

Redes filogenéticas

Kevin I. Sánchez

JOURNAL ARTICLE

Rampant Genome-Wide Admixture across the *Heliconius* Radiation

Krzysztof M Kozak , Mathieu Joron, W Owen McMillan, Chris D Jiggins [Author Notes](#)

Genome Biology and Evolution, Volume 13, Issue 7, July 2021, evab099, <https://doi.org/10.1093/gbe/evab099>

Extensive introgression in a malaria vector species complex revealed by phylogenomics

MICHAEL C. FONTAINE, JAMES B. PEASE, AARON STEELE, ROBERT M. WATERHOUSE, DANIEL E. NEAFSEY, IGOR V. SHARAKHOV, XIAOFANG JIANG, ANDREW B. HALL, FLAMINIA CATTERUCCIA, [...], AND NORA J. BESANSKY [+9 authors](#) [Authors Info & Affiliations](#)

SCIENCE • 27 Nov 2014 • Vol 347, Issue 6217 • DOI: 10.1126/science.1258524

The evolutionary network of whiptail lizards reveals predictable outcomes of hybridization

ANTHONY J. BARLEY , ADRIÁN NIETO-MONTES DE OCA , NORMA L. MANRÍQUEZ-MORÁN , AND ROBERT C. THOMSON  [Authors Info & Affiliations](#)

SCIENCE • 11 Aug 2022 • Vol 377, Issue 6607 • pp. 773-777 • DOI: 10.1126/science.abn1593



ORIGINAL ARTICLE

Historical introgression among the American live oaks and the comparative nature of tests for introgression

Deren A. R. Eaton, Andrew L. Hipp, Antonio González-Rodríguez, Jeannine Cavender-Bares 

JOURNAL ARTICLE

Phenotypic and Genetic Structure Support Gene Flow Generating Gene Tree Discordances in an Amazonian Floodplain Endemic Species

Gregory Thom , Fabio Raposo Do Amaral, Michael J Hickerson, Alexandre Aleixo, Lucas E Araujo-Silva, Camila C Ribas, Erik Choueri, Cristina Y Miyaki

Systematic Biology, Volume 67, Issue 4, July 2018, Pages 700–718, <https://doi.org/10.1093/sysbio/syy004>

MOLECULAR ECOLOGY

ORIGINAL ARTICLE

Speciation and gene flow in two sympatric small mammals from Madagascar, *Microgale fotsifotsy* and *M. soricoides* (Mammalia: Tenrecidae)

Athryn M. Everson , Steven M. Goodman, Link E. Olson

first published: 08 April 2020 | <https://doi.org/10.1111/mec.15433> | Citations: 2



Phenotypic and life-history diversification in Amazonian frogs despite past introgressions

Antoine Fouquet^{a b}  , Berengère Ferrier^{b c}, Jordi Salmona^a, Sourakhata Tirera^d, Jean-Pierre Vacher^a, Elodie A. Courtois^b, Philippe Gaucher^b, Jucivaldo Dias Lima^e, Pedro M. Sales Nunes^f, Sergio Marques de Souza^g, Miguel T. Rodrigues^g, Brice Noonan^h, Benoit de Thoisy^{c d}

JOURNAL ARTICLE

Hybridization and polyploidy in the weeping lizard *Liolaemus chilensis* (Squamata: Liolaemidae)

Raúl Araya-Donoso , Fernando Torres-Pérez, David Véliz, Madeleine Lamborot

Biological Journal of the Linnean Society, Volume 128, Issue 4, December 2019, Pages 963–974, <https://doi.org/10.1093/biolinnean/blz145>

MOLECULAR ECOLOGY

JOURNAL OF Evolutionary Biology



doi: 10.1111/jeb.13273

FROM THE COVER |  [Full Access](#)

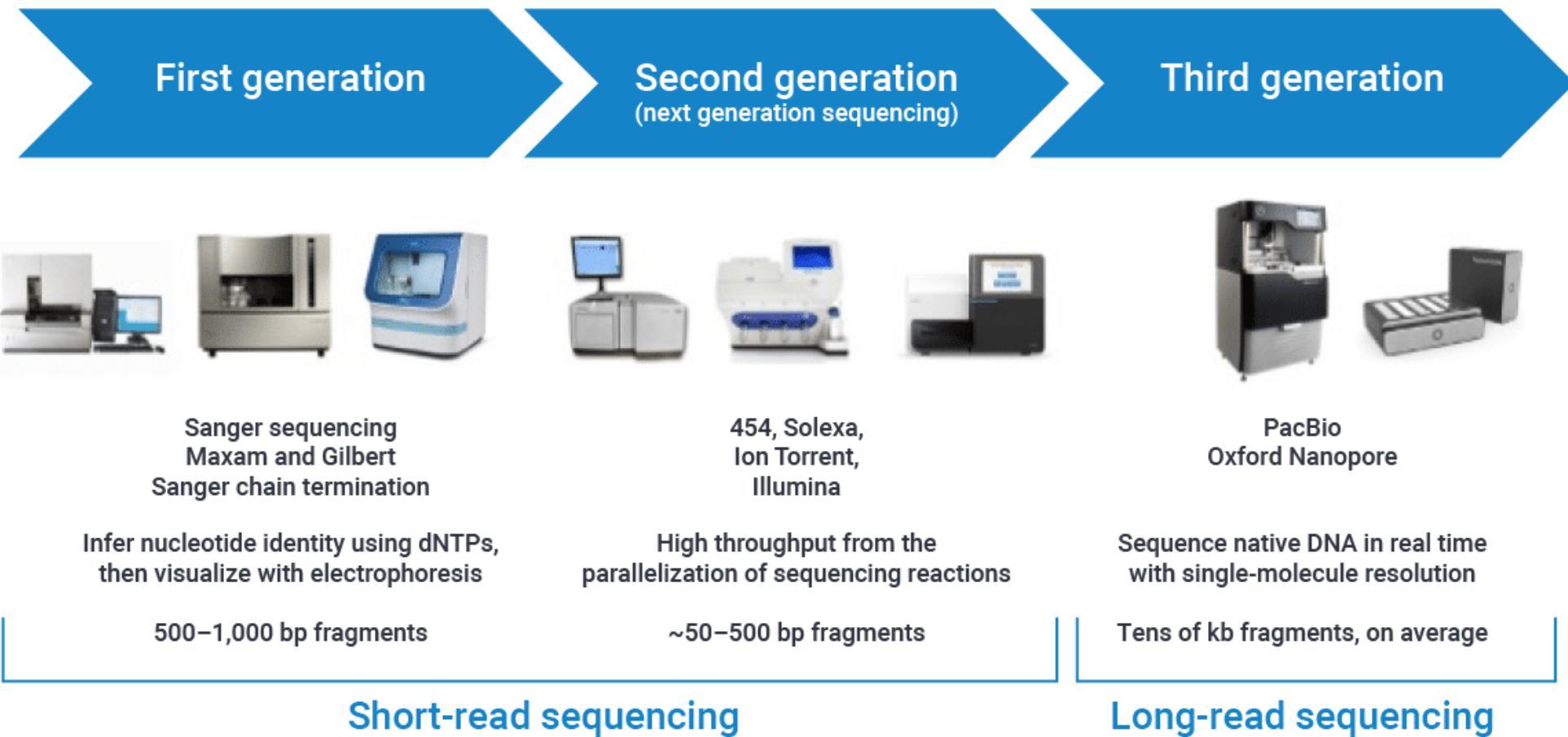
Complex patterns of differentiation and gene flow underly the divergence of aposematic phenotypes in *Oophaga* poison frogs

