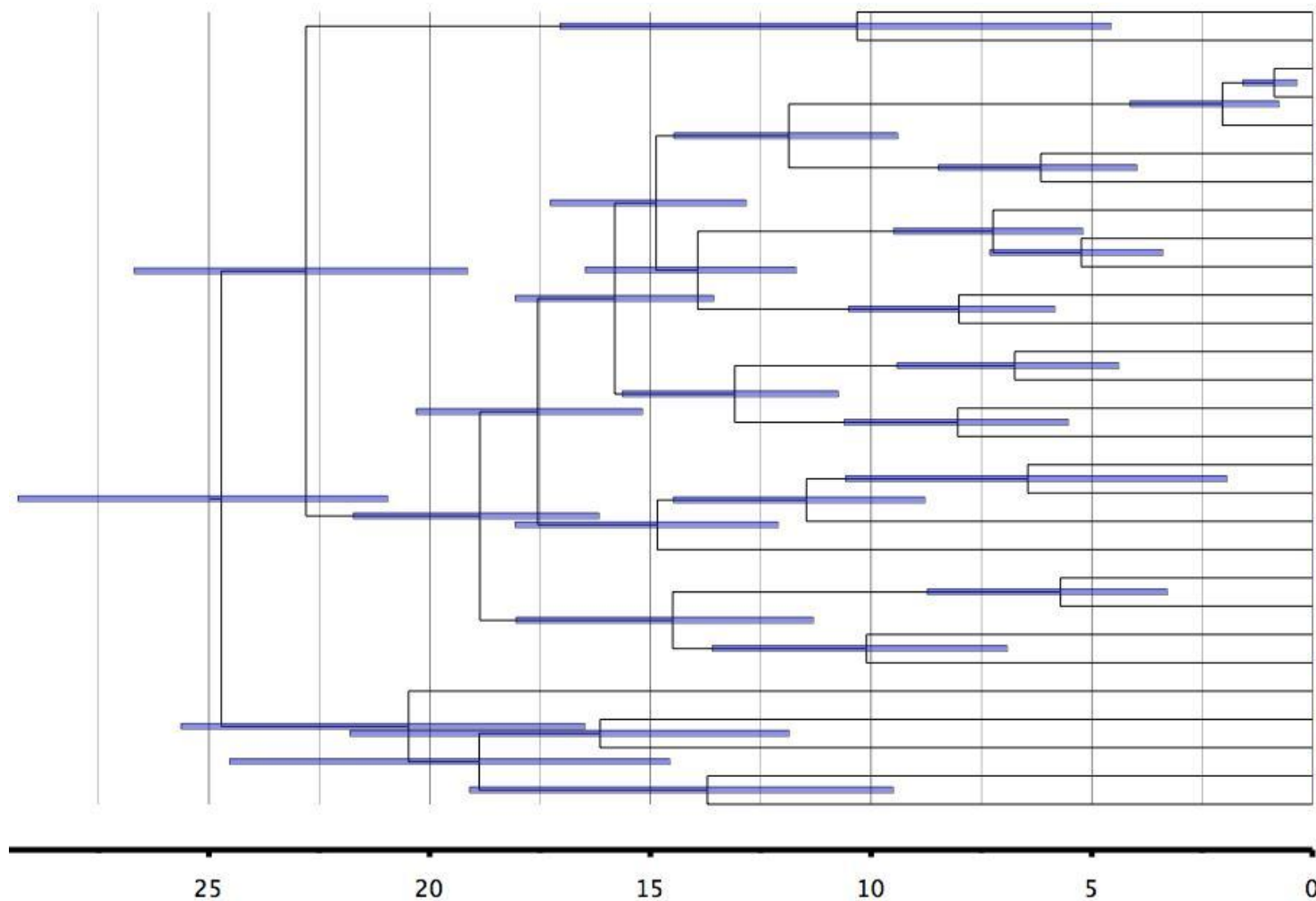
Summary

- It is possible to estimate past diversification and turnover rates from neontological data.
- To estimate diversification rates a reliable timetree is fundamental
- To select the proper method to estimate diversification rates we must focus on what we want to know about diversification dynamics.
- There are no “all-in-one” model, that is why the question will guide the methodological pipeline.

