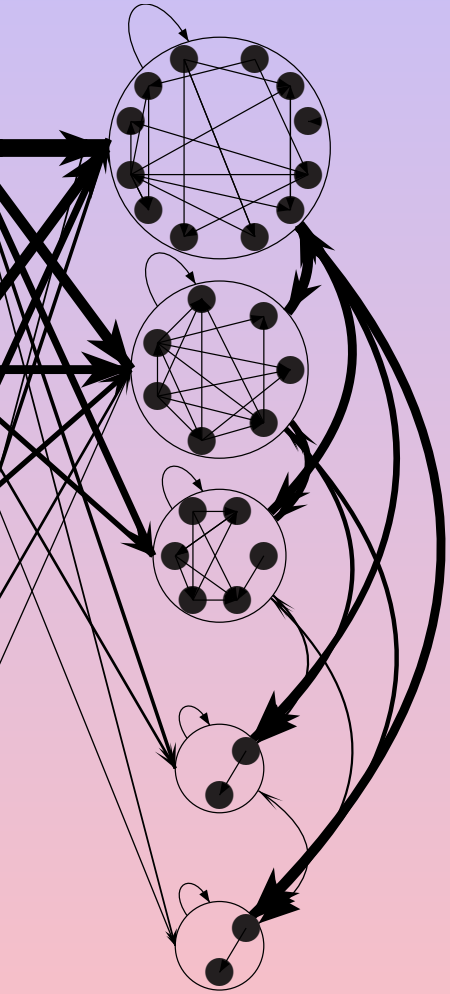
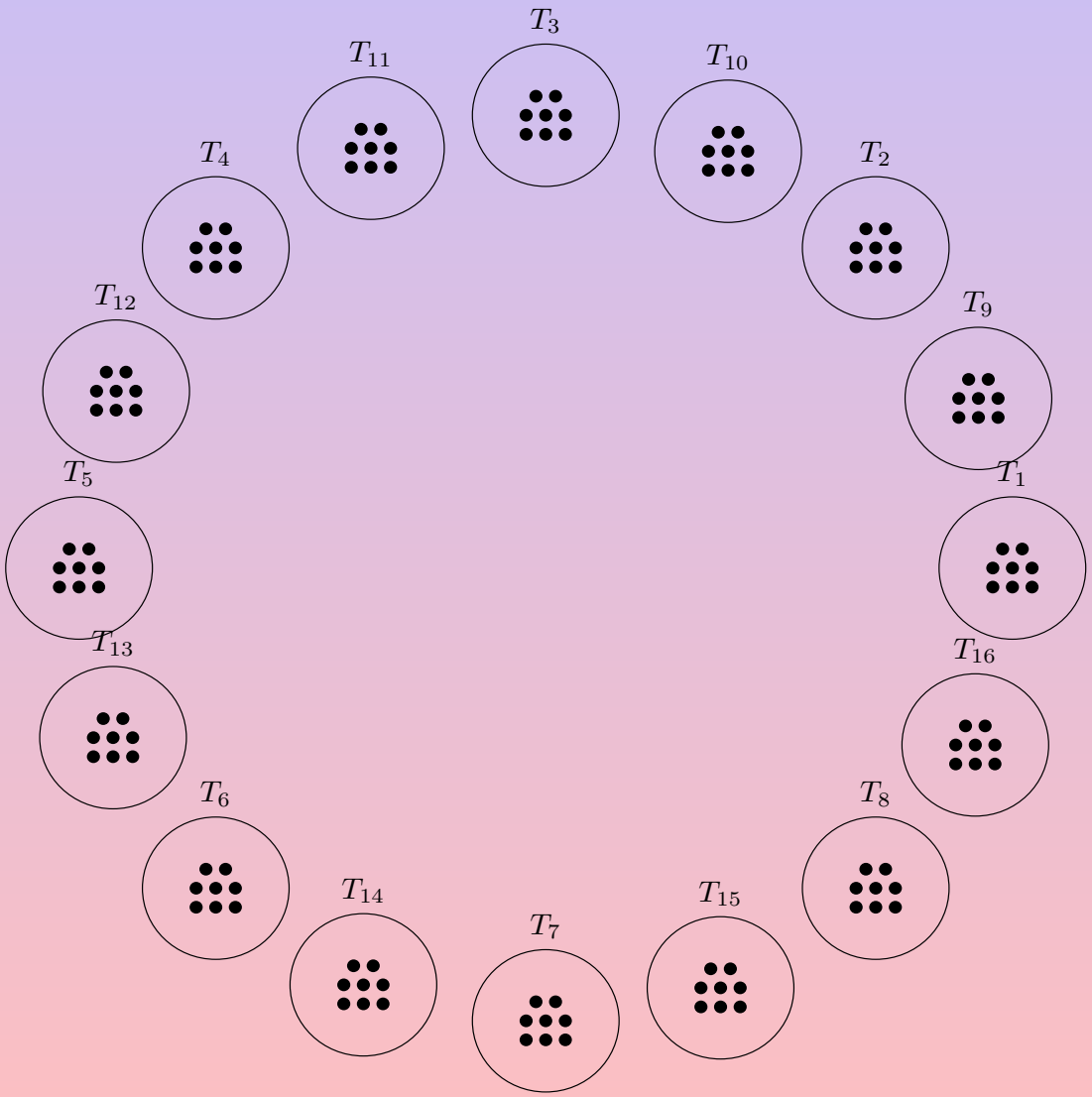
Carlos J. Melián
Center for Ecology, Evolution and Biogeochemistry
Swiss Federal Institute of Aquatic Science and Technology



Diversification Dynamics in Interdependent Networks

SEBES Seminar for Evolutionary Biology and Environmental Studies, U. Zürich, November 12, 2015

Individuals are complex



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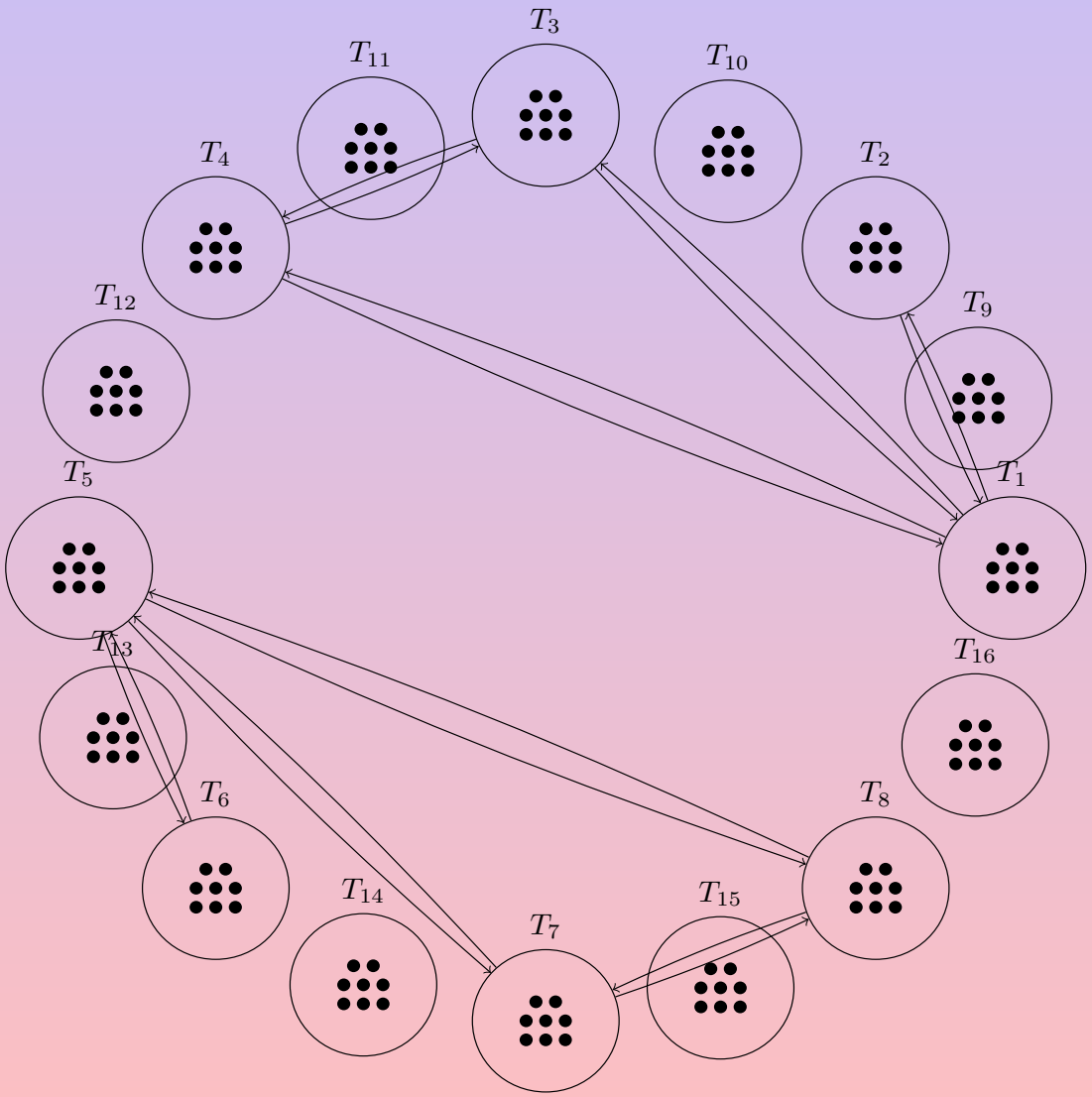