Jana Ebersbach, Andrés Posso-Terranova , Steven Bogdanowicz, Mónica Gómez-Díaz, Ma. Ximena García-González, Wilmar Bolívar-García, José Andrés

Hybridization could be a common phenomenon within the highly diverse lizard genus *Liolaemus*

MELISA OLAVE*† , LUCIANO J. AVILA*, JACK W. SITES JR‡ & MARIANA MORANDO*

Alguns (poucos) exemplos na herpetofauna da América do Sul

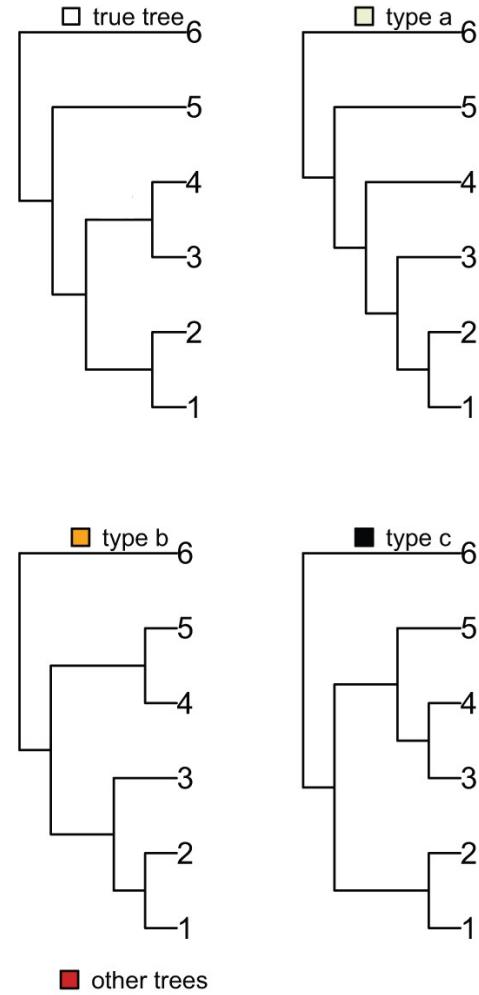
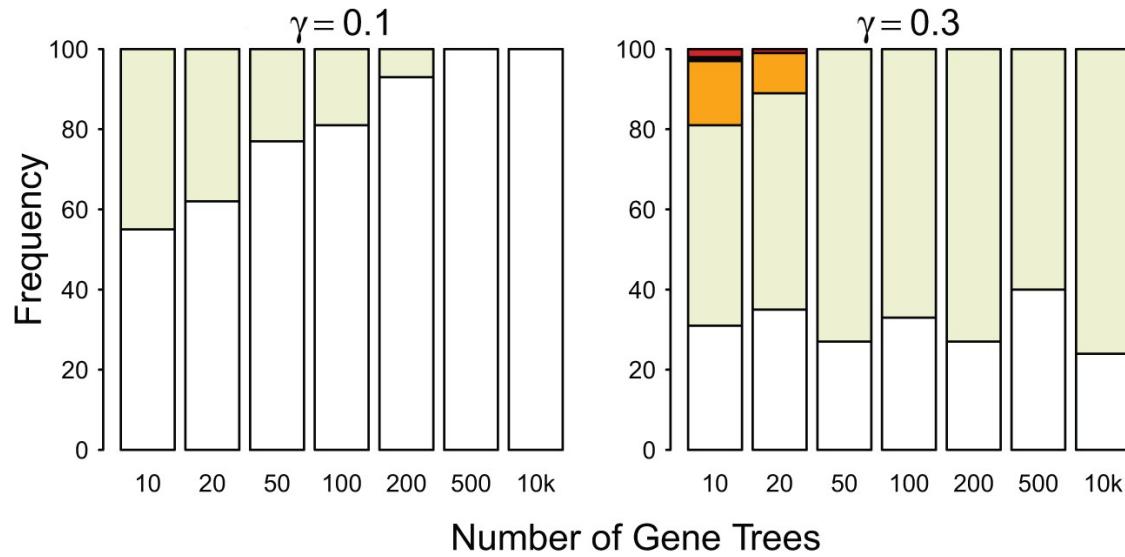
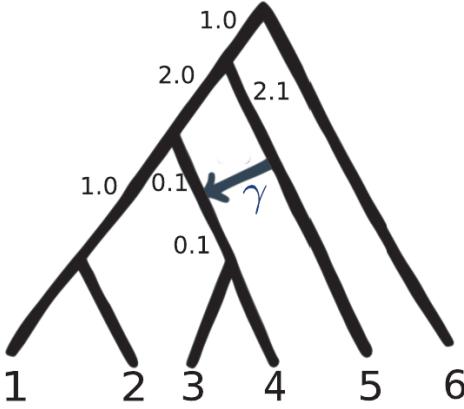