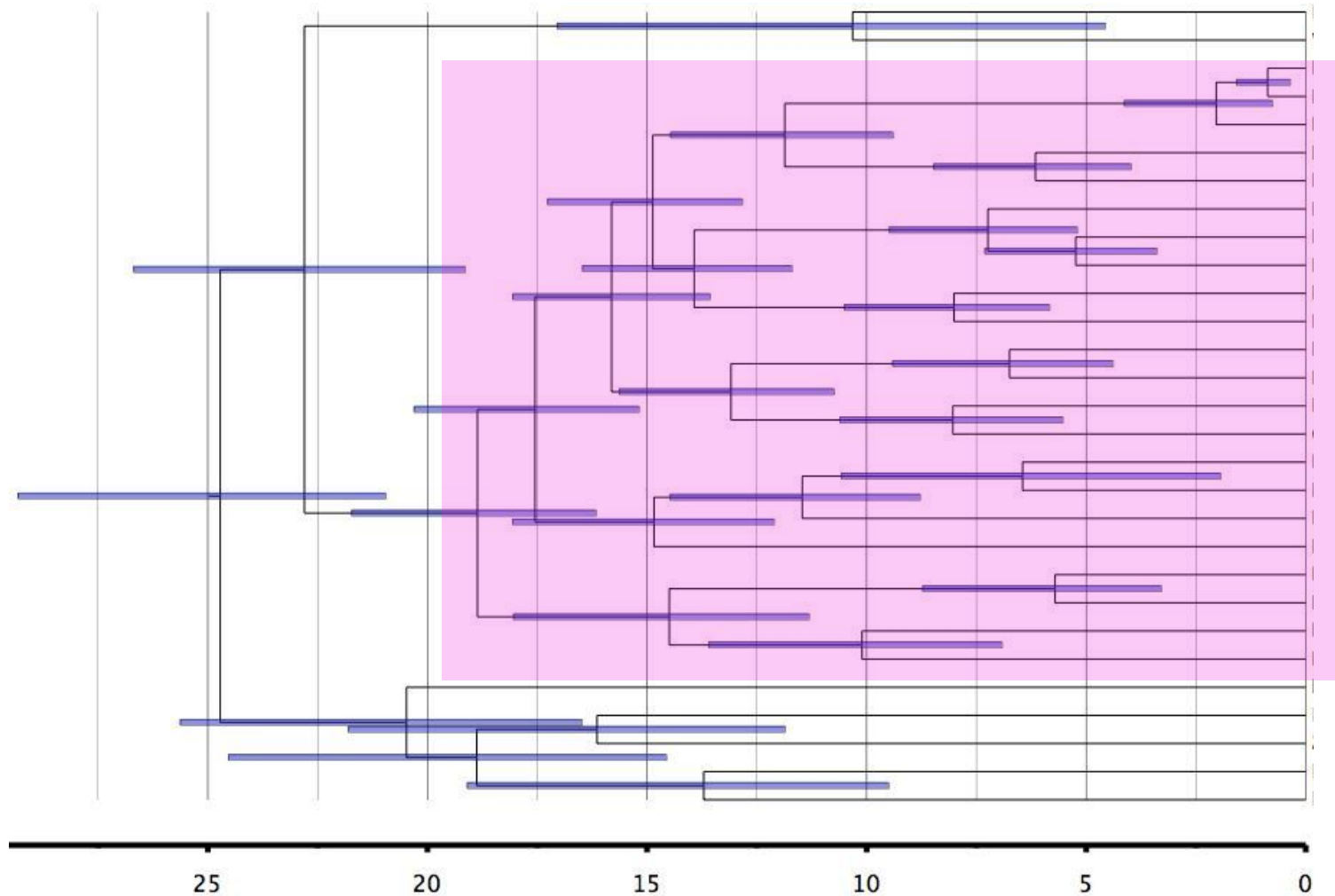
References

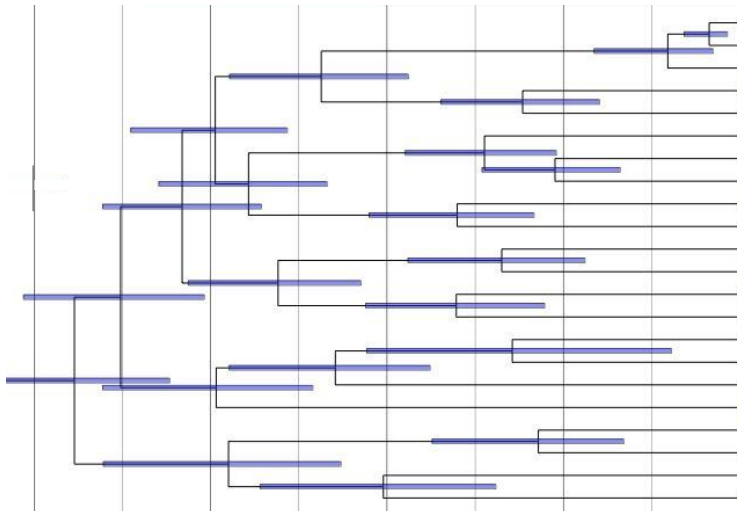
- Barraclough**, T. G., Vogler, A. P., & Harvey, P. H. (1998). Revealing the factors that promote speciation. *Philosophical Transactions of the Royal Society B*, 353(1366), 241–249.
- Beaulieu**, J. M., & O'Meara, B. C. (2016). Detecting hidden diversification shifts in models of trait-dependent speciation and extinction. *Systematic Biology*, 65(4), 583–601.
<https://doi.org/10.1093/sysbio/syw022>
- Caetano**, D. S., O'Meara, B. C., & Beaulieu, J. M. (2018). Hidden state models improve state-dependent diversification approaches, including biogeographical models. *Evolution*, 72(11), 2308–2324.
<https://doi.org/10.1111/evo.13602>
- Condamine**, F. L., Rolland, J., Höhna, S., Sperling, F. A., & Sanmartín, I. (2018). Testing the role of the Red Queen and Court Jester as drivers of the macroevolution of Apollo butterflies. *Systematic Biology*, 67(6), 940–964. <https://doi.org/10.1093/sysbio/syy009>
- Sanmartín**, I., & Meseguer, A. S. (2016). Extinction in phylogenetics and biogeography: from timetrees to patterns of biotic assemblage. *Frontiers in Genetics*, 7, 35. <https://doi.org/10.3389/fgene.2016.00035>
- López-Estrada**, E. K., Sanmartín, I., Uribe, J. E., Abalde, S., Jiménez-Ruiz, Y., & García-París, M. (2022). Mitogenomics and hidden-trait models reveal the role of phoresy and host shifts in the diversification of parasitoid blister beetles (Coleoptera: Meloidae). *Molecular Ecology*, 31(8), 2453–2474.
- López-Estrada**, E. K., Sanmartín, I., García-París, M., & Zaldívar-Riverón, A. (2019). High extinction rates and non-adaptive radiation explains patterns of low diversity and extreme morphological disparity in North American blister beetles (Coleoptera, Meloidae). *Molecular Phylogenetics and Evolution*, 130, 156–168. <https://doi.org/10.1016/j.ympev.2018.09.014>

Estimas de tasas de diversificación y extinción: **Metodología**



Estimas de tasas de diversificación y extinción: **Metodología**





Linajes a lo largo del tiempo

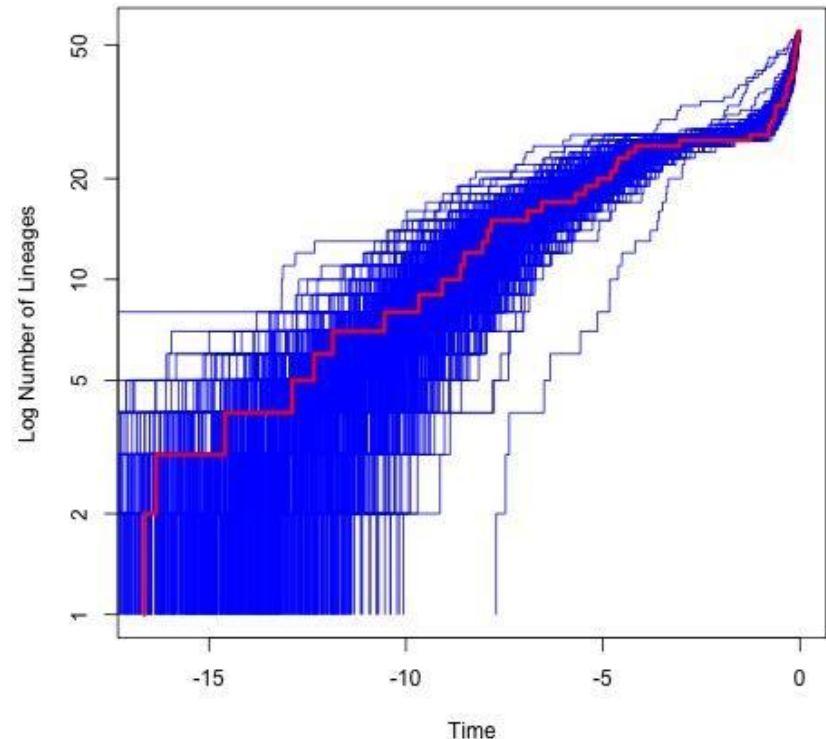
(Lineage through time plot)