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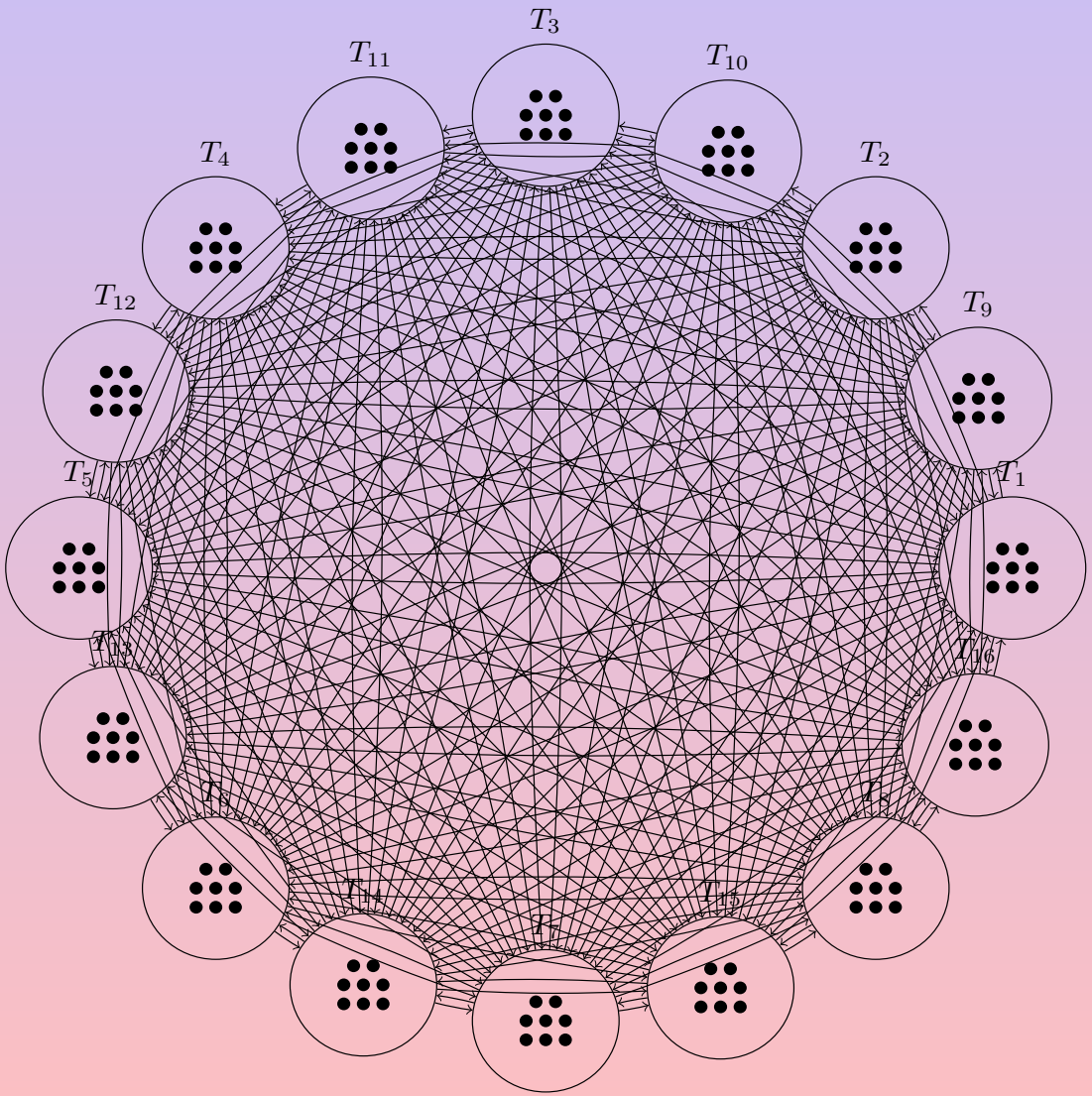
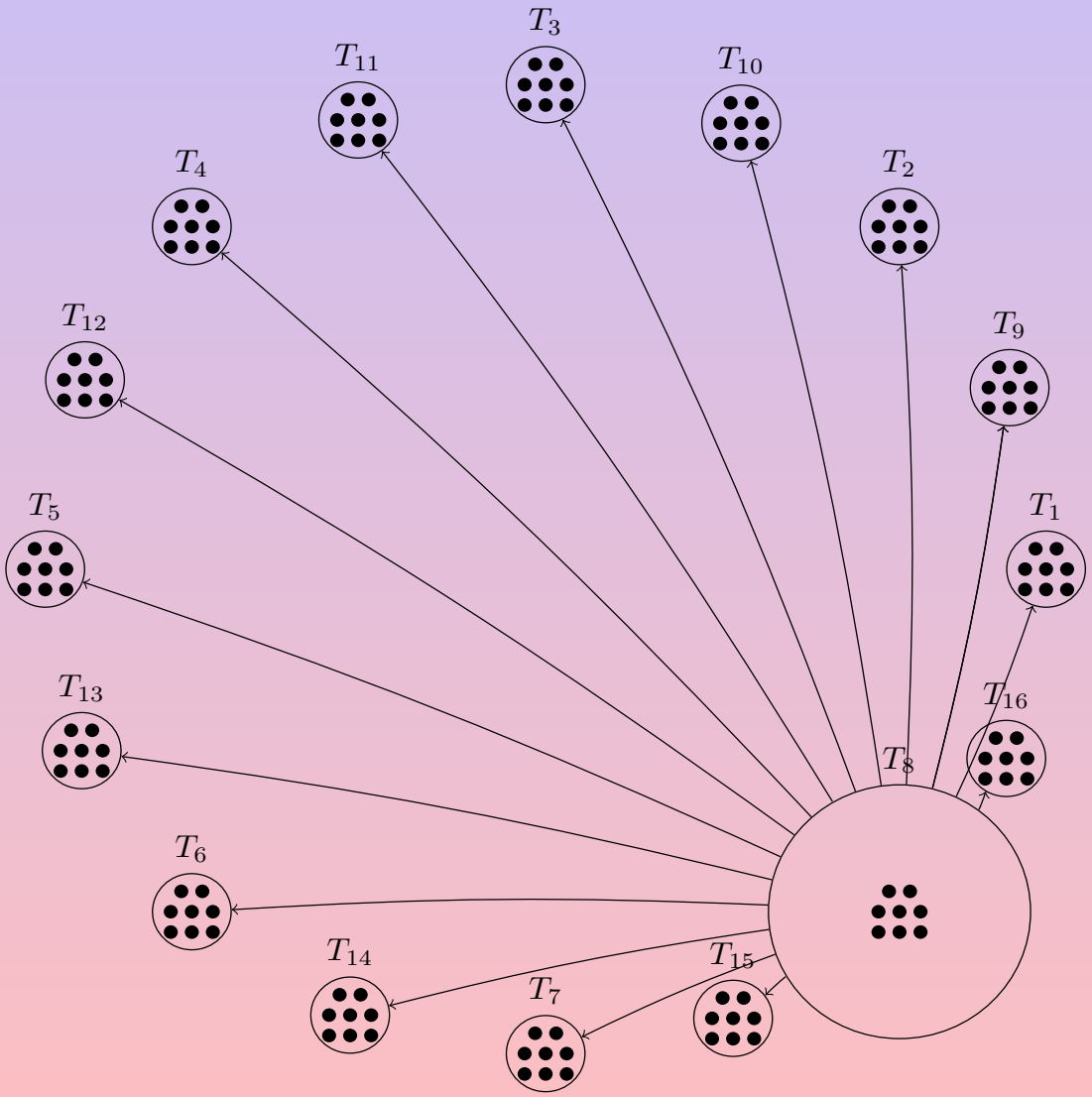
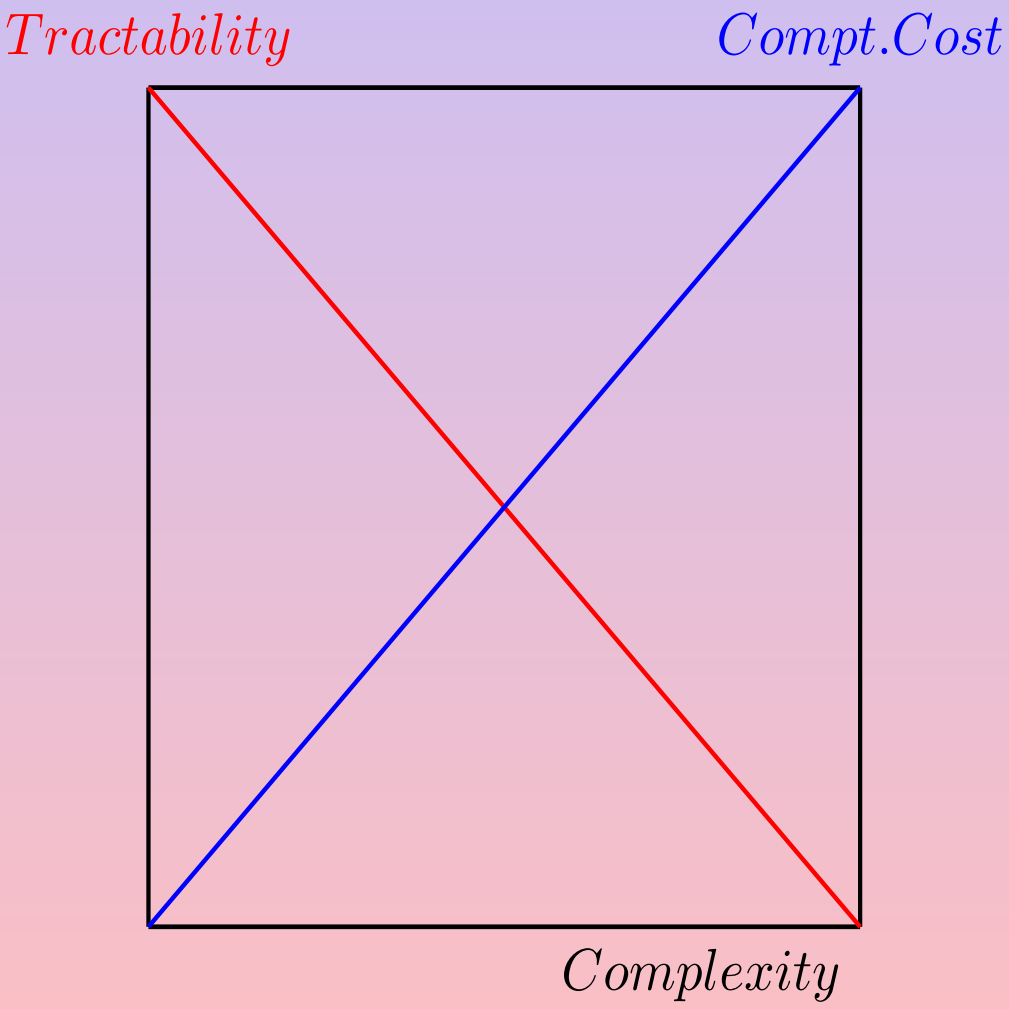