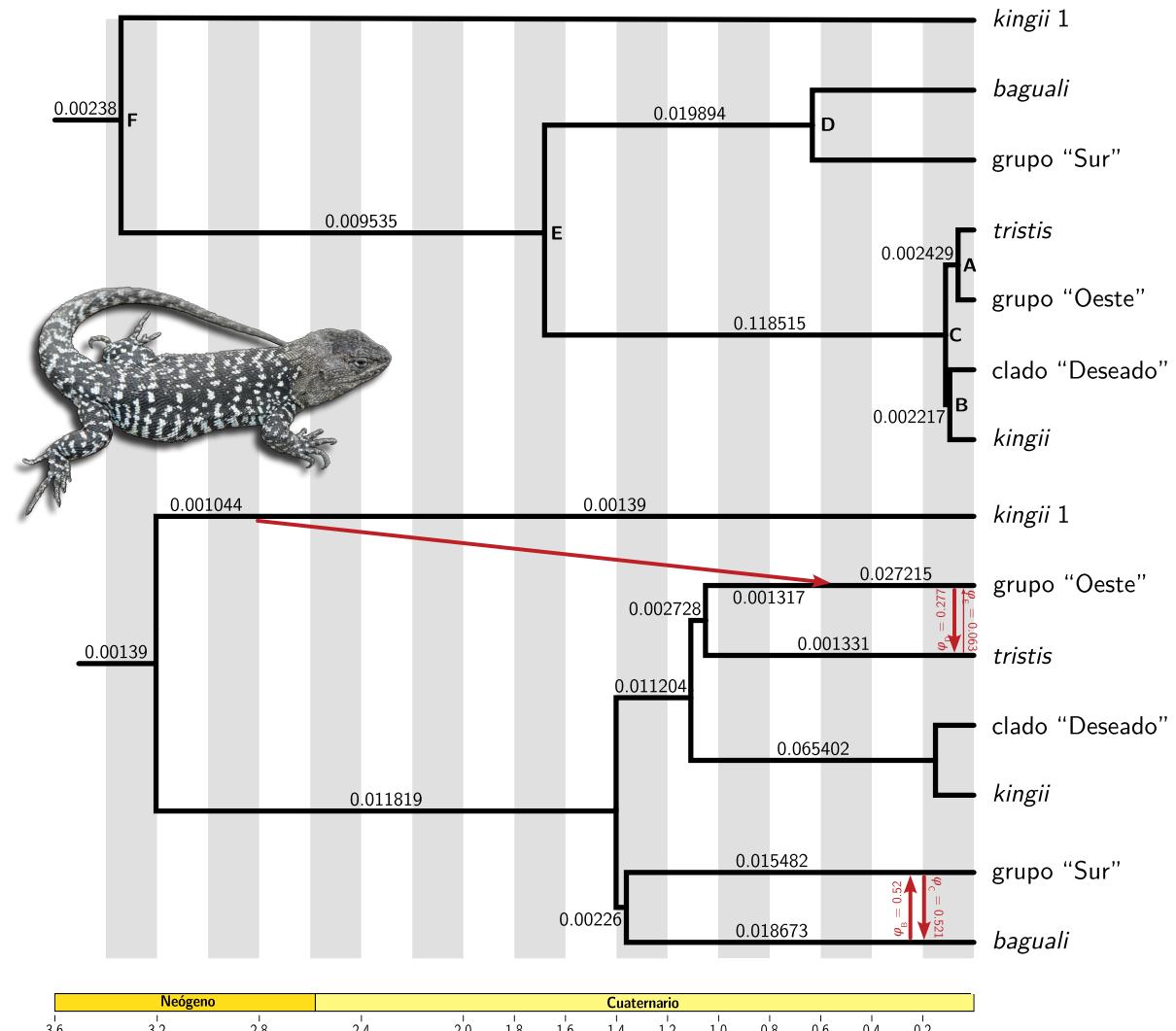
Fluxo gênico → reprodução entre membros de populações geneticamente distintas



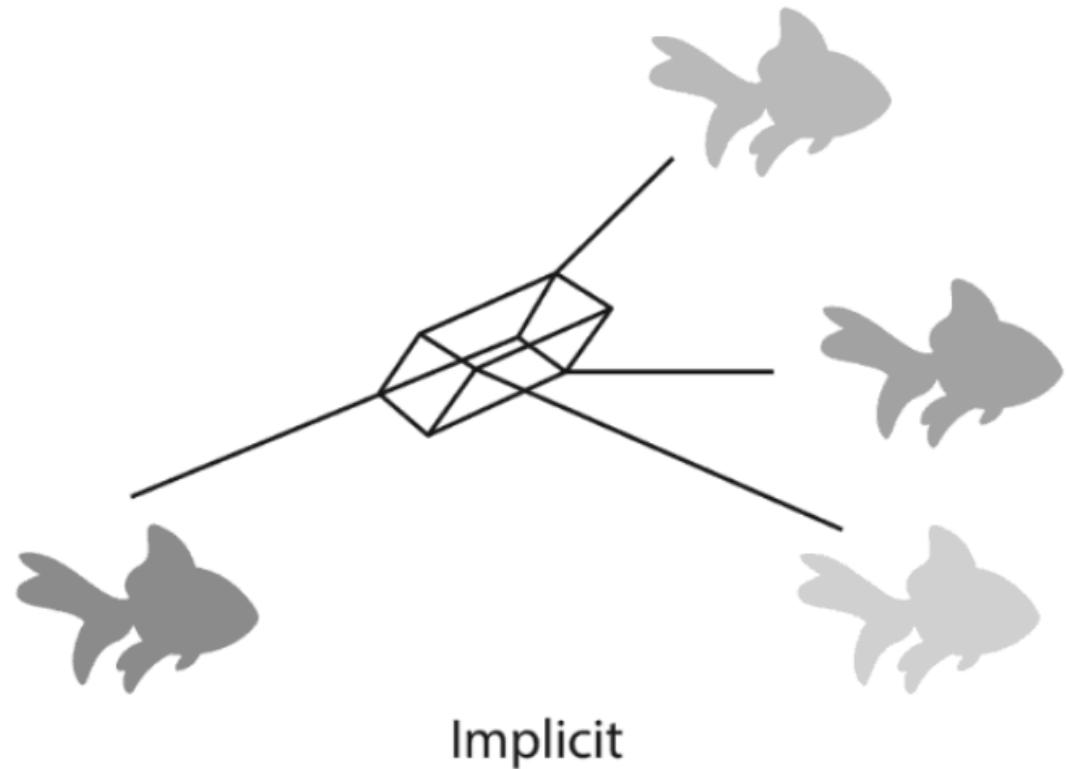
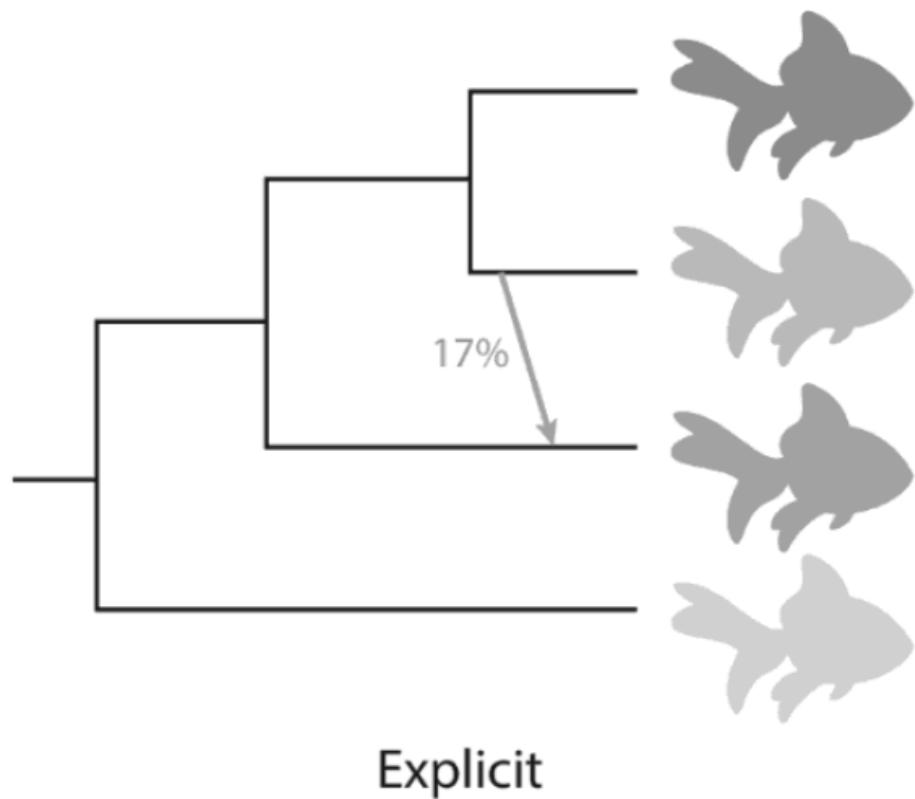
Papel na diversificação e adaptação

