TRAIT EVOLUTION

Identifying complex interactions that modulate trait evolution

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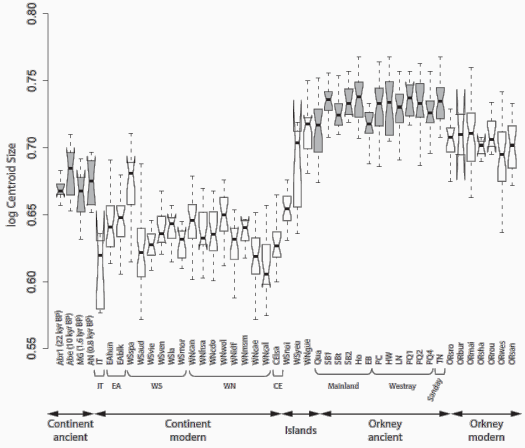
Molar size change during island colonization

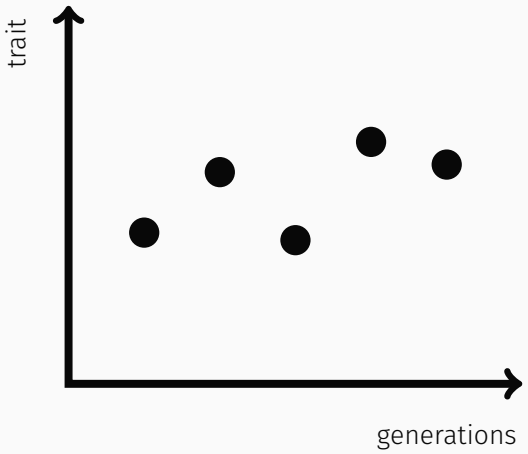
[1]Photo: Andy Belshaw, flikr; Cucchi et al. 2014. Evolution.

Molar size change during island colonization

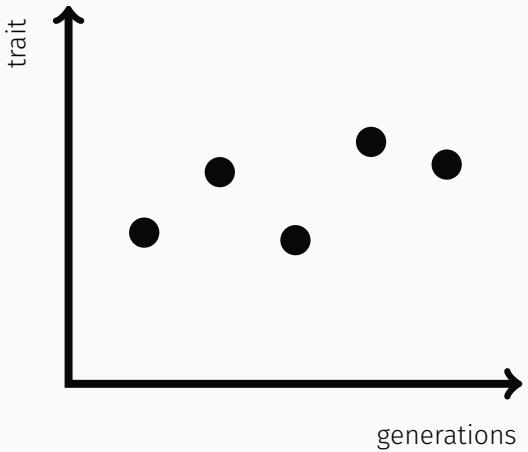


[1]Photo: Andy Belshaw, flikr; Cucchi et al. 2014. Evolution.

Trait evolution



Trait evolution

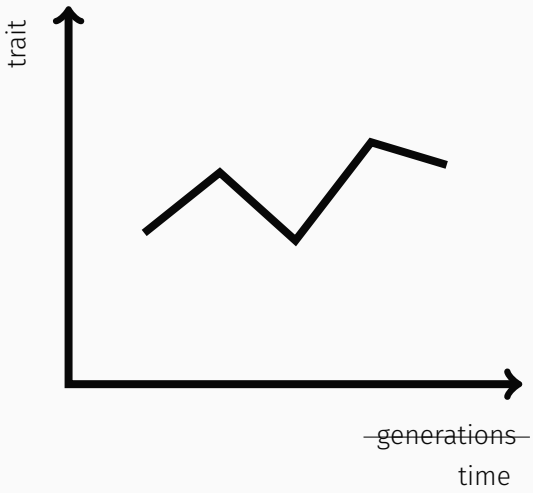


heritable component

changes between generations

mutation accumulation

Trait evolution



Markov chain

heritable component

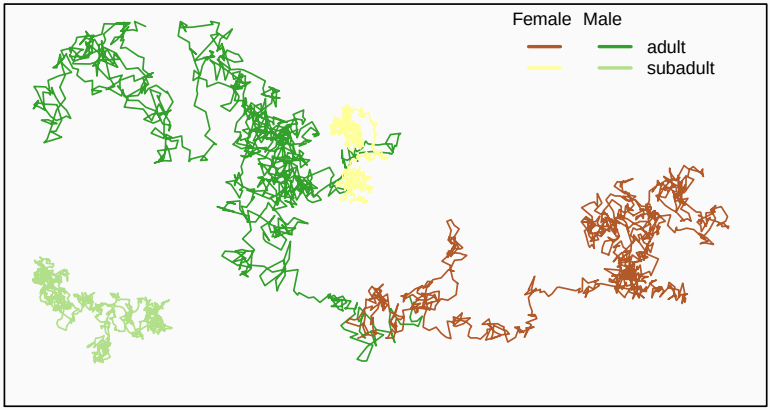
- value depends on the previous value

changes between generations

mutation accumulation

- trait value in a child adds a random component

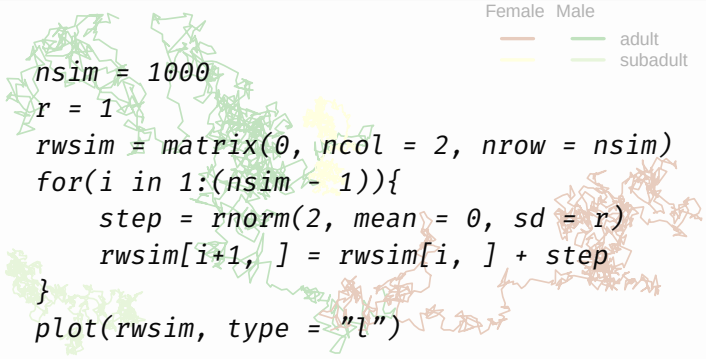
Markov chains in a random walk



$\mathcal{N}(0, \sigma^2)$

[1] Smolinský et al. 2021. J. Vertebr. Biol.