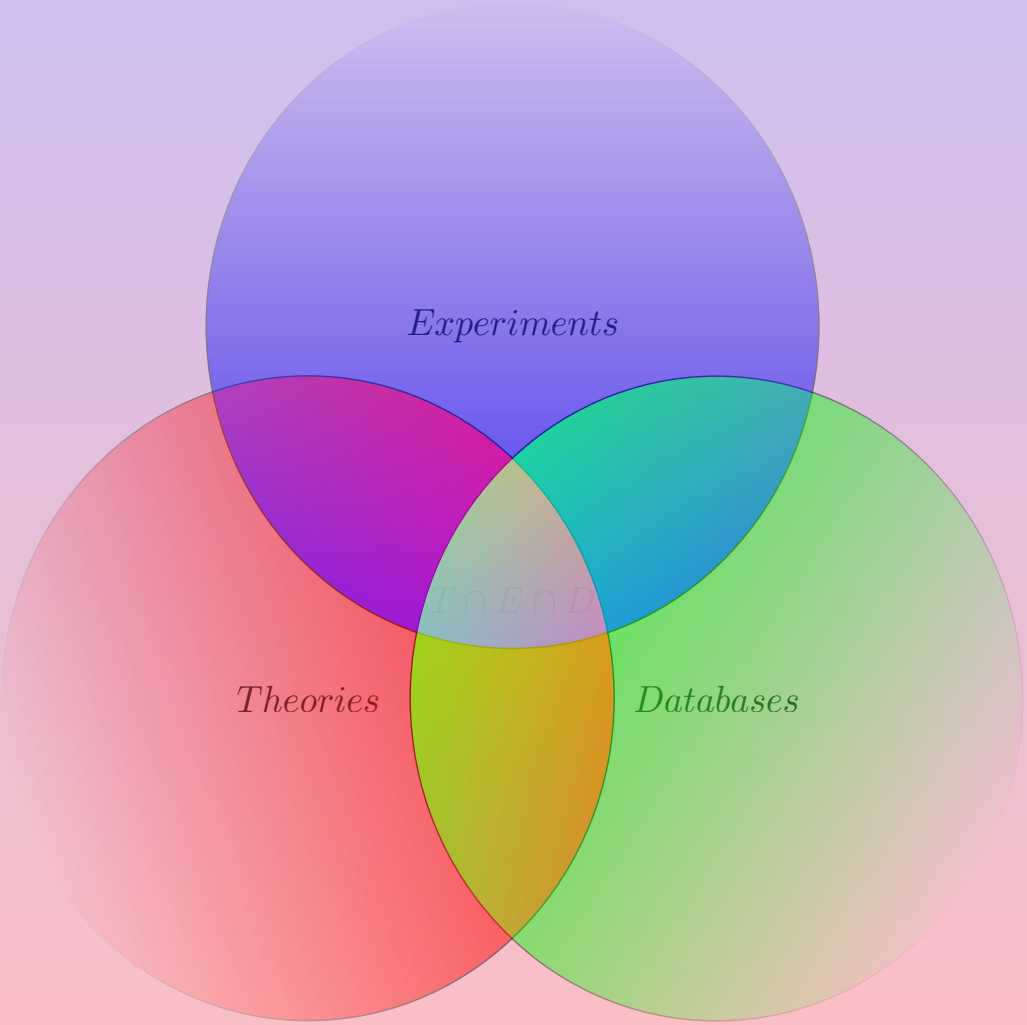
Individuals are complex



Tractability and replicability



Tractability and replicability

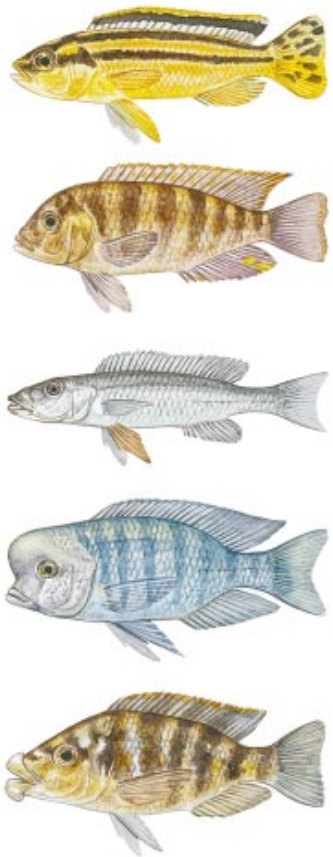


- What is an INTERDEPENDENT NETWORK?

- What is an INTERDEPENDENT NETWORK?
- "...Broadly defined a INTERDEPENDENT NETWORK (IN) may represent the interaction between at least two networks being those for example two biological levels (the genotype-phenotype map), two interaction types (antagonistic-mutualistic in ecological networks or expression-inhibition in gene regulatory networks). IN can also capture spatial scales (local-regional) or the interaction between spatial topology and mating dynamics of diverging or converging lineages..."