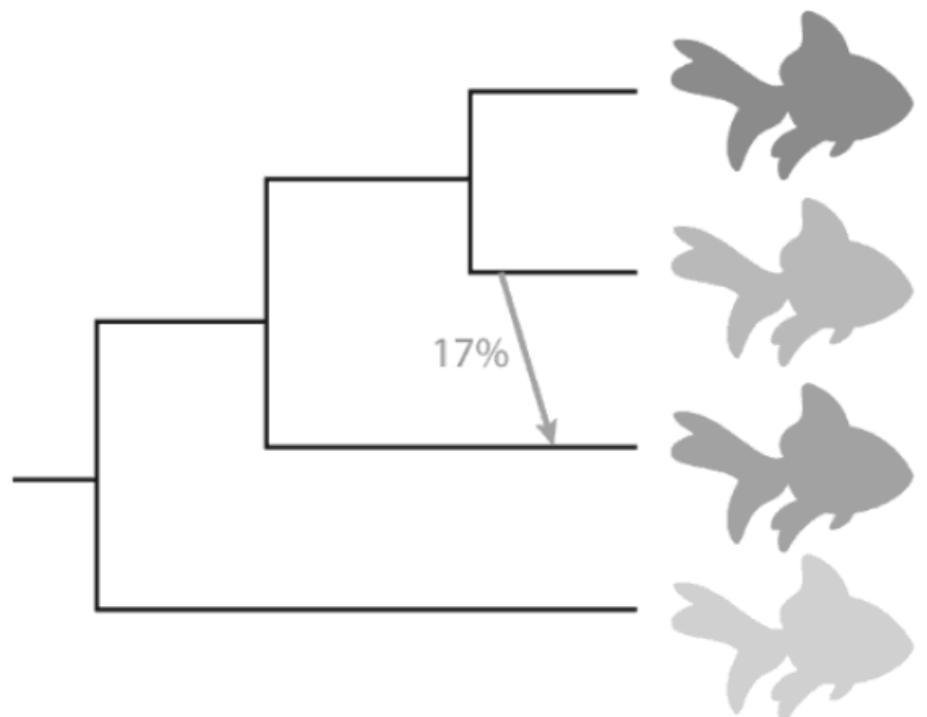
Redes filogenéticas → modelo





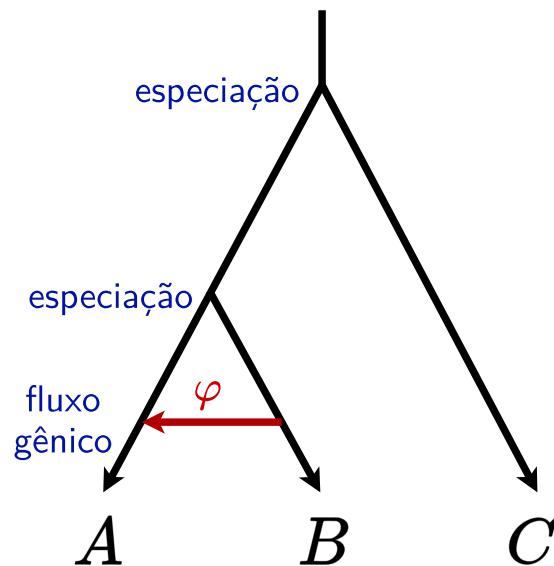
Lagartixas *Liolaemus* (Sánchez et al. 2023)