Markov chains in a random walk



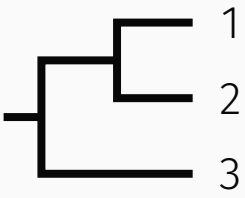

```
nsim = 1000
r = 1
rwsim = matrix(0, ncol = 2, nrow = nsim)
for(i in 1:(nsim - 1)){
    step = rnorm(2, mean = 0, sd = r)
    rwsim[i+1, ] = rwsim[i, ] + step
}
plot(rwsim, type = "l")
```

$\mathcal{N}(0, \sigma^2)$

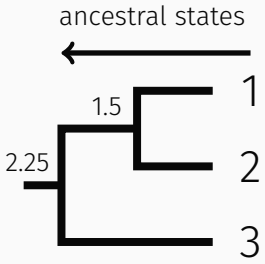
[1] Smolinský et al. 2021. J. Vertebr. Biol.

1D – TRAIT EVOLUTION WITH SPECIES DIVERGENCE

Brownian motion – neutral evolution



Brownian motion – neutral evolution



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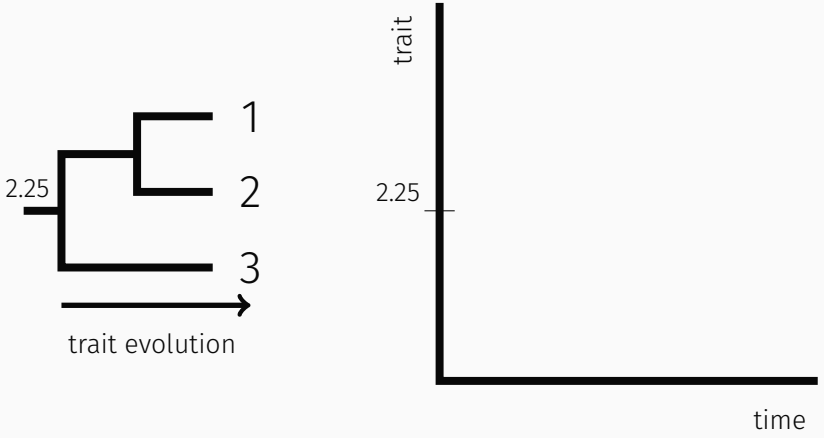

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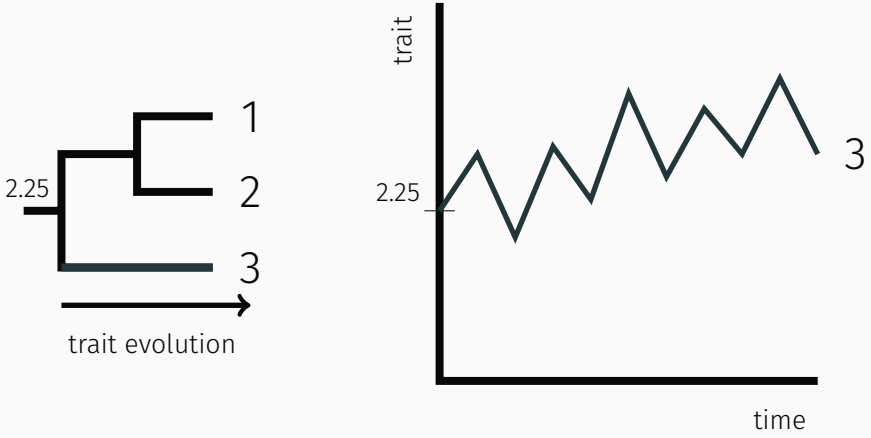

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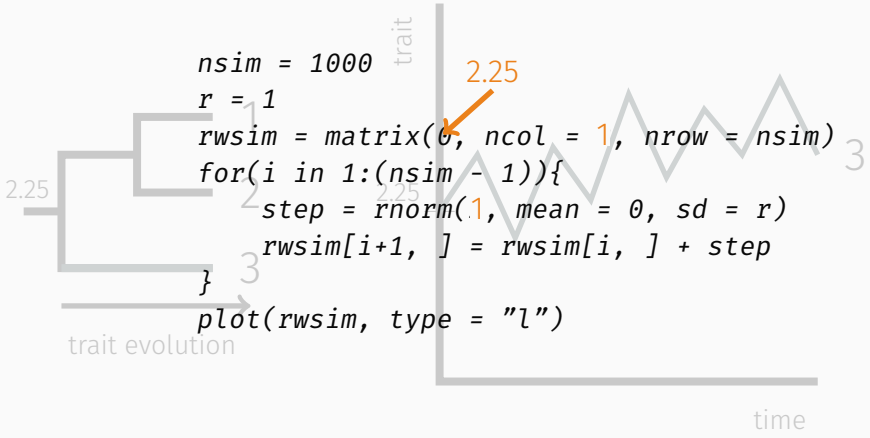

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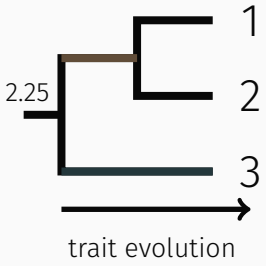