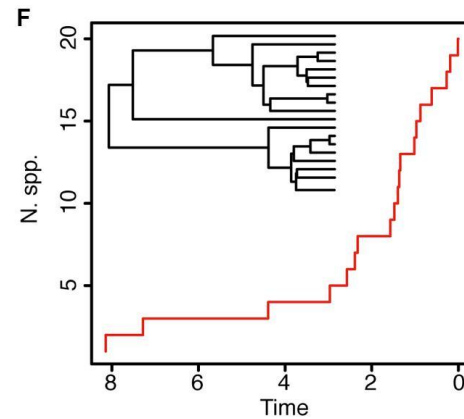
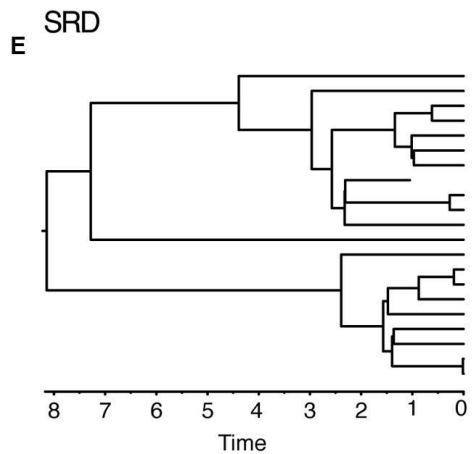
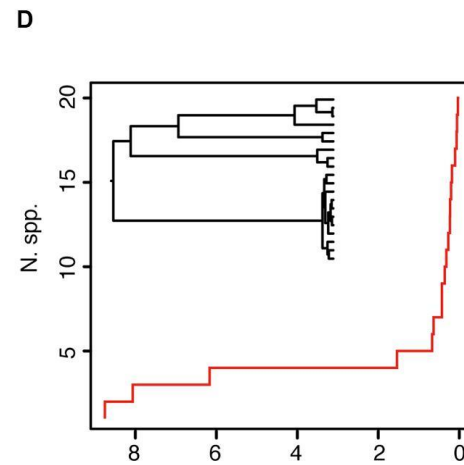
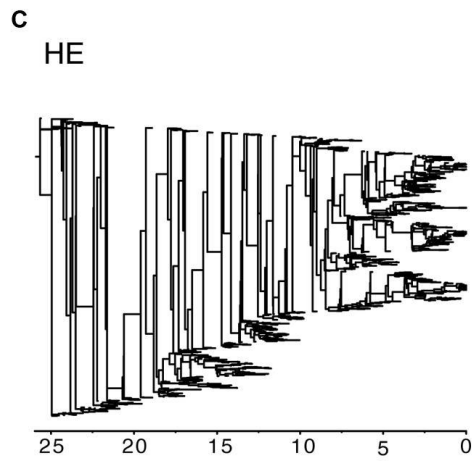
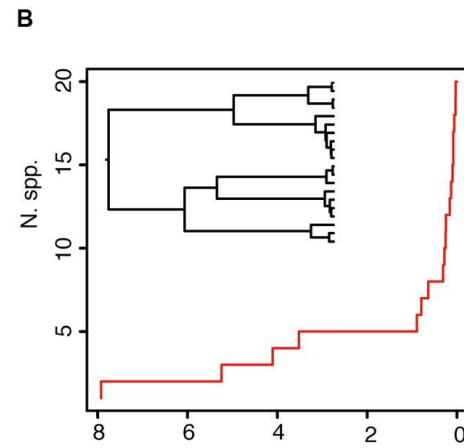
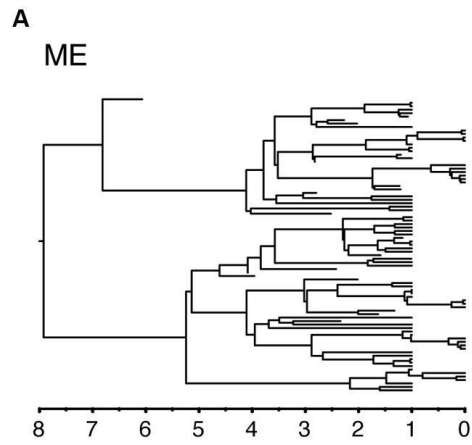
ltt.plot (ape R package)