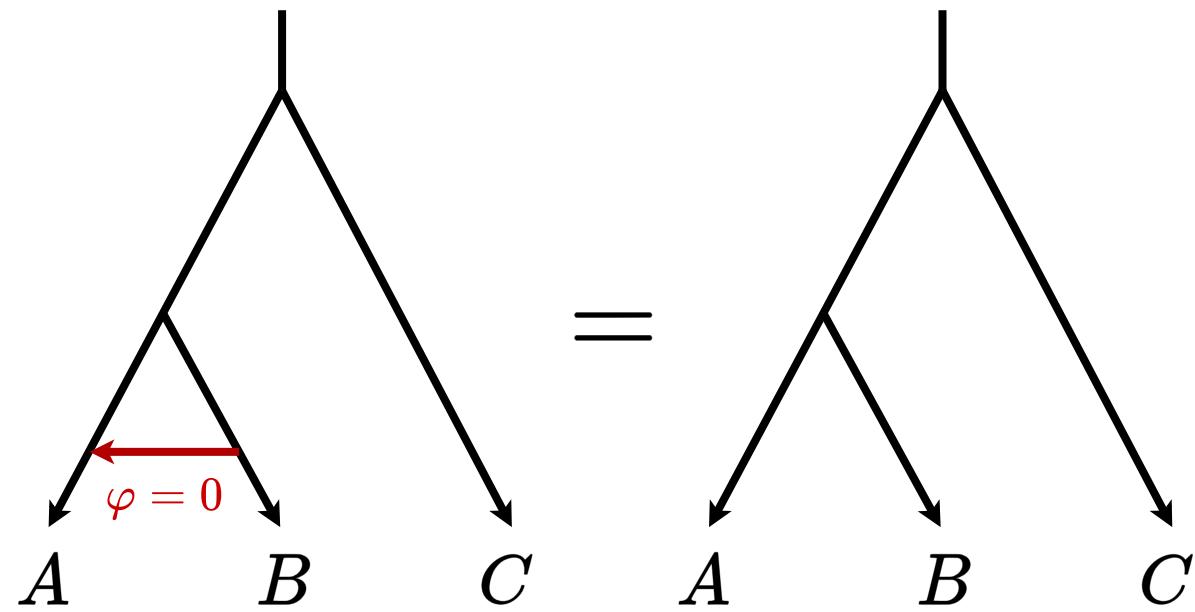


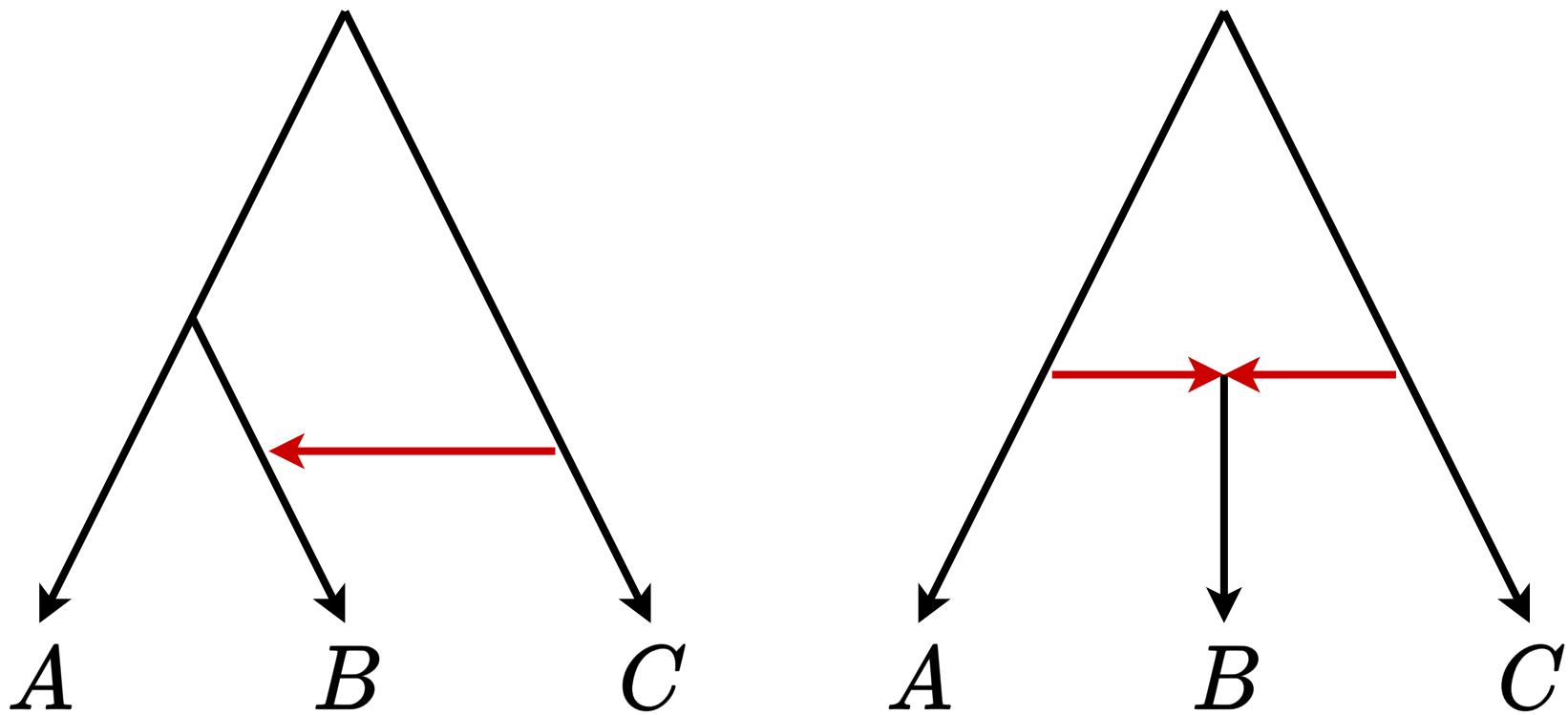
Explicit

Redes filogenéticas (explícitas)

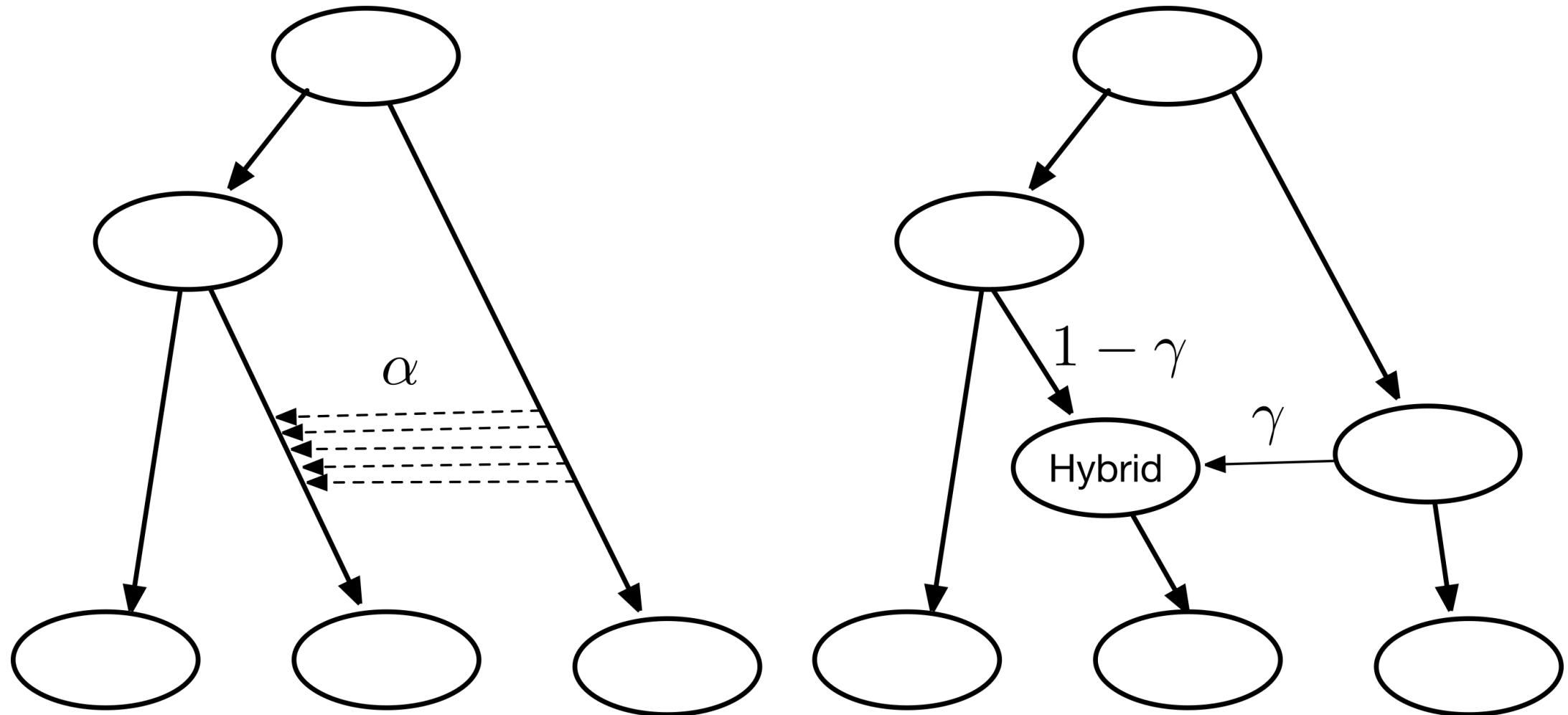


$\varphi, \gamma \rightarrow$ prop. de material genético transferido/probabilidade de introgessão