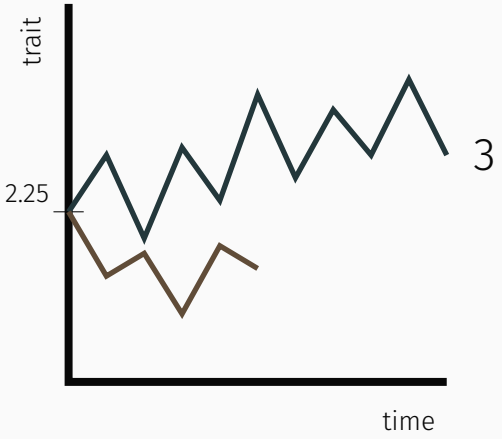

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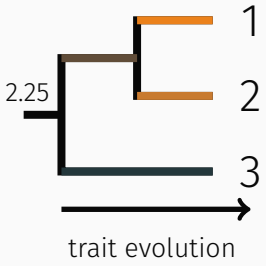
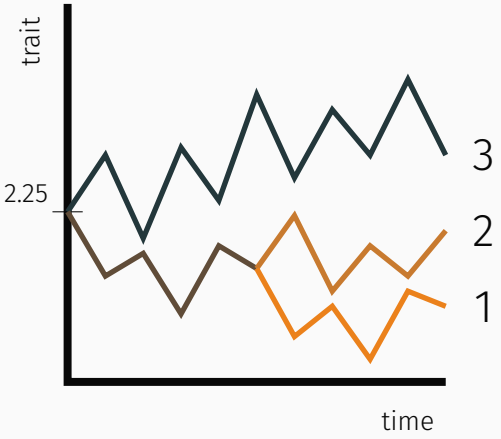
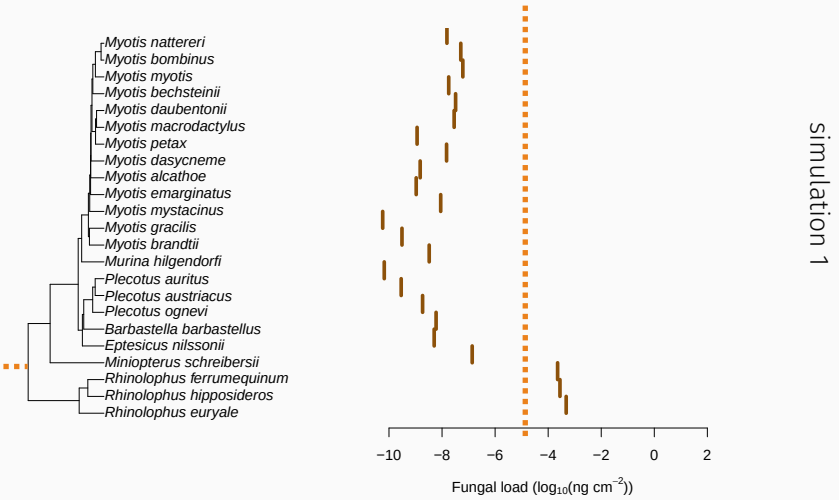




Simulation of trait evolution on a phylogeny



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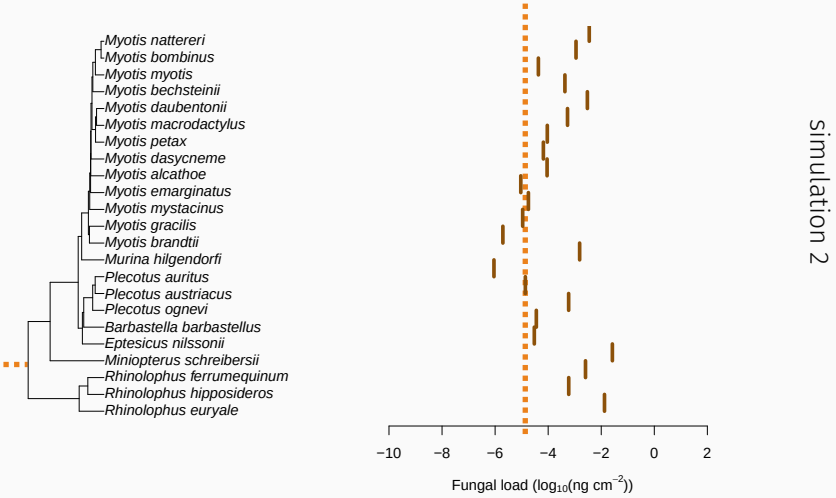

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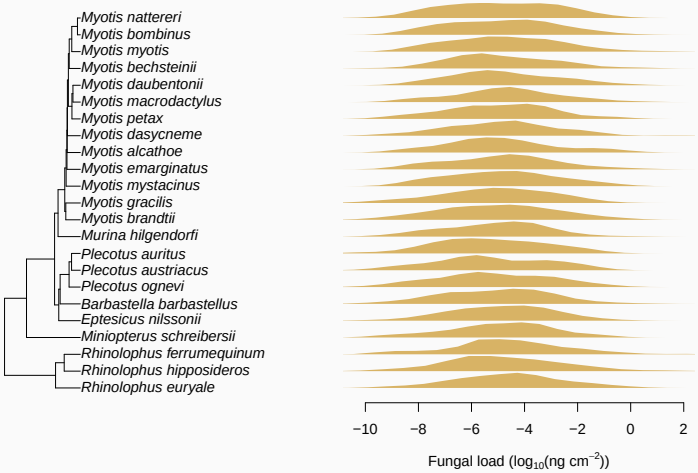