Individuals are complex

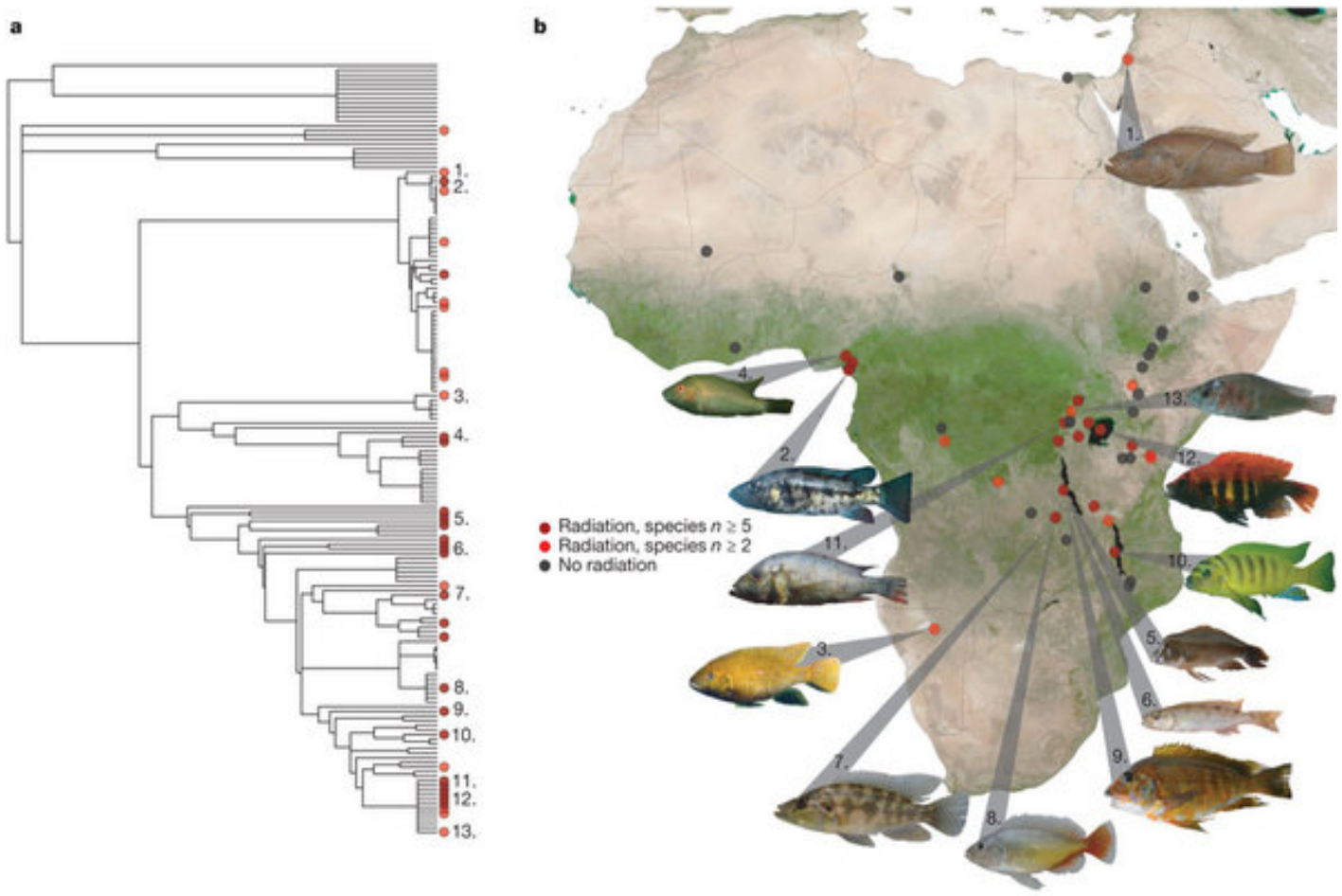
L. TANGANYIKA



L. MALAWI

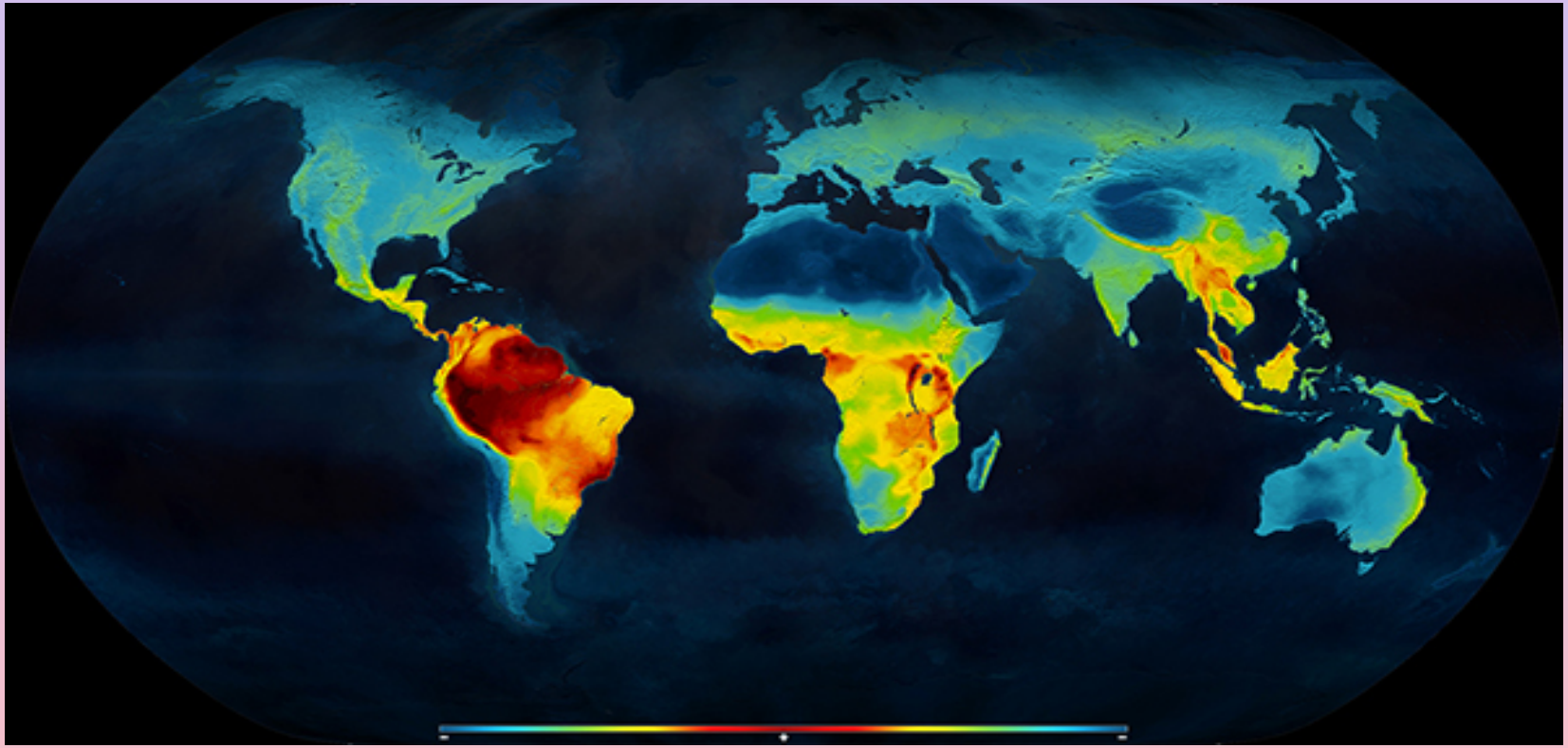
Stiassny, M. J., and Meyer, A. (1999). Cichlids of the Rift Lakes. *Scientific American*, 64-69.

Model system: geographic variation in Cichlids radiations



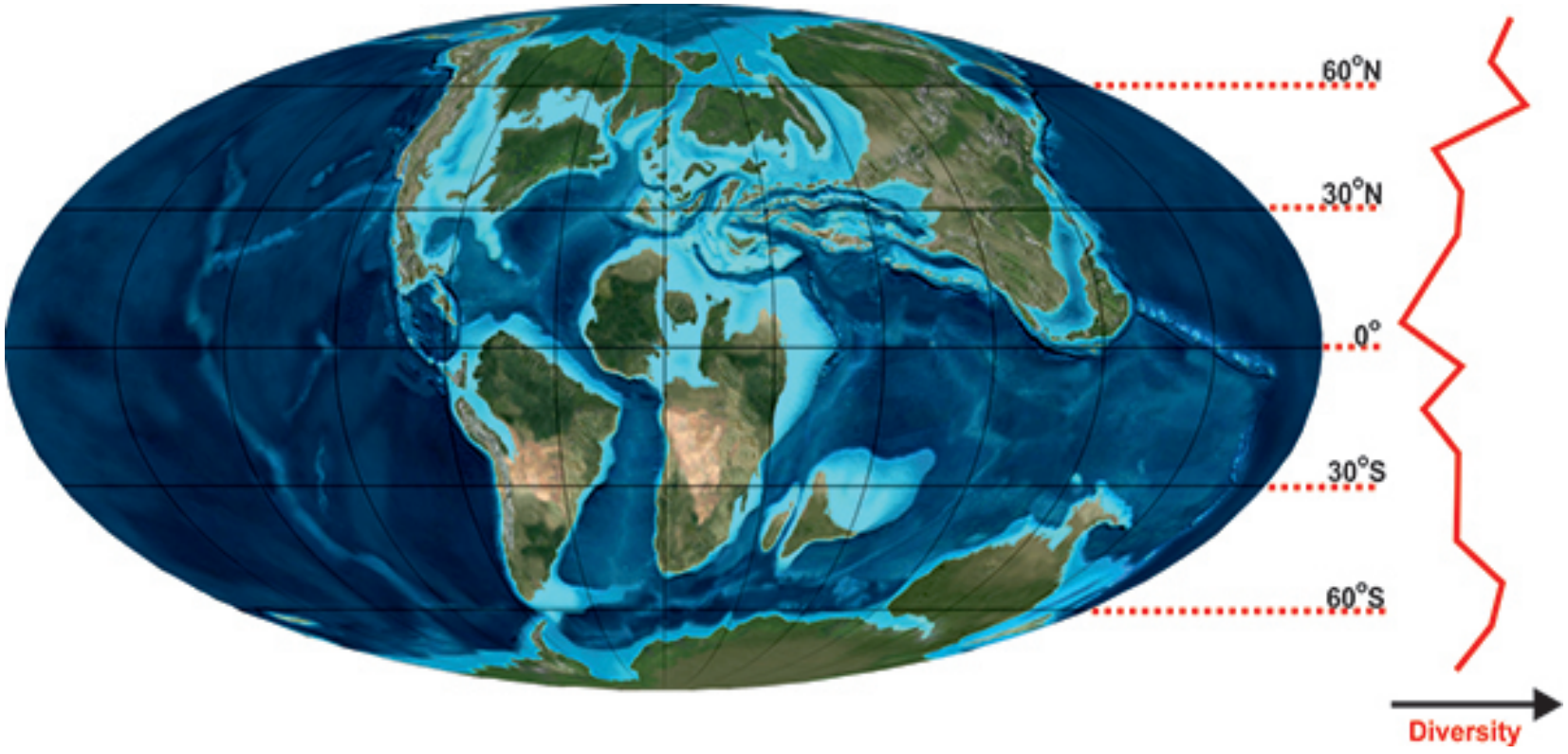
Wagner, C. E., et. al (2012). Ecological opportunity and sexual selection together predict adaptive radiation, *Nature*, 487:366-369.

Latitudinal biodiversity gradient: Contemporary time



Mannion, P. D., et al. (2014). The latitudinal biodiversity gradient through deep time. *TREE*, 29:42-50