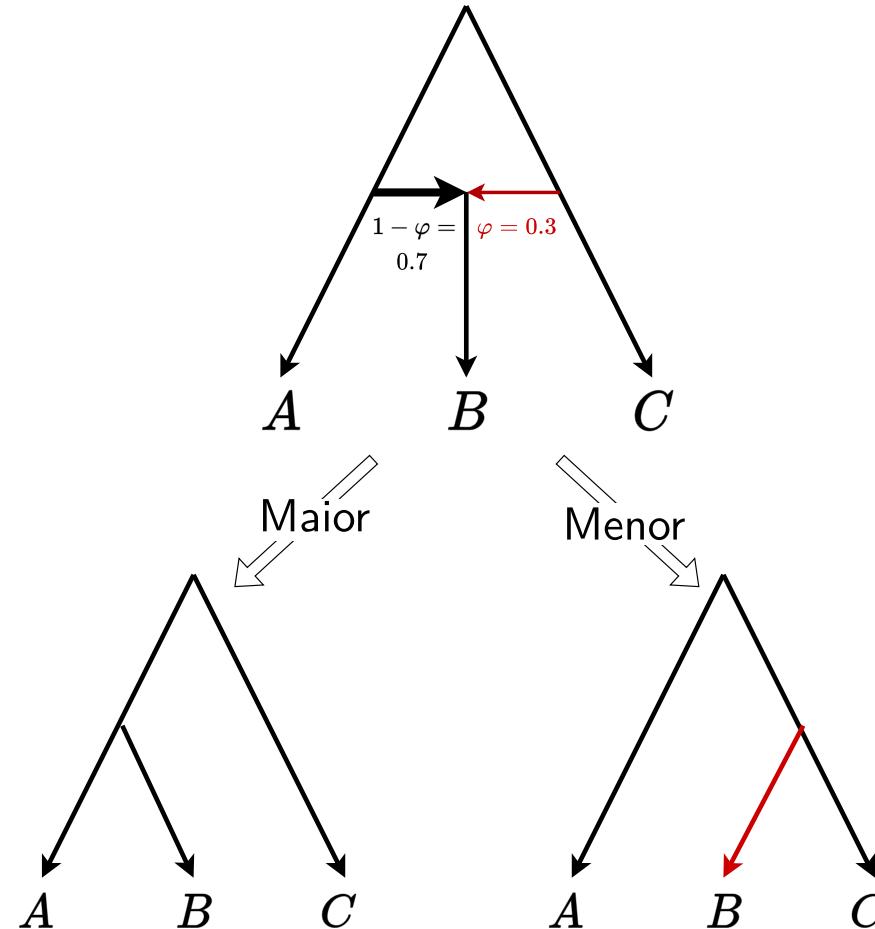




introgressão | especiação híbrida



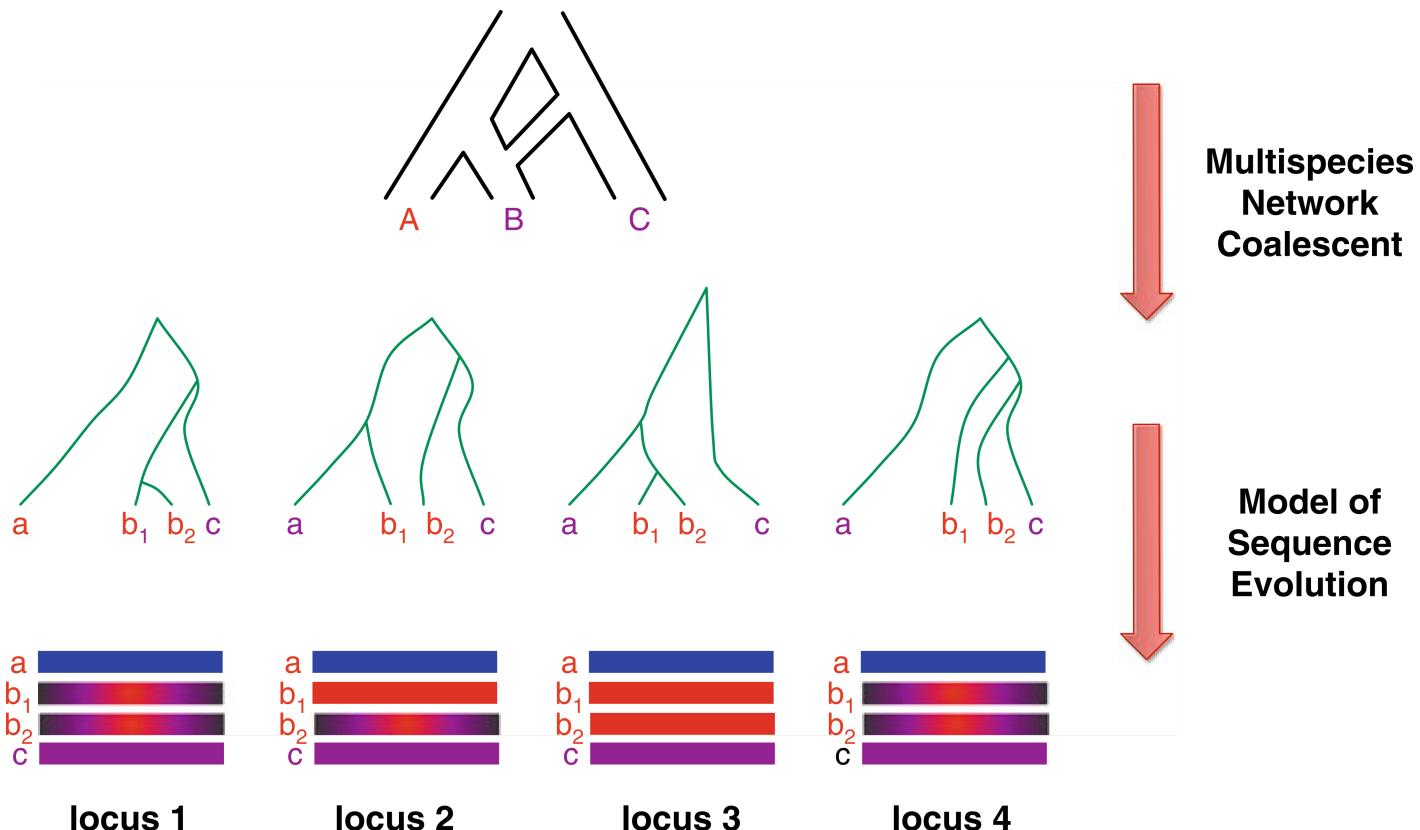
Árvore maior vs árvore menor



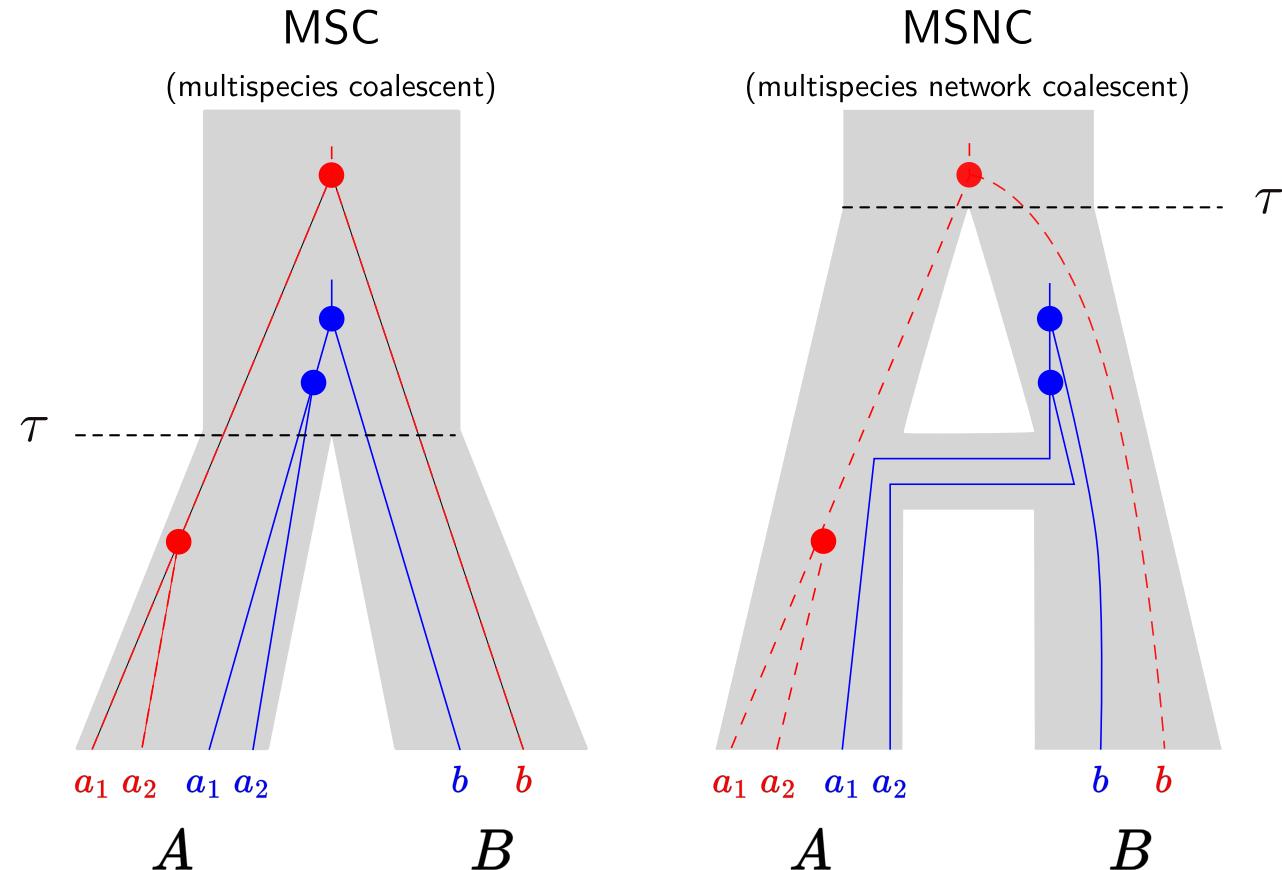
Multispecies Network Coalescent (MSNC; Yu et al. 2014)



Distribuição de probabilidade de árvores gênicas na presença de ILS e reticulação



Coalescência de alelos



- MSC → ILS
- MSNC → ILS + introgressão

Estimação de redes filogenéticas

1. Métodos de resumo

- Resumo de sequências → + rápidos; não são estimados todos os parâmetros
- Software: PHYLONETWORKS, PHYLONET (InferNetwork_ML, InferNetwork_MPL, MCMC_GT, MLE_BiMarkers)

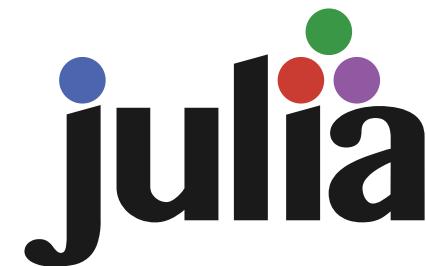
2. Verossimilhança completa (*full likelihood*)

- Uso direto de sequências → + demandantes; estimam todos os parâmetros
- Software: PHYLONET (MCMC_SEQ, MCMC_BiMarkers), SPECIESNETWORKS, BPP