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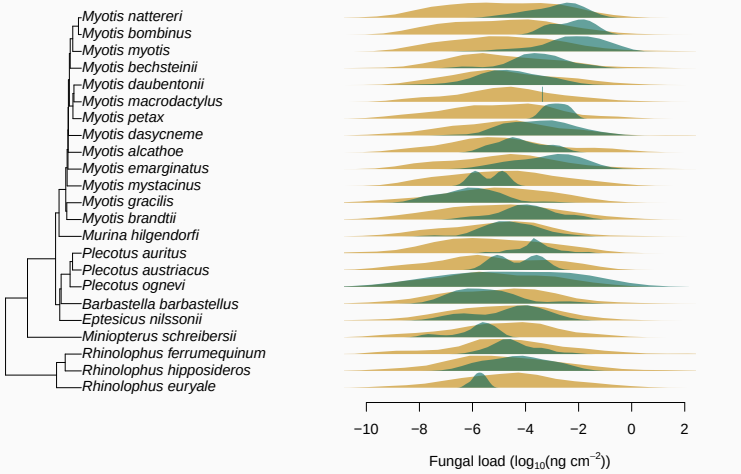
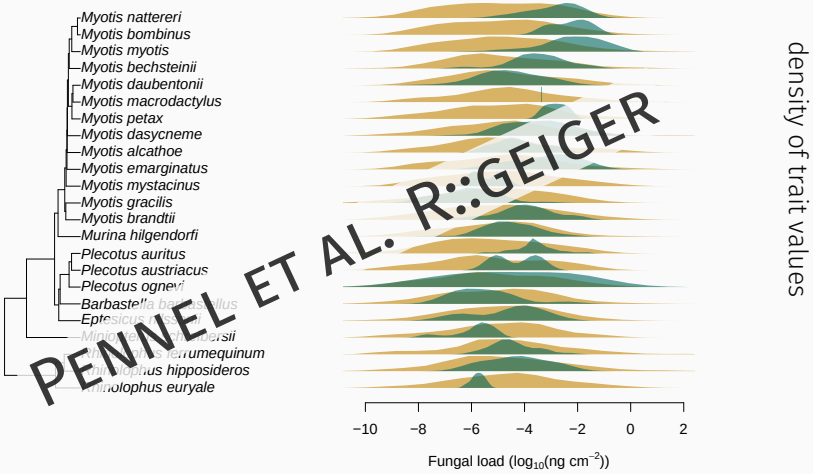


[1]Zukal et al. 2016. Sci. Rep.

Simulation of trait evolution on a phylogeny



2D – MOVING ACROSS SPACE

Geographically explicit phylogeography

[1]Králová I. 2016. Master Thesis. MUNI.

Geographically explicit phylogeography

each sequence has two geographic coordinates

each coordinate evolves with Brownian motion as a trait

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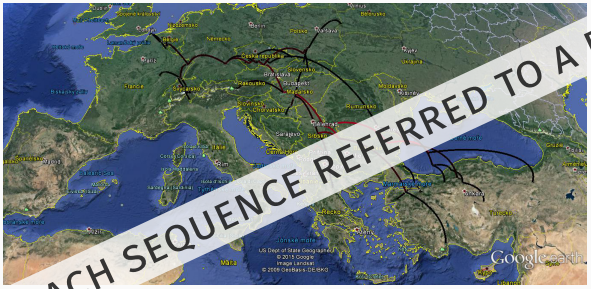


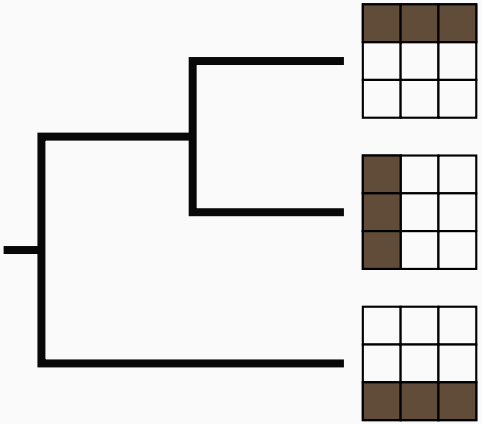
What if each sequence referred to a range?

each sequence has two geographic coordinates

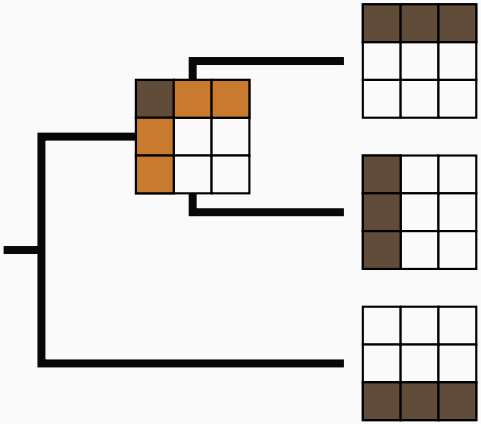
each coordinate evolves with Brownian motion as a trait

[1]Králová I. 2016. Master Thesis. MUNI.