Latitudinal biodiversity gradient: Late Cretaceous

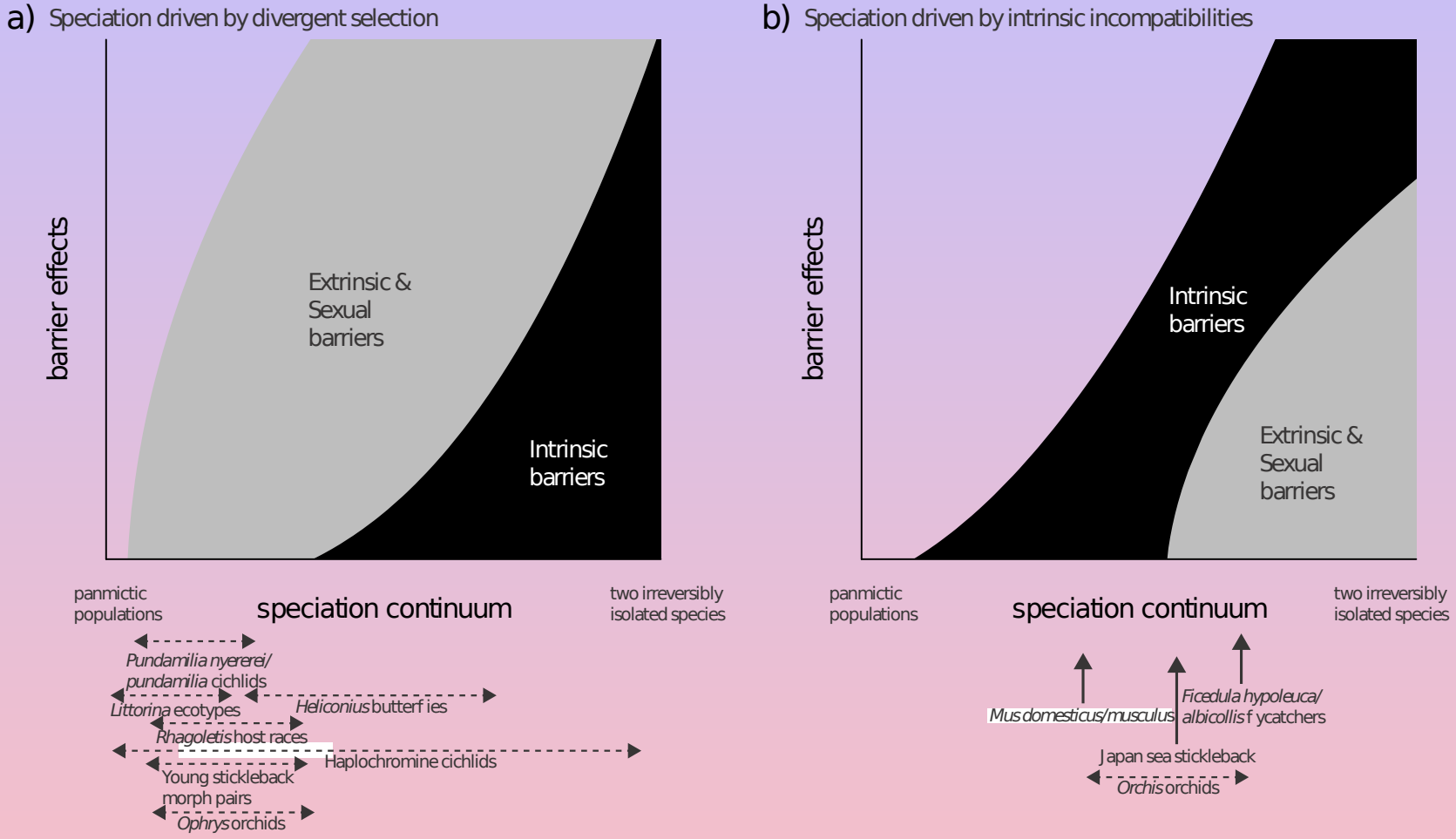


Mannion, P. D., et al. (2014). The latitudinal biodiversity gradient through deep time. *TREE*, 29:42-50

Questions

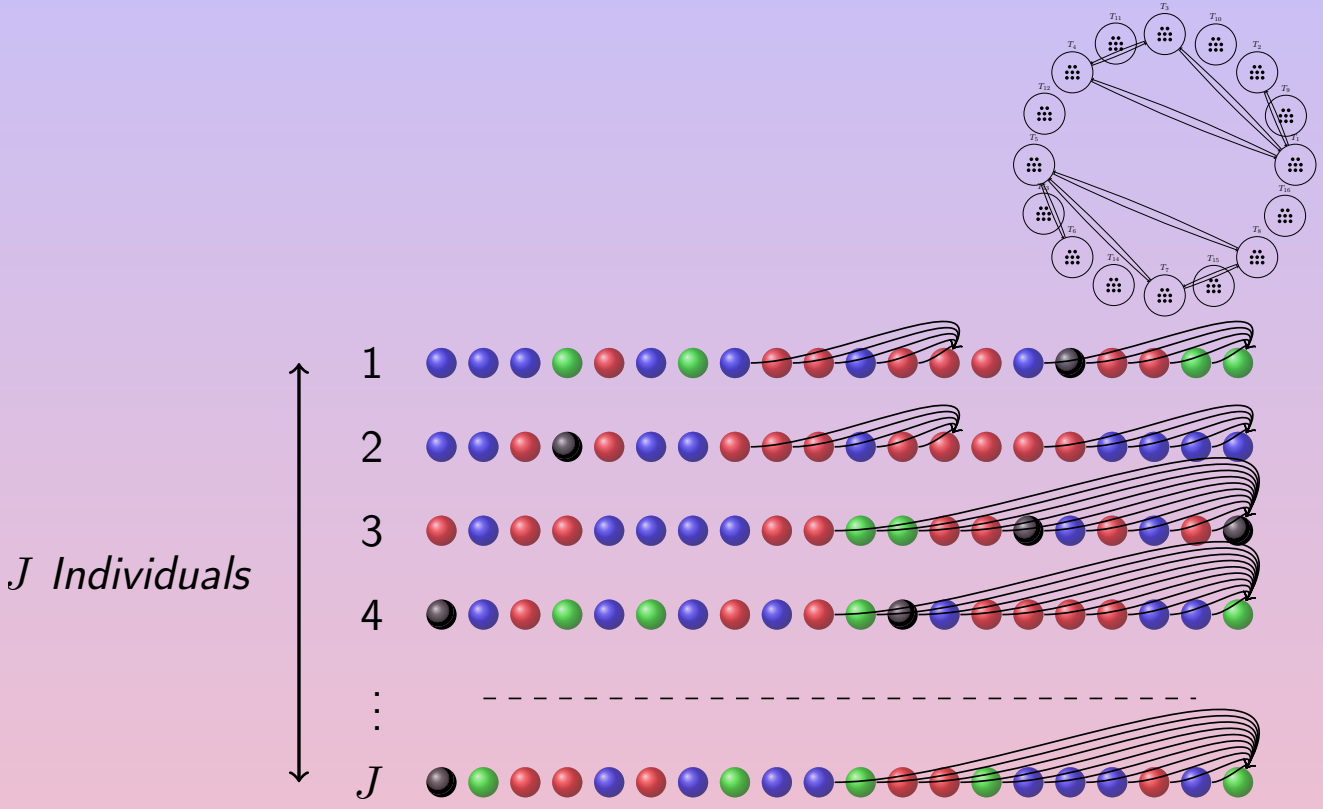
- How do a INTERDEPENDENT NETWORK containing gene flow in a spatial network and mating graphs interact to predict the biogeography of hot and cold spots?

Ecological and non-ecological speciation

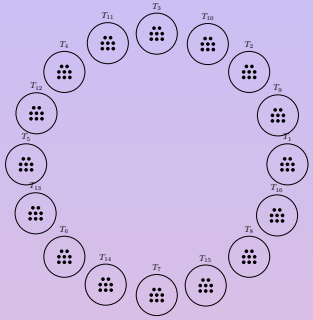


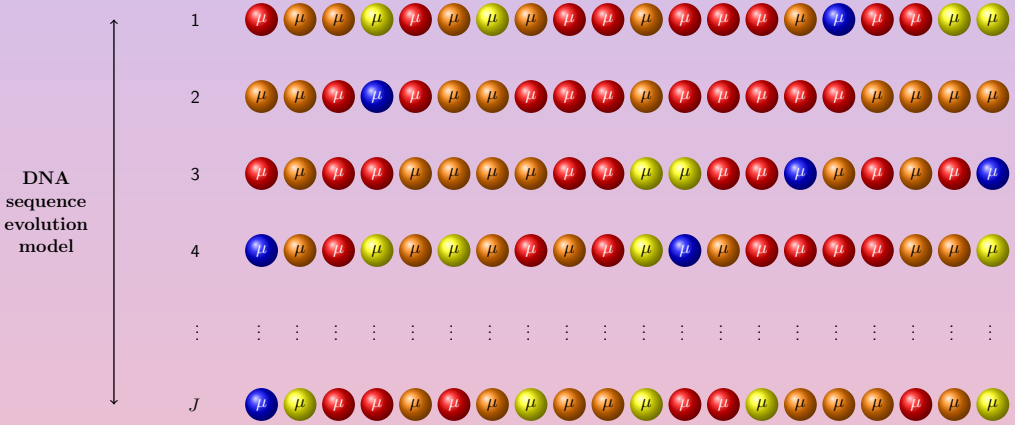
Seehausen, O., et al. (2014). Genomics and the origin of species. *Nature Reviews Genetics*, 15:176-192