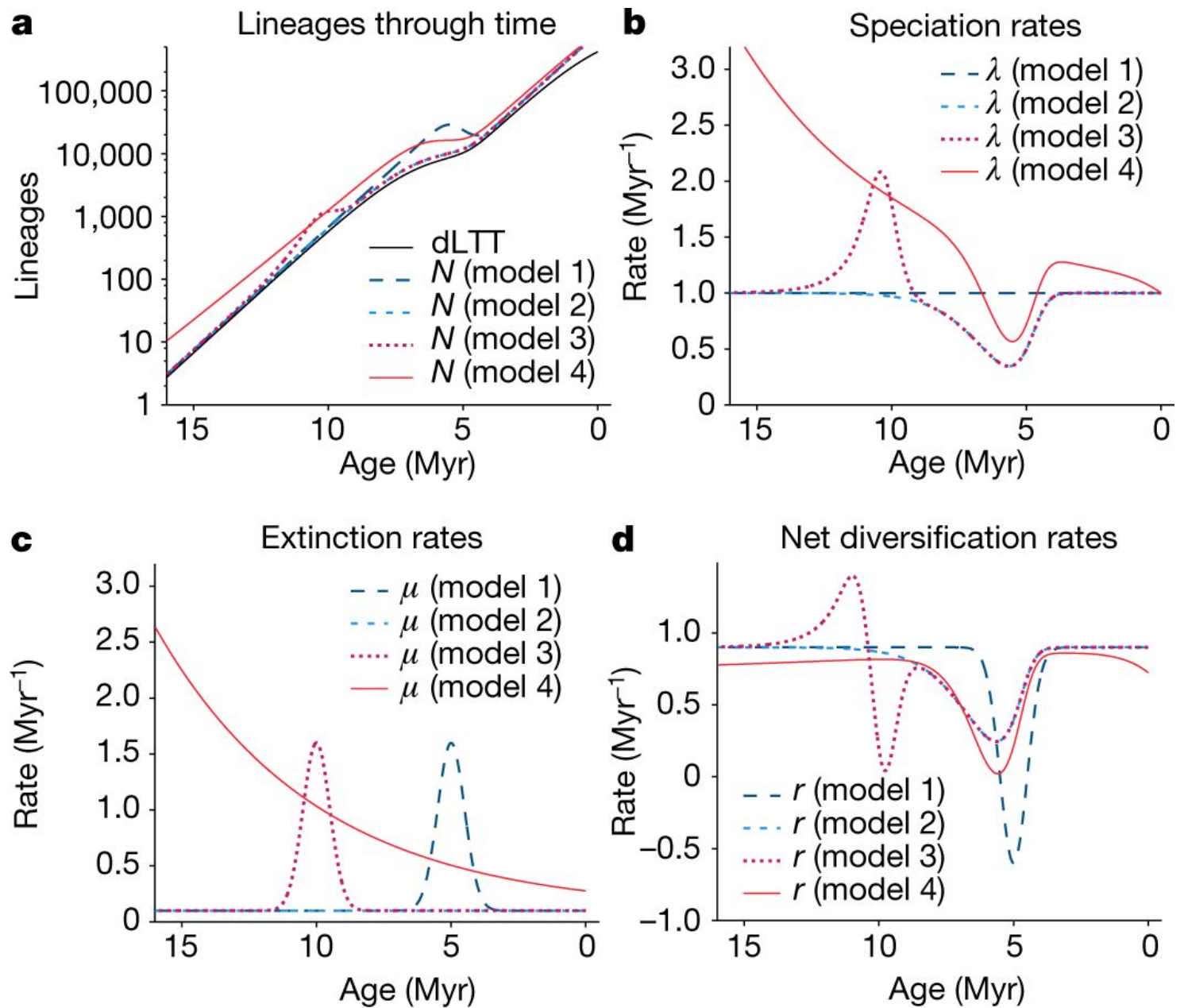
Explorar el patrón GENERAL
de diversificación

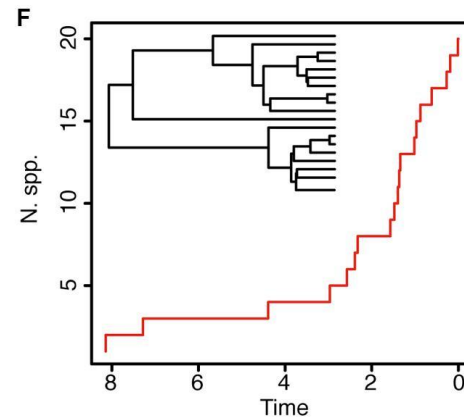
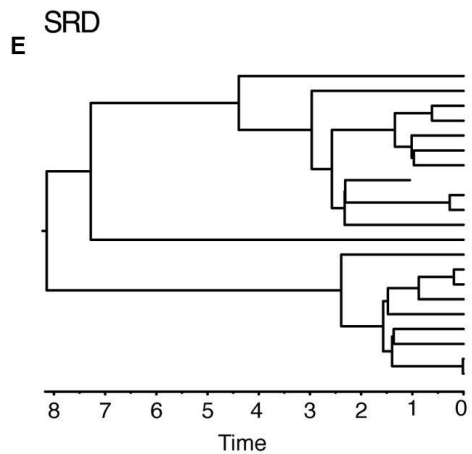
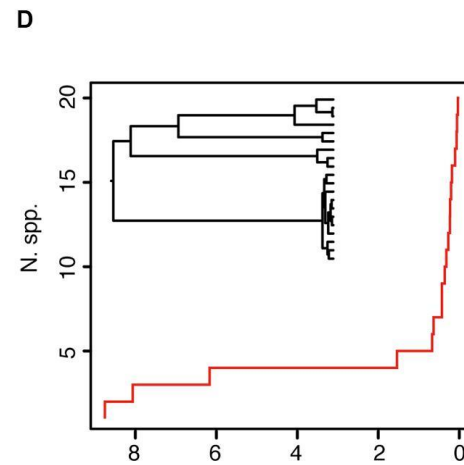
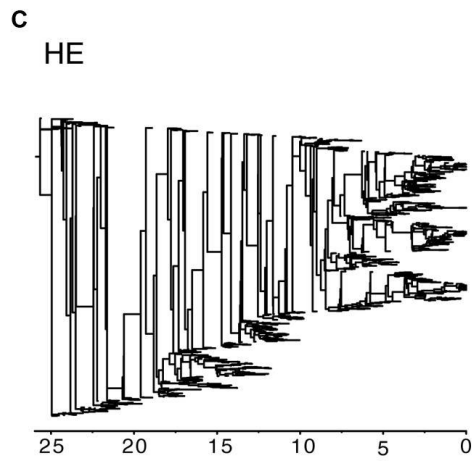
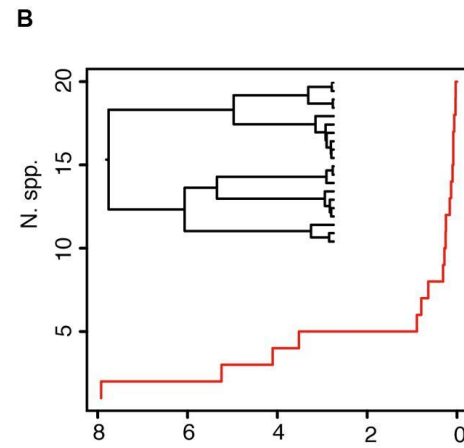
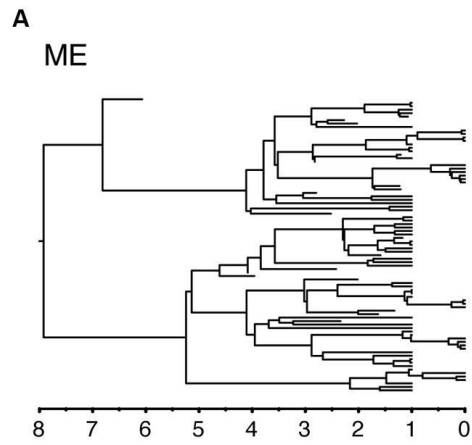
Diferentes historias evolutivas
reconstruyen
el mismo patrón