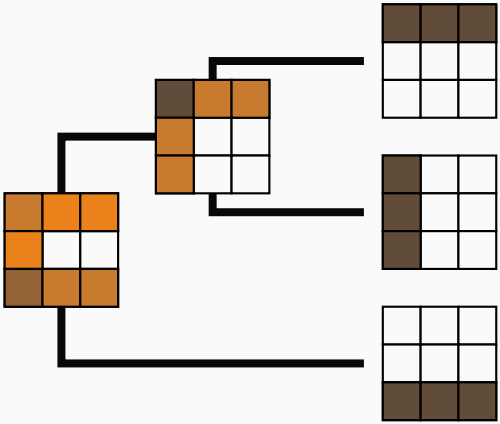
Discrete traits



Discrete traits

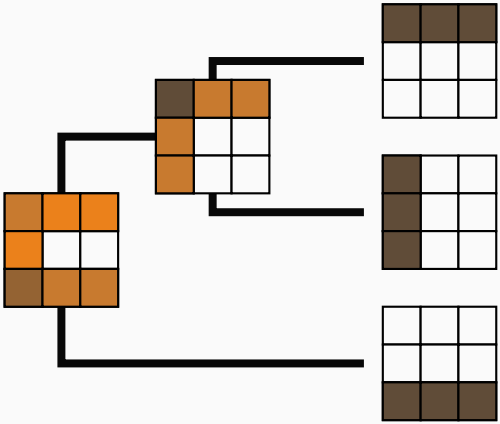


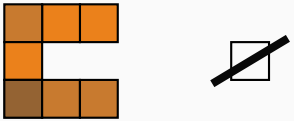
Discrete traits



ancestral range

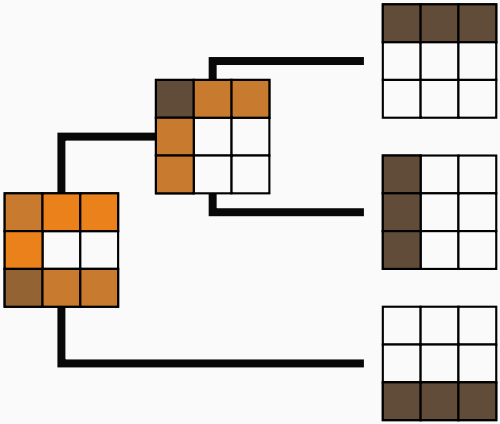
Discrete traits





ancestral range

Discrete traits



ancestral range

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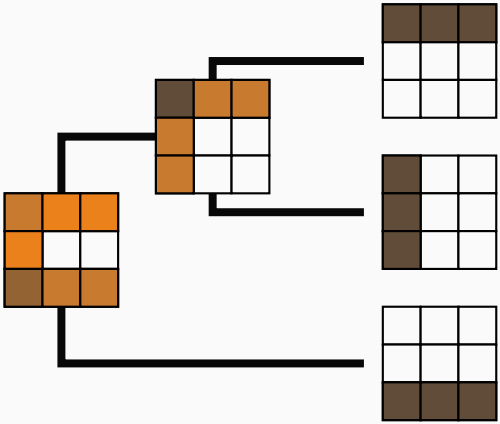
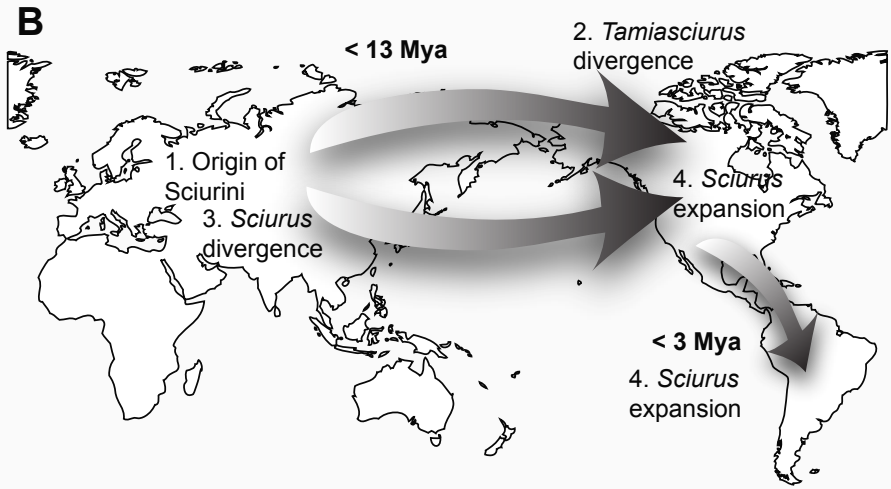


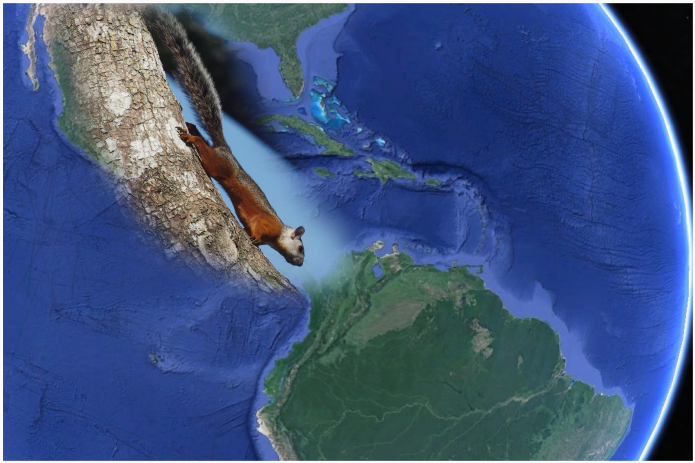
ancestral range

Tree squirrel divergence and dispersal



[1]Pečnerová & Martínková. 2012. Zool. Scr.