Population size, $\mathcal{J}$, Genome size, $\mathcal{L}$, and mutation rate, μ

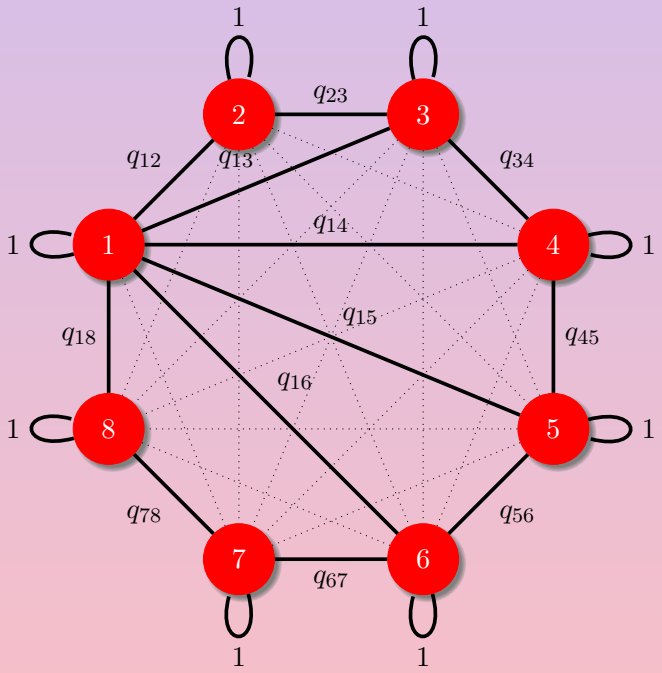


Population size, $\mathcal{J}$, Genome size, $\mathcal{L}$, and mutation rate, μ



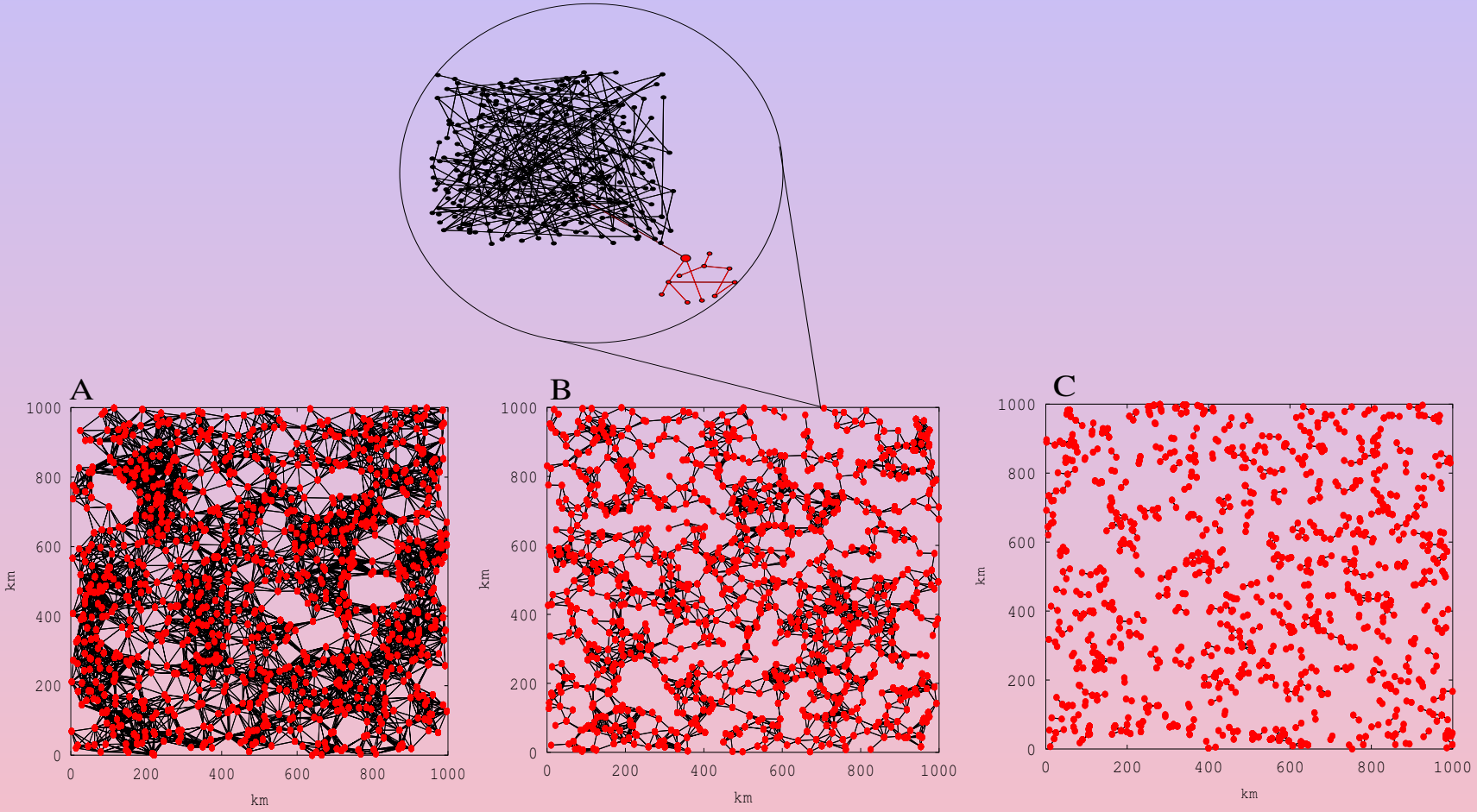


Genomes in a mating graph (threshold, $\mathcal{Q}_{min}$); Q = $[q_{ij}]$ and $q_{ij} > \mathcal{Q}_{min}$



$$\mathbf{Q} = \begin{bmatrix} & \mathbf{1} & \mathbf{2} & \mathbf{3} & \mathbf{4} & \mathbf{5} & \mathbf{6} & \mathbf{7} & \mathbf{8} \\ \mathbf{1} & 1 & q_{12} & q_{13} & q_{14} & q_{15} & q_{16} & 0 & q_{18} \\ \mathbf{2} & q_{21} & 1 & q_{23} & 0 & 0 & 0 & 0 & 0 \\ \mathbf{3} & q_{31} & q_{32} & 1 & q_{34} & 0 & 0 & 0 & 0 \\ \mathbf{4} & q_{41} & 0 & q_{43} & 1 & q_{45} & 0 & 0 & 0 \\ \mathbf{5} & q_{51} & 0 & 0 & q_{54} & 1 & q_{56} & 0 & 0 \\ \mathbf{6} & q_{61} & 0 & 0 & 0 & q_{65} & 1 & q_{67} & 0 \\ \mathbf{7} & 0 & 0 & 0 & 0 & 0 & q_{76} & 1 & q_{78} \\ \mathbf{8} & q_{81} & 0 & 0 & 0 & 0 & 0 & q_{87} & 1 \end{bmatrix}$$

Genomes in the landscape (threshold, $\mathcal{D}_{max}$); D = $[d_{ij}]$ and $d_{ij} \leq$ D$_{max}$



Gene flow, ($\mathcal{M}$)

Symmetric gene flow

$$m_{ij}^{k} = \frac{\mathcal{M}}{d_{ij}} \tag{1}$$

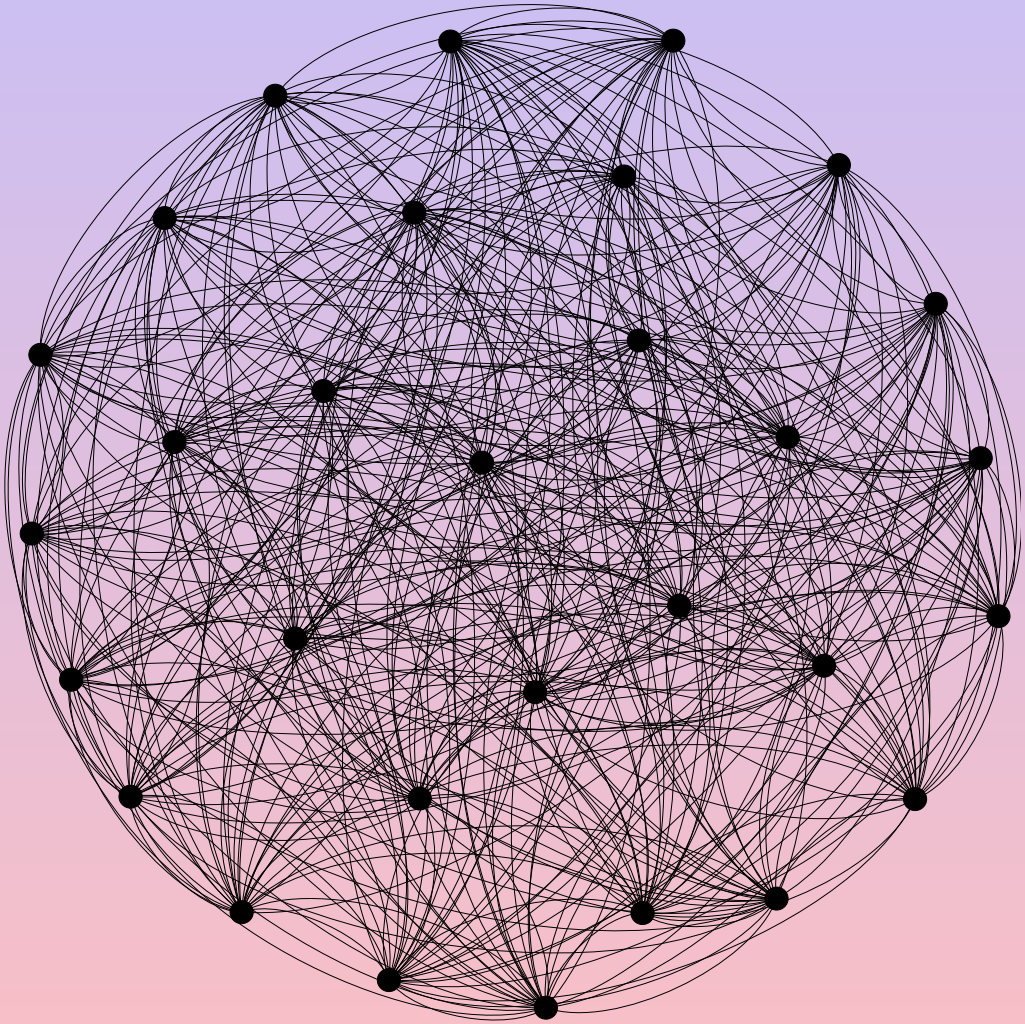
Centripetal gene flow

$$m_{ij}^{k} = \begin{cases} \frac{\mathcal{M}}{d_{ij}} & \text{if } \sum_{l=1}^{\mathcal{S}} d_{il} \leq \sum_{l=1}^{\mathcal{S}} d_{jl}, \\ 0 & \text{if } \sum_{l=1}^{\mathcal{S}} d_{il} > \sum_{l=1}^{\mathcal{S}} d_{jl} \end{cases} \tag{2}$$

Centrifugal gene flow

$$m_{ij}^{k} = \begin{cases} \frac{\mathcal{M}}{d_{ij}} & \text{if } \sum_{l=1}^{\mathcal{S}} d_{il} \geq \sum_{l=1}^{\mathcal{S}} d_{jl}, \\ 0 & \text{if } \sum_{l=1}^{\mathcal{S}} d_{il} < \sum_{l=1}^{\mathcal{S}} d_{jl} \end{cases} \tag{3}$$

Given $\mathcal{J}$, μ, $\mathcal{Q}_{min}$ and $\mathcal{D}_{max}$ = 1, do we find isolated clusters in the graph?