“Pull of the present”

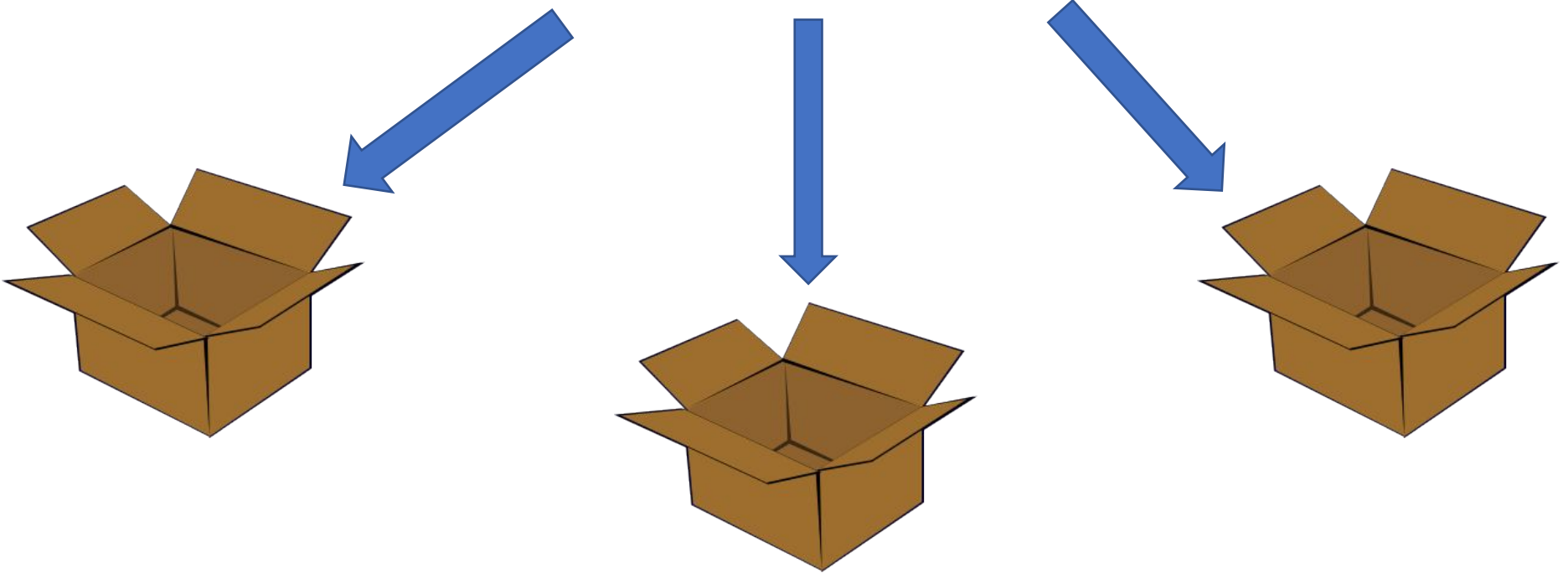
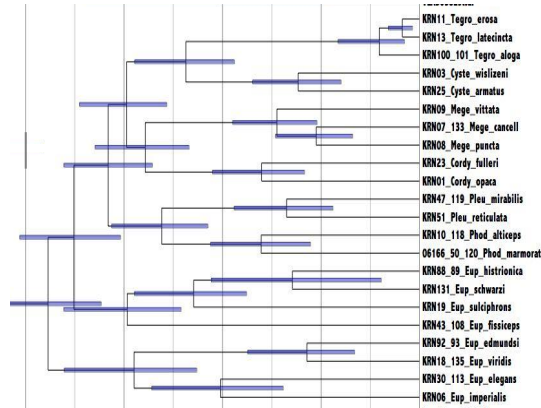








Ajuste estadístico a modelos de especiación







Welsh Corgi



Siberian Husky



Dachshund



Beagle



Rottweiler



Pug



Akita Inu



Jack Russell Terrier



Pomeranian



Dalmatian



Chihuahua



Golden Retriever



Doberman Pinscher



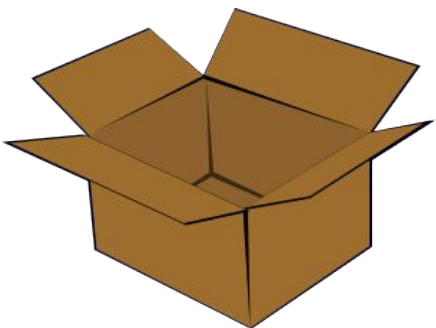
Saint Bernard



Shih Tzu



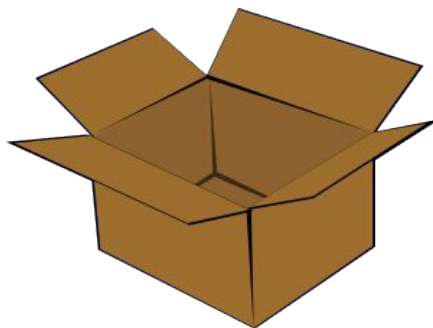
Riesenschнауzer



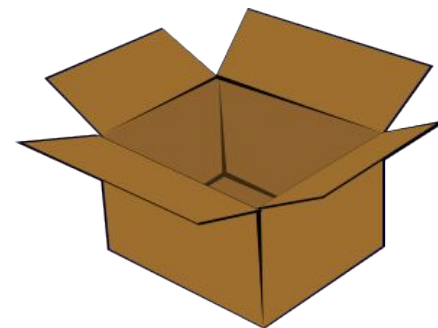
Modelo Yule

$$\lambda = \text{cte.}$$

$$\mu = 0$$



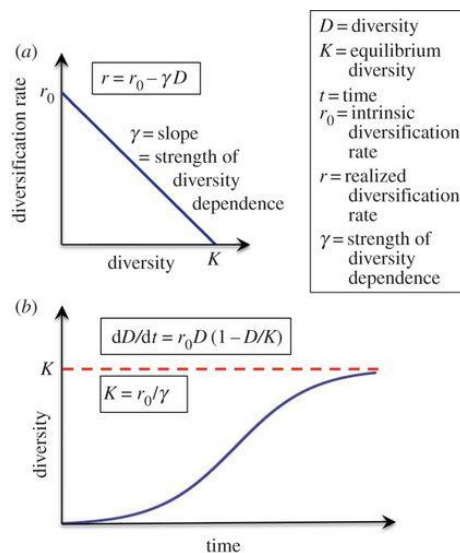
Diversificación
Dependiente de
la densidad