Tree squirrel speciation explosion in South America



[1]Photo: T. Bartoničkа

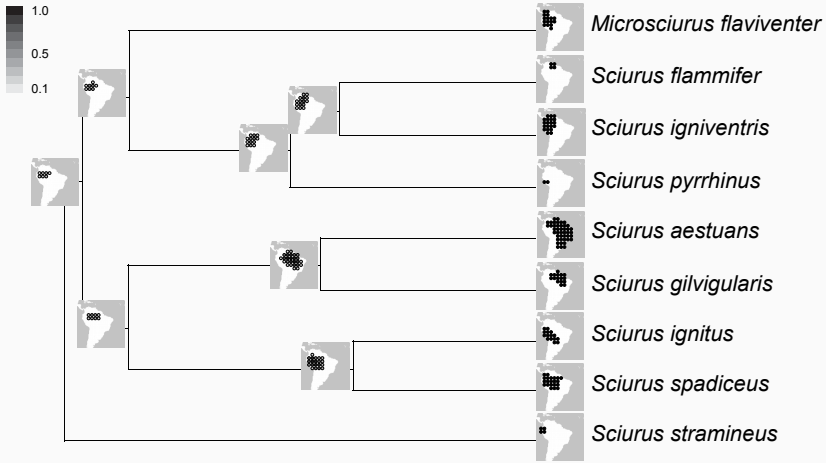
Tree squirrel speciation explosion in South America

distribution ranges in a grid with presence/absence data

modelled as evolution of discrete characters

[1]Pečnerová et al. 2015. Syst. Biol.

Tree squirrel speciation explosion in South America



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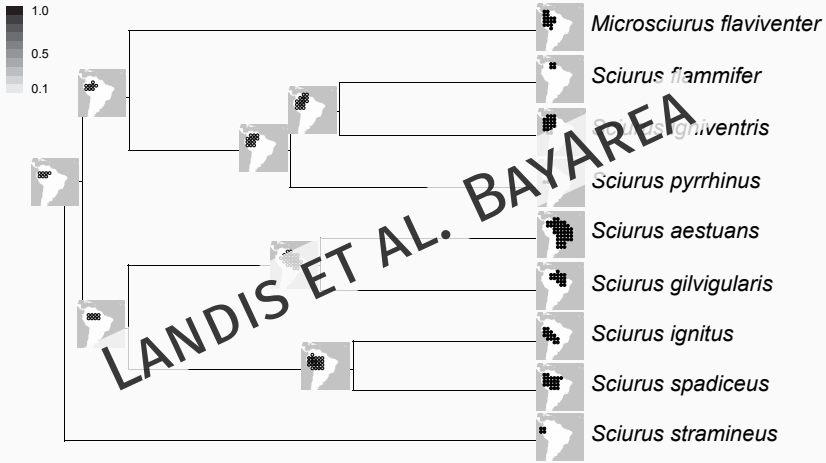

[1]Pečnerová et al. 2015. Syst. Biol.

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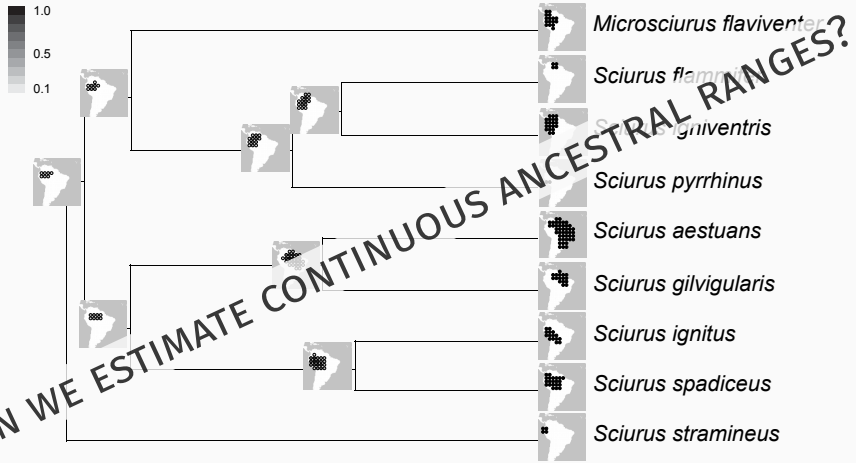
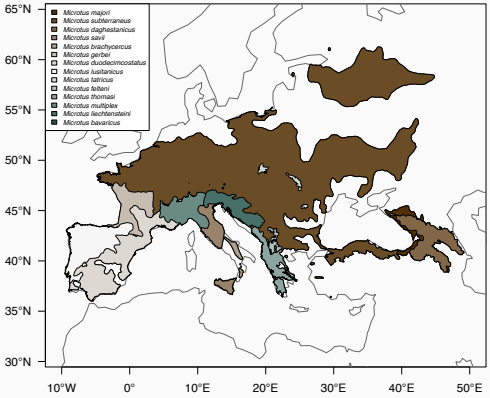
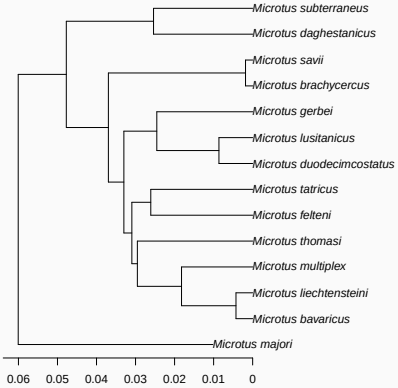


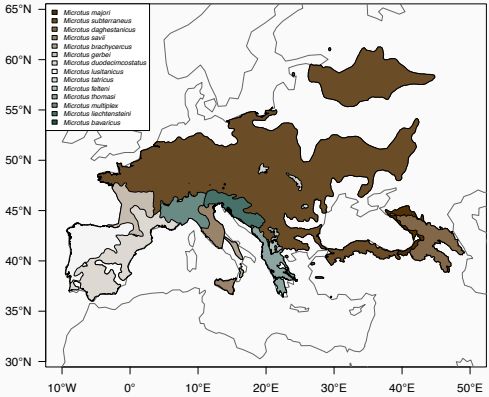
[1]Pečnerová et al. 2015. Syst. Biol.