(Solís-Lemus et al. 2017)

- Inferência (presença, localização e magnitude do fluxo gênico)
- Manipulação (enraizamento, etc.)
- Visualização
- Análise a partir de redes (PCMs)

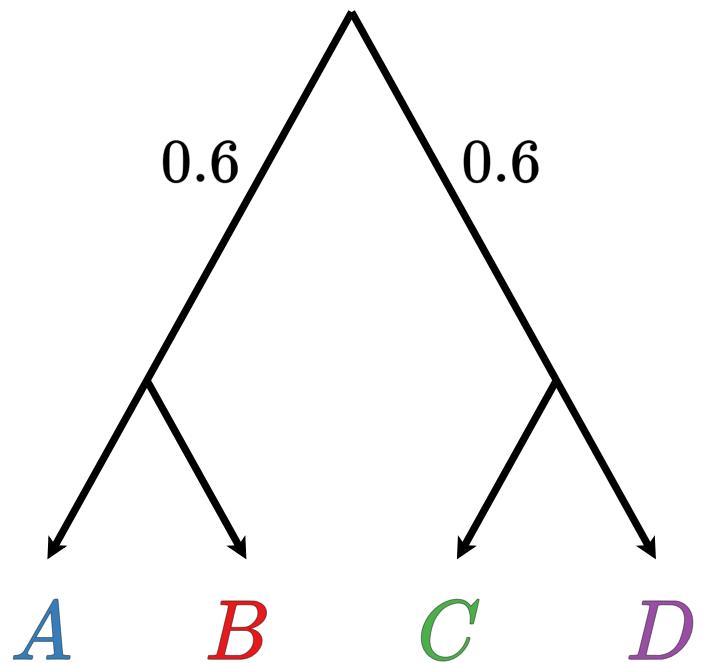




Species Networks applying Quartets (Solís-Lemus et al. 2016)

```
snaq!(sppTree, CFtable, hmax = 1, filename = "net1", runs = 1)
```

Probabilidades de topologias com base no MSC

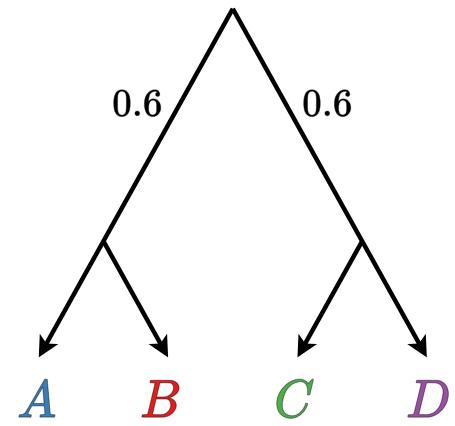


$$P\left(\begin{array}{c} A \\ \textcolor{red}{B} \\ \textcolor{green}{C} \\ \textcolor{violet}{D} \end{array}\right) = 0.8$$

$$P\left(\begin{array}{c} A \\ \textcolor{green}{C} \\ \textcolor{red}{B} \\ \textcolor{violet}{D} \end{array}\right) = 0.1$$

$$P\left(\begin{array}{c} A \\ \textcolor{violet}{D} \\ \textcolor{red}{B} \\ \textcolor{green}{C} \end{array}\right) = 0.1$$