↓ ↓

$$\lambda \mu \neq 0$$

Modelo nacimiento/
Muerte



Modelo	Características principales	Supuestos	Aplicaciones específicas
Yule (Pure Birth)			
Birth-Death			
Density-Dependent (DD)			

bd.shifts.optim

(TreePar R package)

bd.densdep.optim

bd.shifts.optim(tr,rho,grid,start,end,yule=TRUE)

bd.shifts.optim

(TreePar R package)

bd.densdep.optim

Longitud de las ramas



bd.shifts.optim(*tr*,rho,grid,start,end,yule=TRUE)

bd.shifts.optim

(TreePar R package)

bd.densdep.optim

Porcentaje de efectividad del muestreo



bd.shifts.optim(tr,rho**,grid,start,end,yule=TRUE)**

bd.shifts.optim

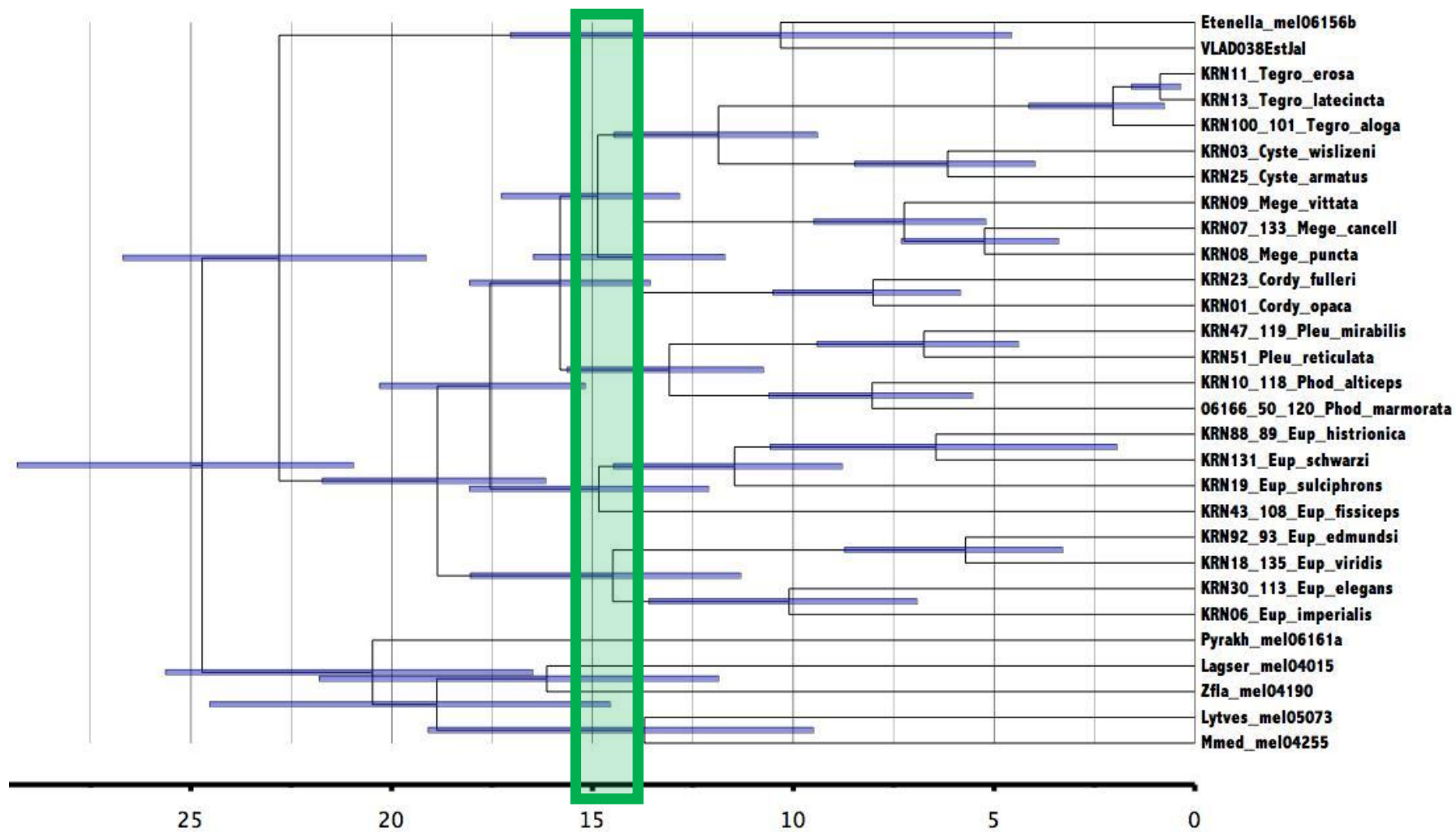
(TreePar R package)