Pine vole ancestral range



Pine vole ancestral range





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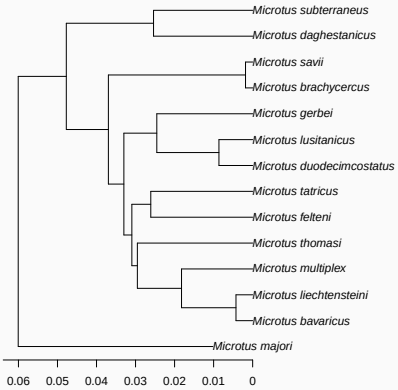

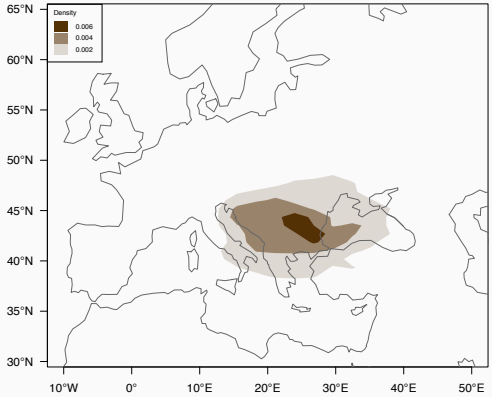

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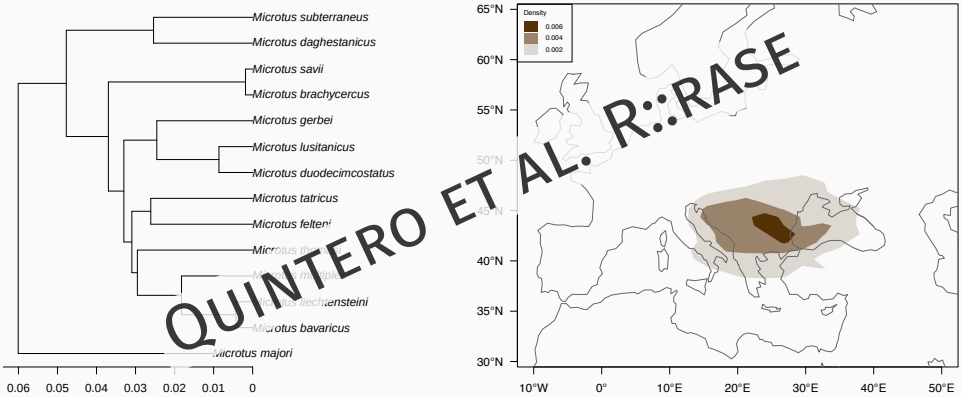
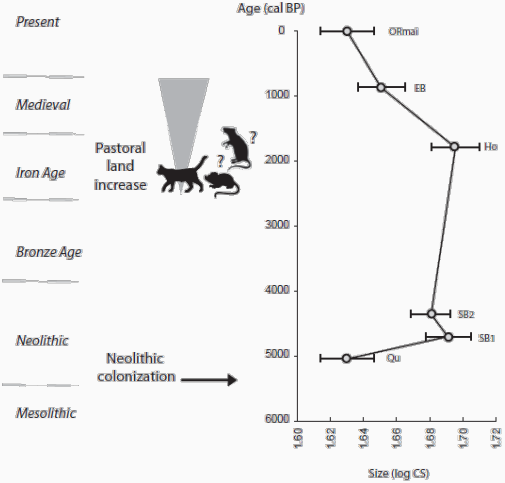


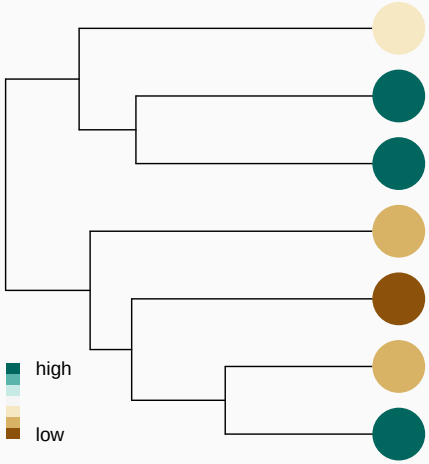
3D – BIOTIC INTERACTIONS ACROSS SPACE

Other species interactions influence trait evolution



[1]Photo: Andy Belshaw, flikr; Cucchi et al. 2014. Evolution.