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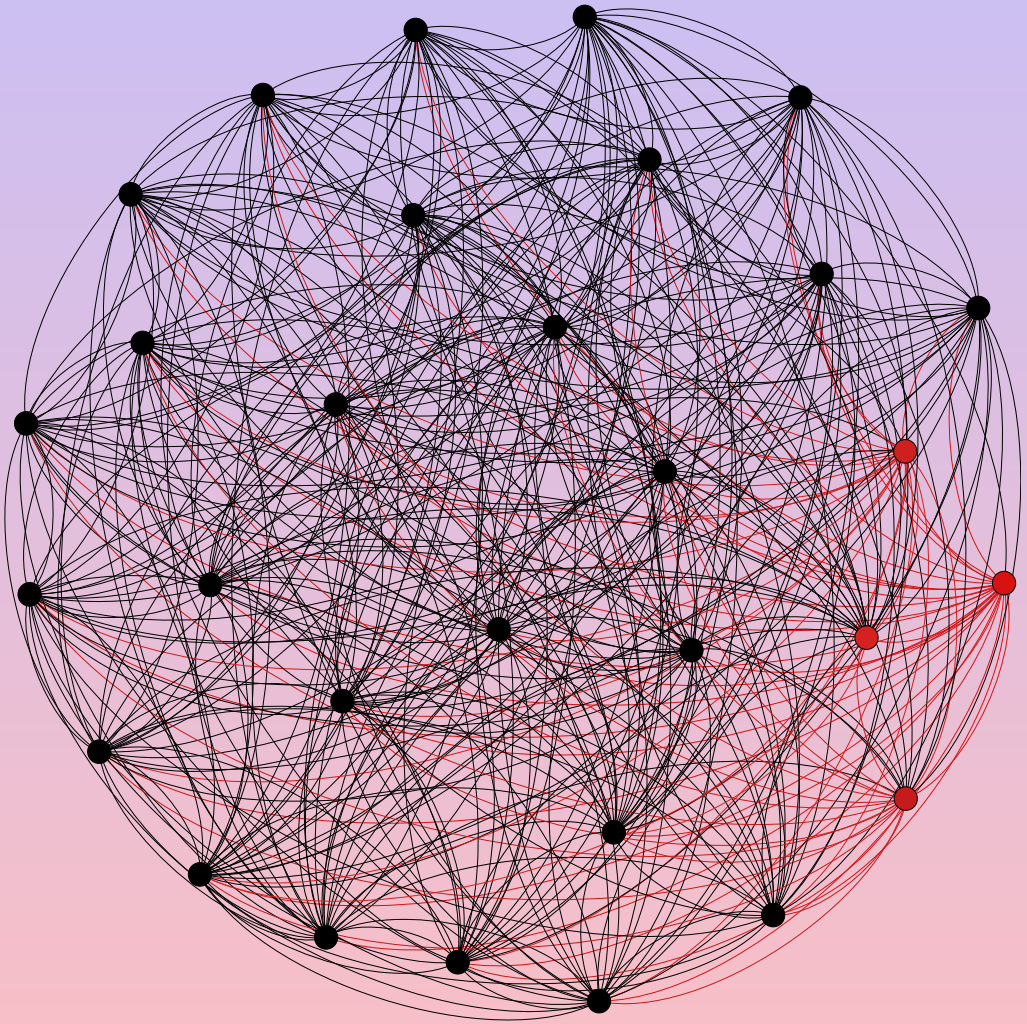

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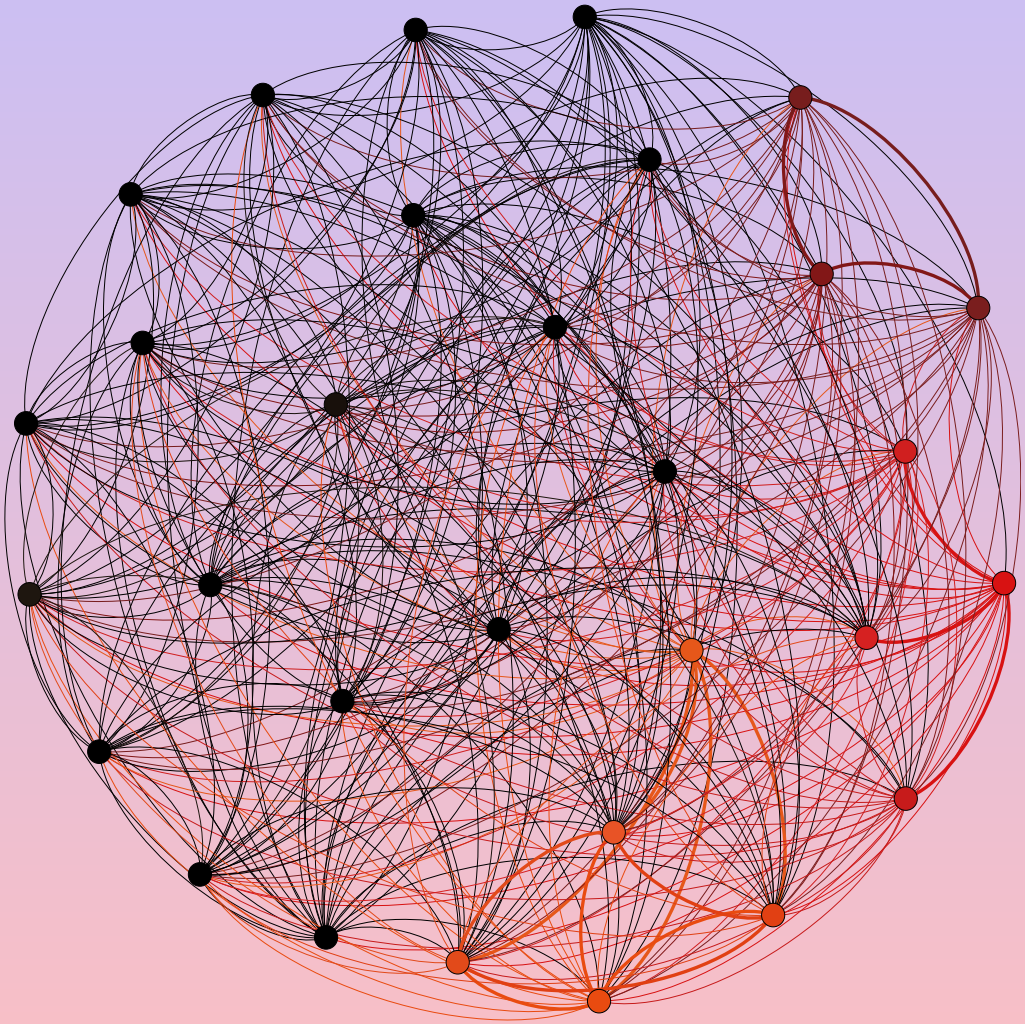