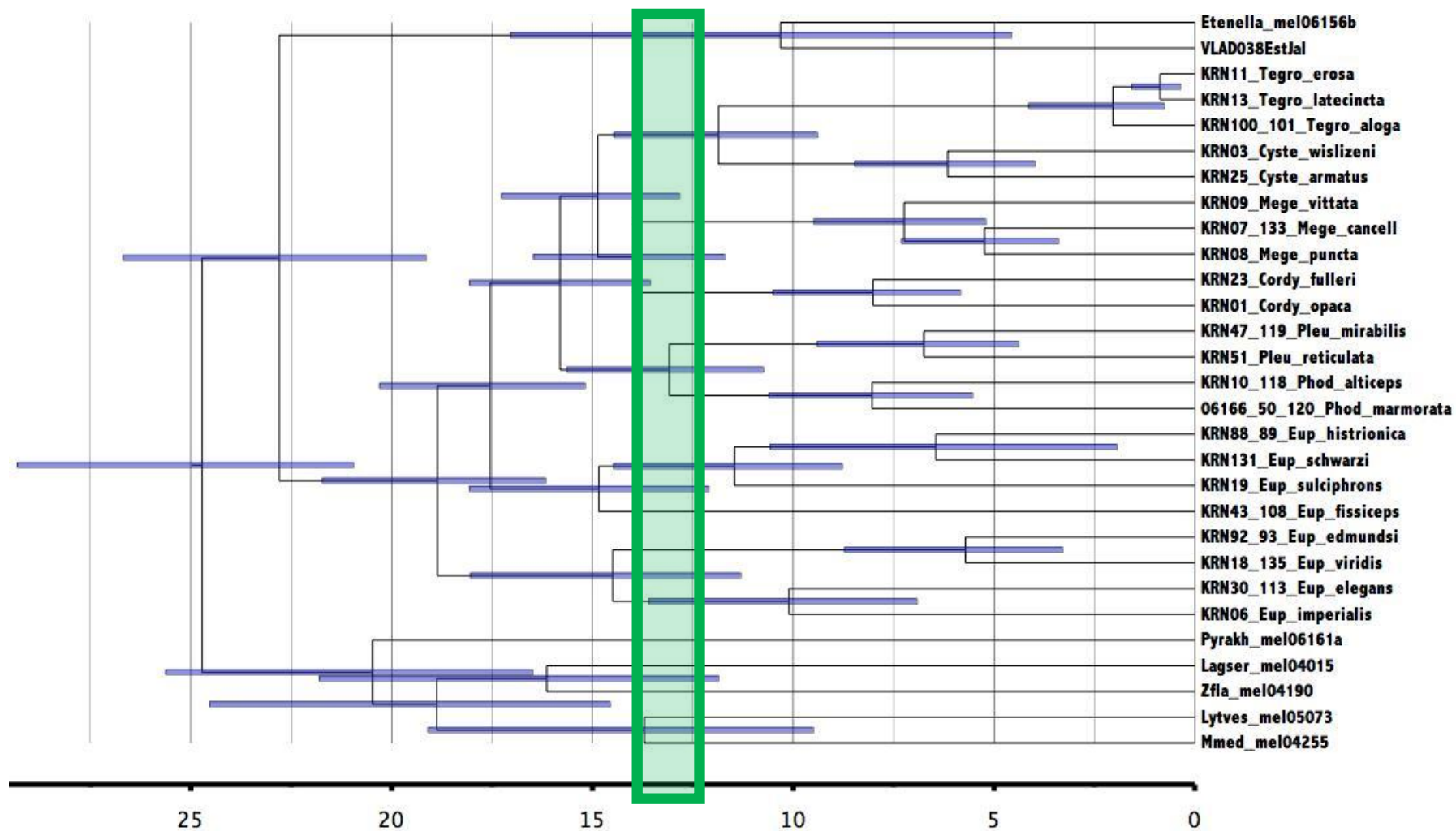
bd.densdep.optim

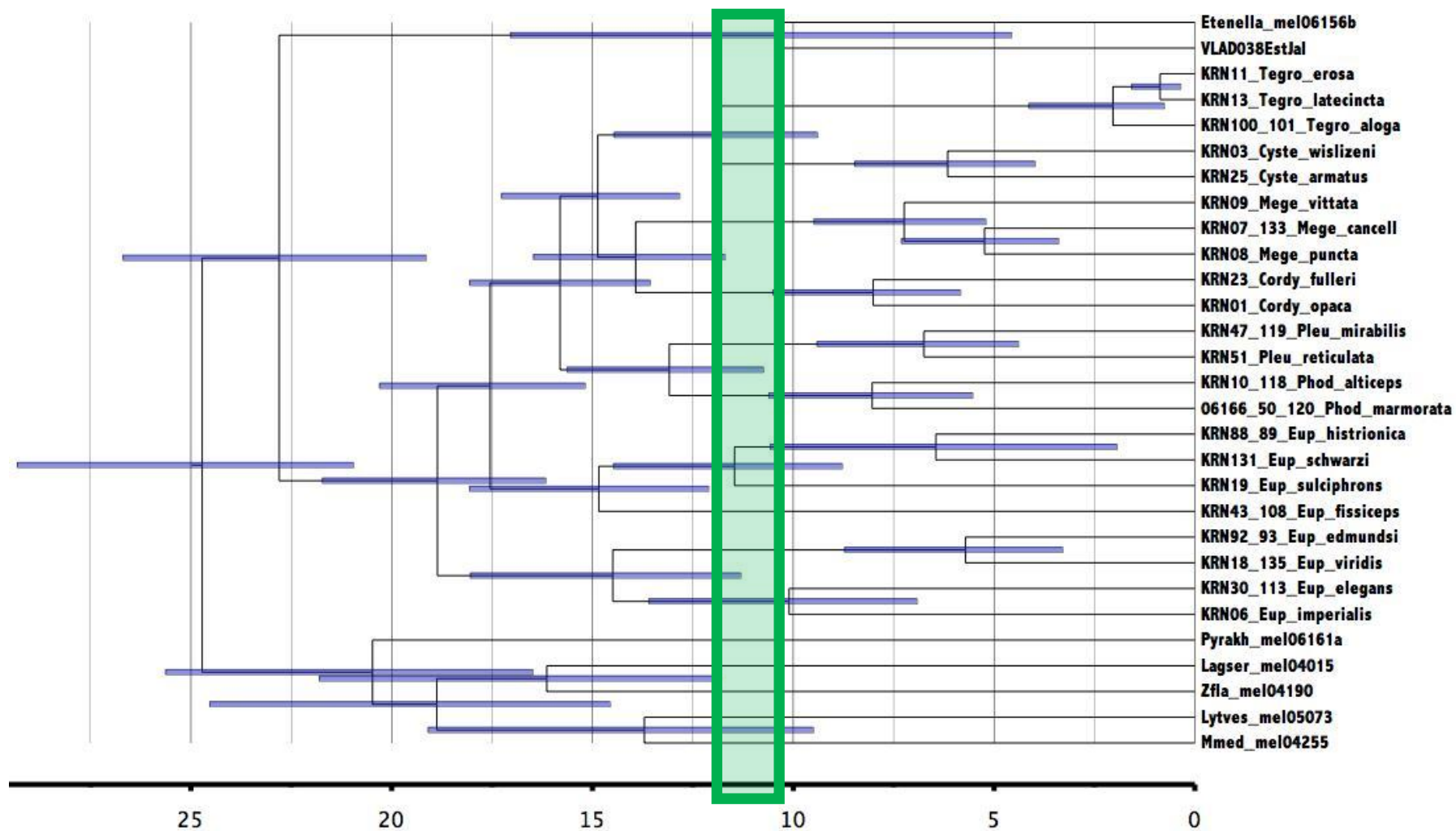
“ventana” de actualización



bd.shifts.optim(tr,rho,grid,start,end,yule=TRUE)







bd.shifts.optim

(TreePar R package)

bd.densdep.optim

t_0



bd.shifts.optim(tr,rho,grid,start**,end,yule=TRUE)**

bd.shifts.optim

(TreePar R package)

bd.densdep.optim

Último evento de especiación



bd.shifts.optim(tr,rho,grid,start,end,yule=TRUE)

bd.shifts.optim

(TreePar R package)