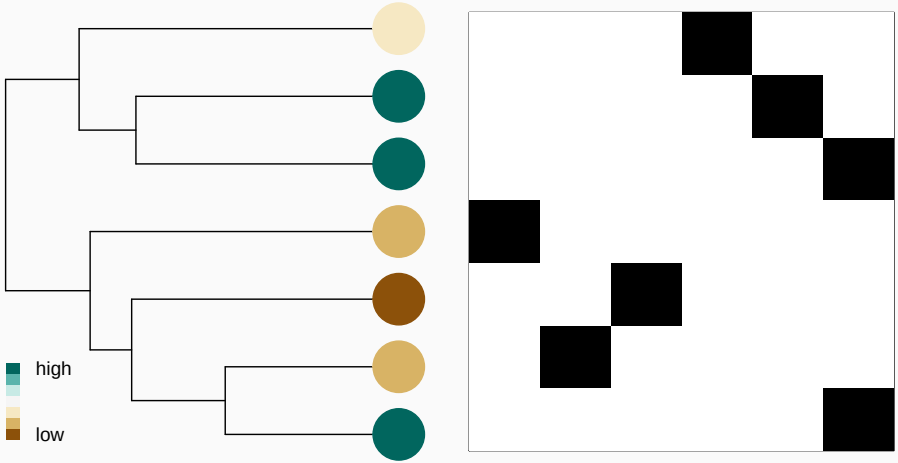
Bat ecological diversity



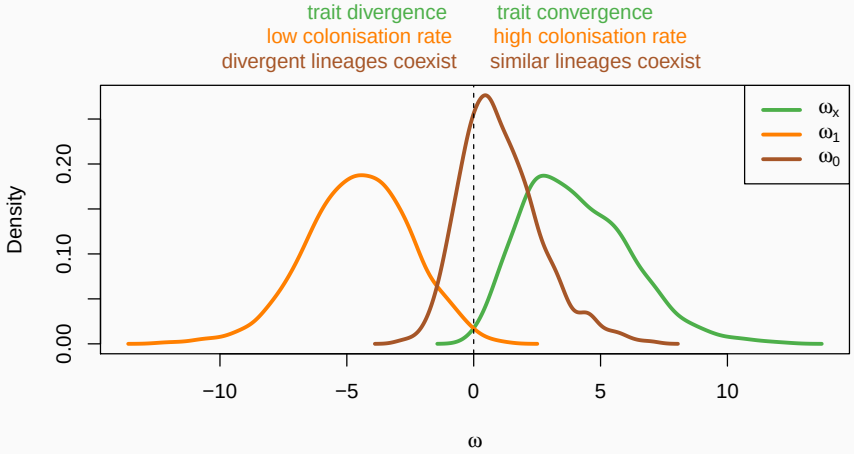
[1]Barracuda1983, wikimedia

Bat ecological diversity

continuous trait, discrete space

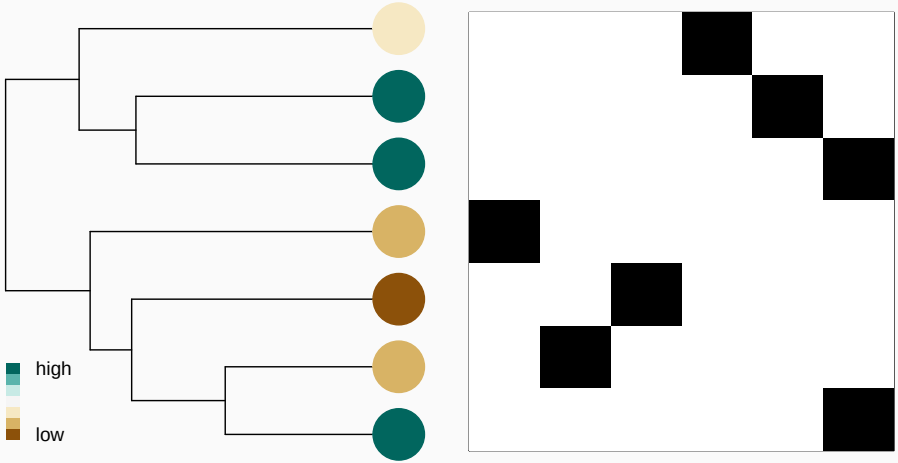


Bat ecological diversity



Bat ecological diversity

low colonisation rate, trait convergence



Bat ecological diversity

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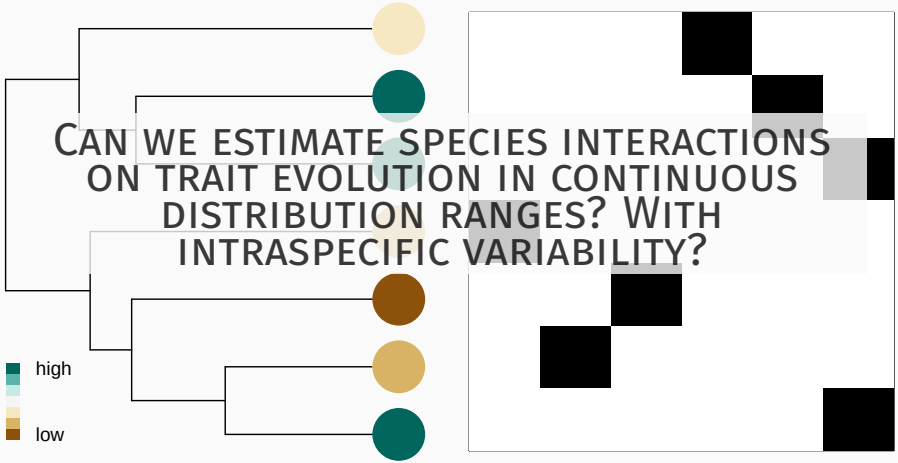

Can we estimate species interactions on trait evolution in continuous distribution ranges? With intraspecific variability?

Not that I know of :(

Thank you for your attention