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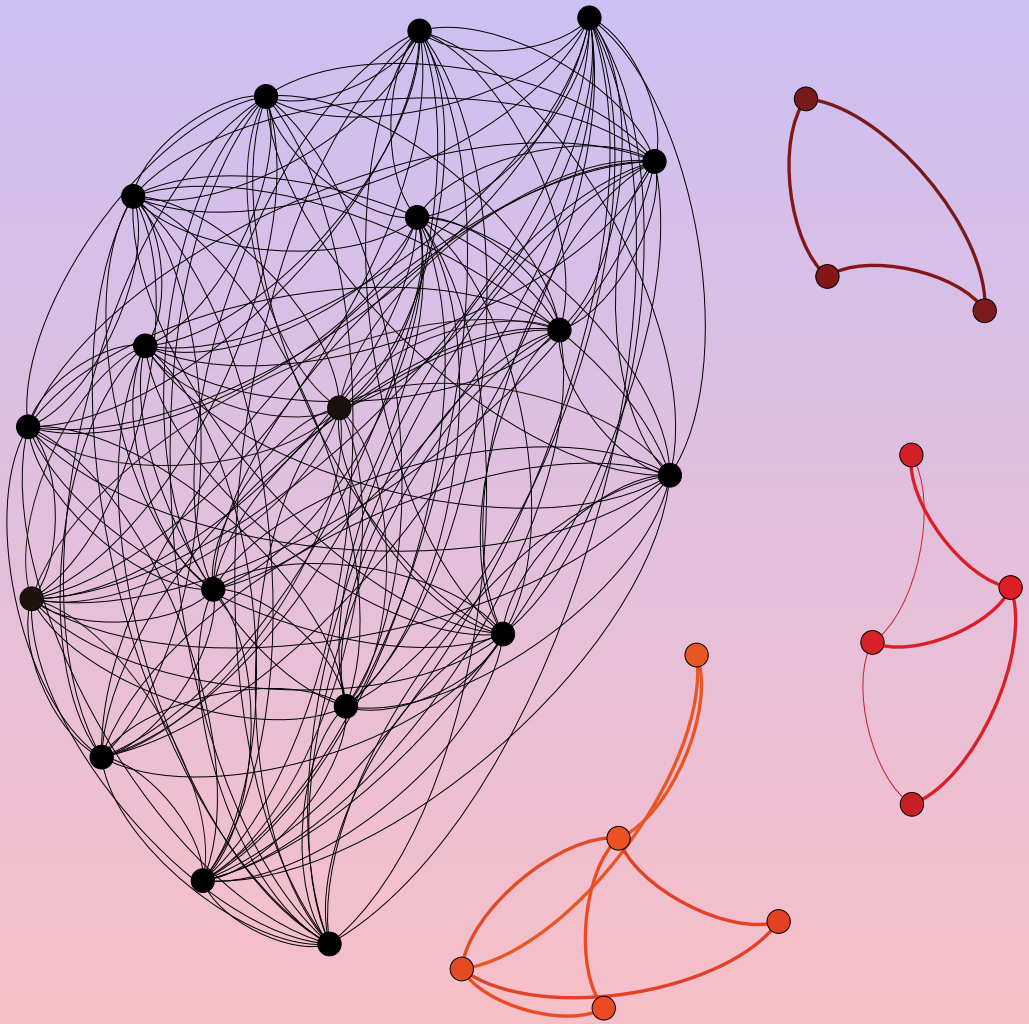
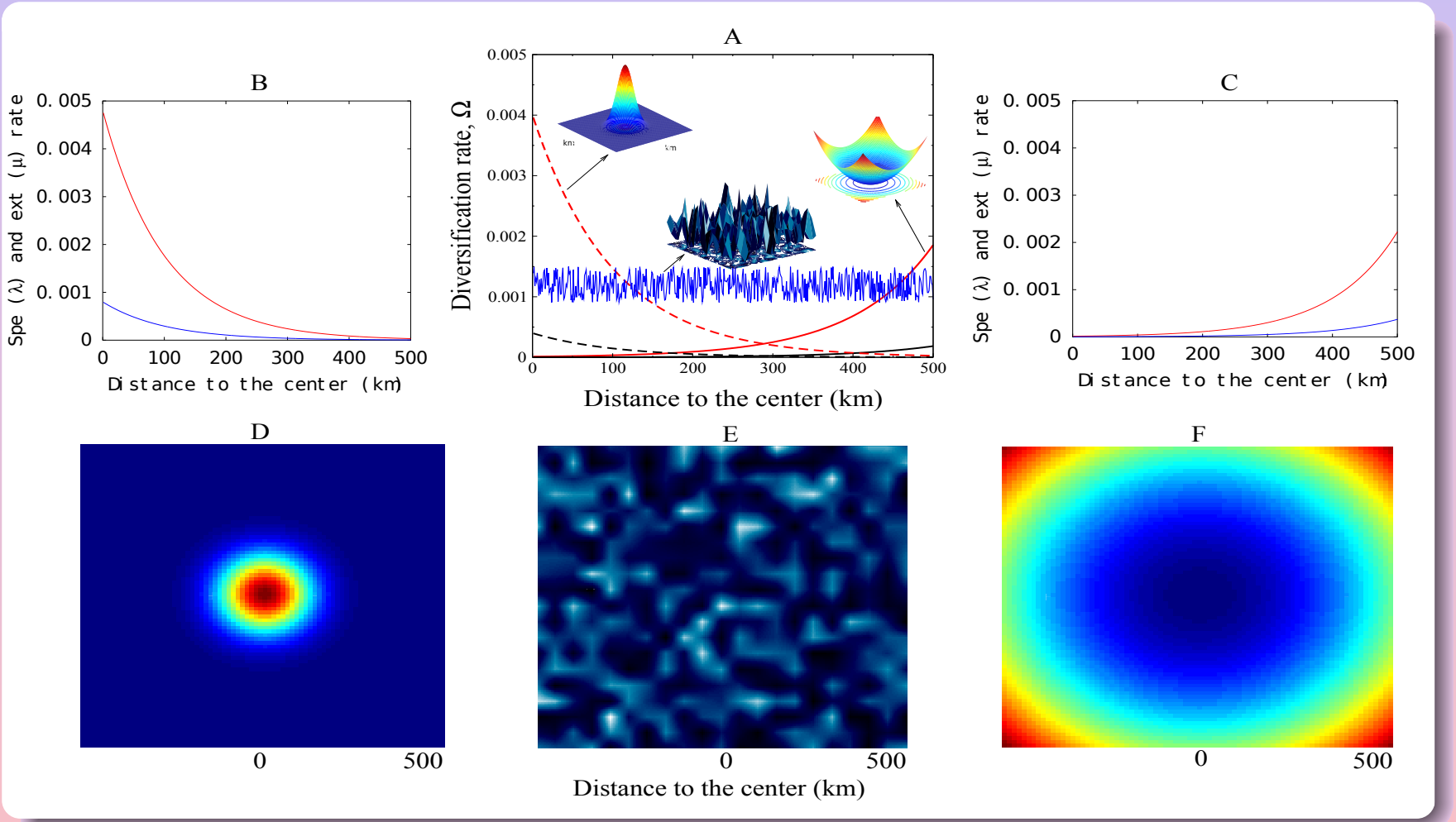


- Given $\mathcal{J}$, μ, $\mathcal{D}_{max}$ = 1, and $\mathcal{Q}_{min} > Q^* \rightarrow Q^*$ = $\frac{1}{4J\mu+1}$
  Sexual reproduction: $\rightarrow n^*_{sex}$ = $\frac{log(\mathcal{Q}_{min})}{-2\mu+log[(\mathcal{Q}_{min}+3)/4]}$

Melián, C. J., et al. (2010). Frequency-dependent selection predicts patterns of radiations and biodiversity. *PLoS Comput Biol*, 6(8):1000892.

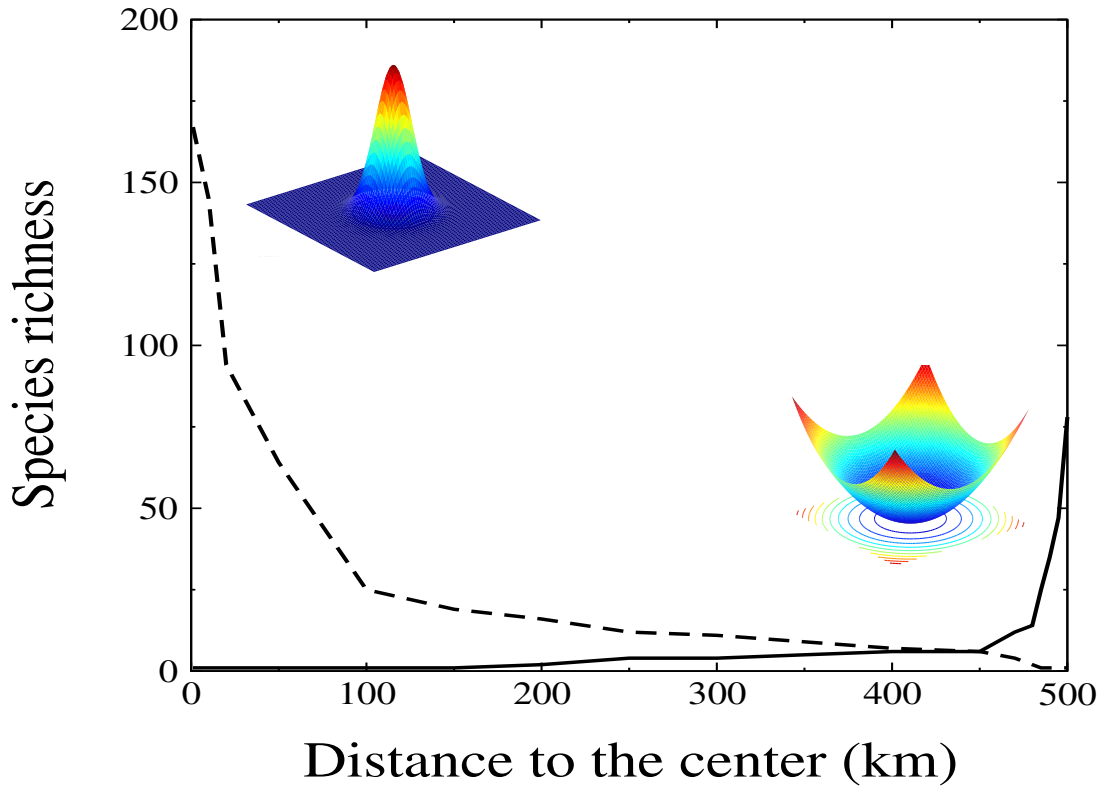
Melián, C. J., et al. (2012). Does sex speed up evolutionary rate and increase biodiversity. *PLoS Comput Biol*, 8(3):1002414.

Hot and cold spots ($\mathcal{J}$,$\mathcal{L}$,μ,$\mathcal{Q}_{min}$,$\mathcal{D}_{max}$,$\mathcal{M}$)



Melián, C. J., et al. Diversification and biodiversity dynamics of hot and cold spots (2015). *Ecography*, 38:393–401.

Hot spots and species richness



Outlook

- BIG CHALLENGE: Join genotype phenotype maps to large scale biodiversity patterns

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- Landscape structure, the strength of assortative mating and the intensity and directionality of gene flow in structured landscapes may play a critical role to anticipate the formation of hot and cold spots

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- BIG CHALLENGE: Join genotype phenotype maps to large scale biodiversity patterns
- Landscape structure, the strength of assortative mating and the intensity and directionality of gene flow in structured landscapes may play a critical role to anticipate the formation of hot and cold spots
- Centripetal gene flow model predicts hot spots in the center of the distribution ranges of diversifying lineages

Thank you!

- Computing-scientist staff at NCEAS, University of California Santa Barbara.
- Swiss National Foundation
- Charles N. de Santana (SNSF), Jan Klecka (SCIEX), Gregor Kalinkat (DAAD and SNSF)