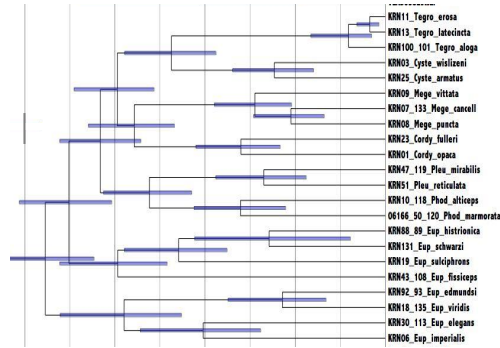
bd.densdep.optim

bd.shifts.optim(tr,rho,grid,start,end,yule=TRUE)

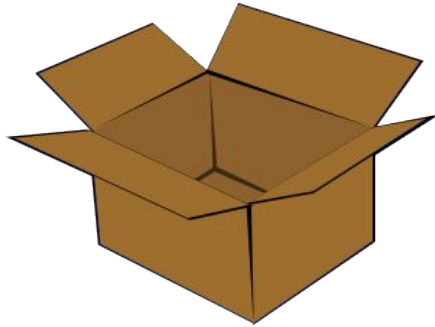


$\mu = 0$

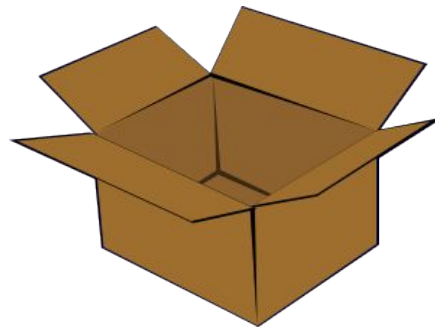
$\mu \neq 0$



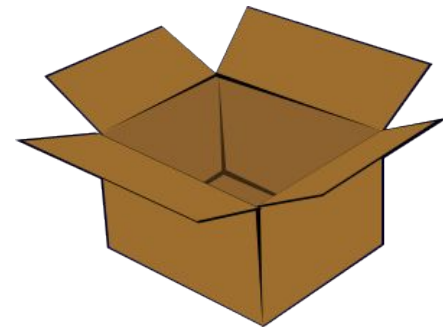
Likelihood ratio test



Yule

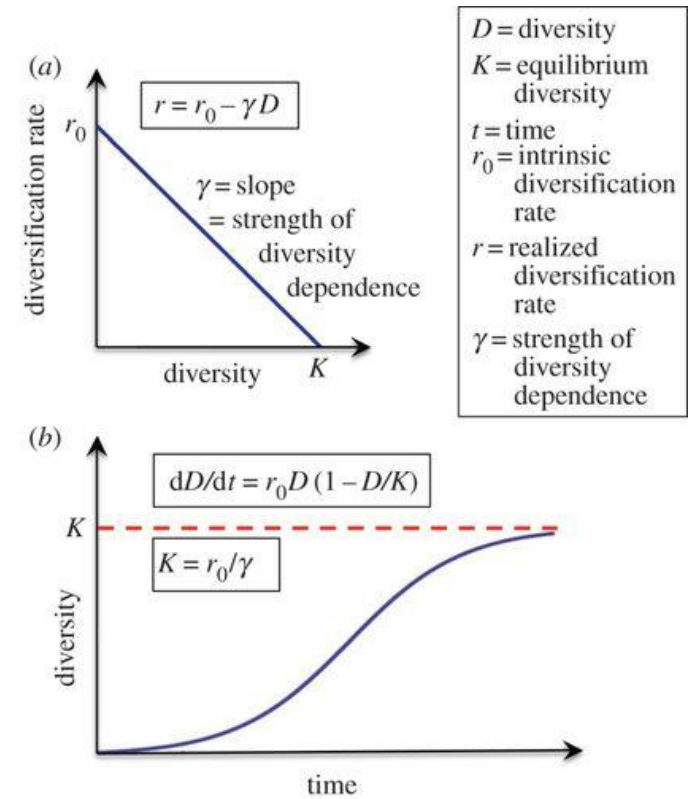


DD



BD

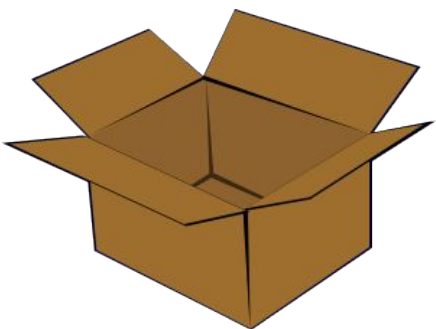
bd.densdep.optim



```
bd.densdep.optim(x,minK,maxK,discrete=TRUE,continuous=FALSE,
lambdainit=2,
muinit=1,Kinit=0,Yule=FALSE,muset=0,rho=1,model=-1)
```

Prueba de razón de verosimilitud

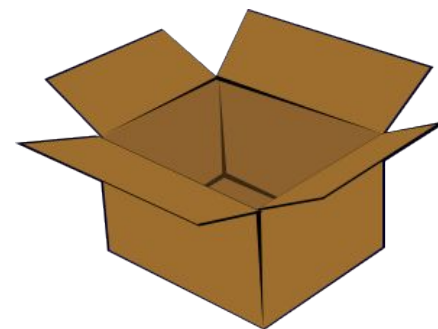
- La prueba de razón de verosimilitud es una prueba de la suficiencia de un modelo más pequeño frente a un modelo más complejo. La hipótesis nula de la prueba indica que el modelo más pequeño proporciona un ajuste tan bueno para los datos como el modelo más grande. Si se rechaza la hipótesis nula, el modelo alternativo más grande proporciona una mejora significativa sobre el modelo más pequeño.
- Para utilizar la prueba de razón de verosimilitud, el modelo de hipótesis nula debe ser un modelo anidado dentro, es decir, un caso especial del modelo de hipótesis alternativo



Diversificación
constante

$$\lambda = \text{cte.}$$

$$\mu = 0$$



↓ ↓

$$\lambda \quad \mu \neq 0$$

$$LR = 2 * (\ln L1 - \ln L2)$$



RevBayes tutorial

**¿Qué otros parámetros
podríamos incluir a los modelos
para calcular la tasa de
diversificación de un clado?**