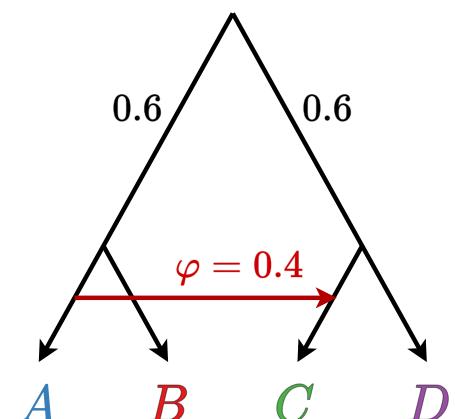
Simulações



$$P\left(\begin{array}{c} A \\ | \\ B & C \\ | \\ D \end{array}\right) \approx 0.8$$

$$P\left(\begin{array}{c} A \\ | \\ C & B \\ | \\ D \end{array}\right) \approx 0.1$$

$$P\left(\begin{array}{c} A \\ | \\ D & B \\ | \\ C \end{array}\right) \approx 0.1$$



$$P\left(\begin{array}{c} A \\ | \\ B & C \\ | \\ D \end{array}\right) \approx 0.2$$

$$P\left(\begin{array}{c} A \\ | \\ C & B \\ | \\ D \end{array}\right) \approx 0.6$$

$$P\left(\begin{array}{c} A \\ | \\ D & B \\ | \\ C \end{array}\right) \approx 0.2$$

Dados de entrada para snaq

```
snaq!(sppTree, CFtable, hmax = 1, filename = "net1", runs = 1)
```



- Árvore de espécies

Dados de entrada para snaq

```
snaq!(sppTree, CFtable, hmax = 1, filename = "net1", runs = 1)
```



- Tabela de fatores de concordância (FC) ← árvores de genes/SNPs

Taxon 1	Taxon 2	Taxon 3	Taxon 4	CF _{12_34}	CF _{13_24}	CF _{14_23}
A	B	C	D	0.2	0.6	0.2
...

Dados de entrada para snaq

```
snaq!(sppTree, CFtable, hmax = 1, filename = "net1", runs = 1)
```



- Número de eventos de introgressão

SNPs2CF (Olave y Meyer 2020)

Locus →	1	2	3	4	5	6	7	8	9	10
A	1	1	0	1	0	1	1	0	0	1
B	1	1	0	1	0	0	0	1	1	0
C	0	0	1	0	1	1	1	0	1	0
D	0	0	1	0	1	0	0	1	0	1

$$AB_CD = 5/10$$

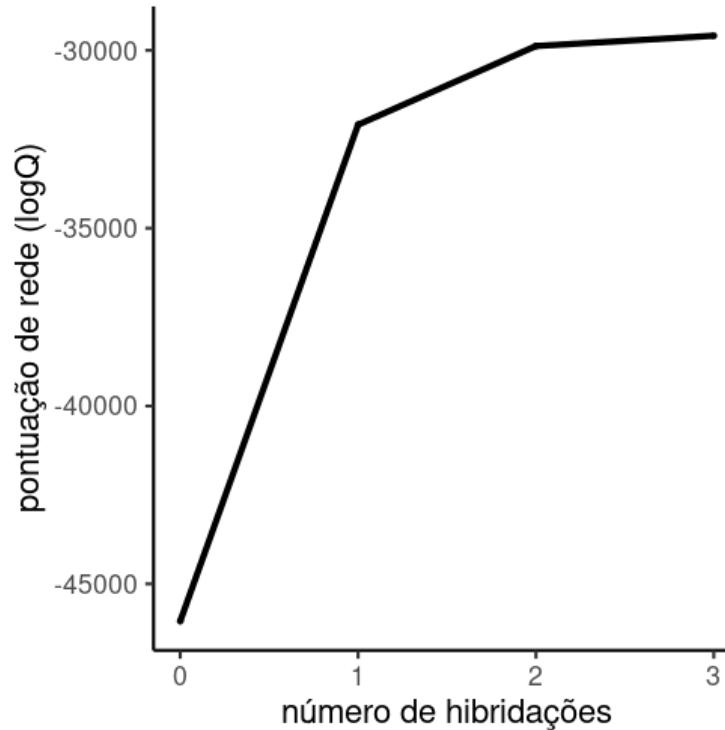
CF _{AB_CD}	CF _{AC_BD}	CF _{AD_BC}
0.5	0.3	0.2

$$AC_BD = 3/10$$

$$AD_BC = 2/10$$

Pseudo-likelihood

$$\max Q = \max \left\{ \prod_{s \in \mathcal{S}} (\text{CF}_{q_1})^{X_{q_1}} \times (\text{CF}_{q_2})^{X_{q_2}} \times (\text{CF}_{q_3})^{X_{q_3}} \right\}$$



Otimização de:

- Topologia
- Extensões dos ramos
- φ

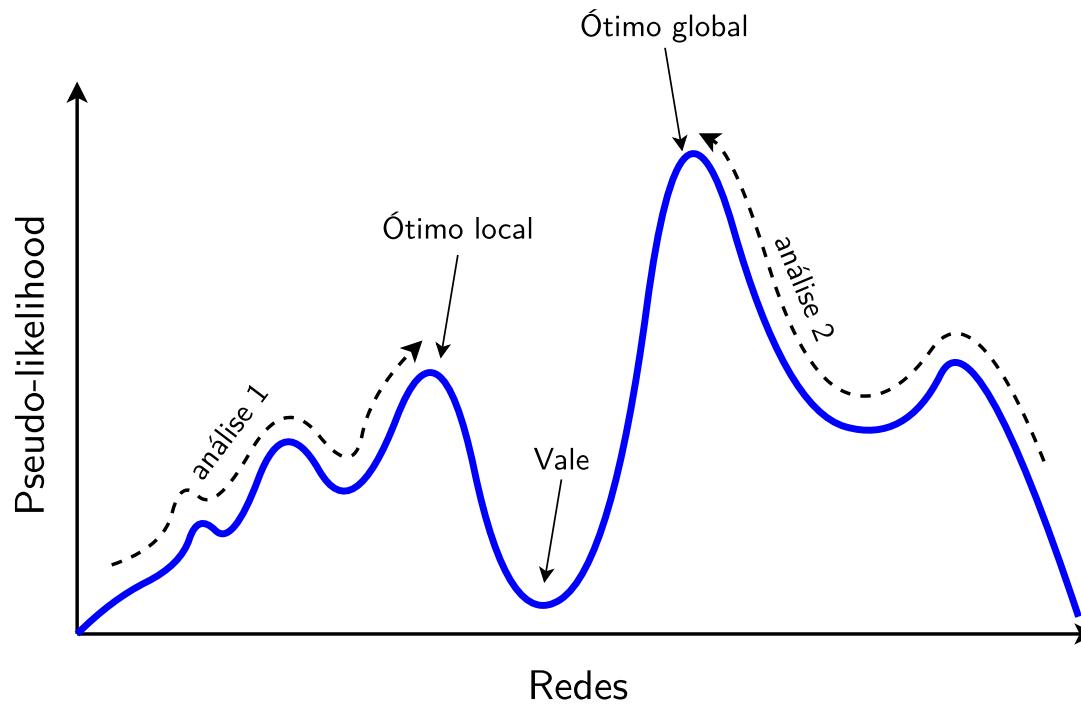
Como são propostas as redes filogenéticas?



operadores



hill-climbing



realizar análises independentes!

```
snaq!(sppTree, CFTable, hmax = 1, filename = "net1", runs = 10)
```

Referências

- Elworth R.A.L. et al., in *Bioinformatics and Phylogenetics* 29, 317–360 (2019).
- Jiao X., Yang Z., *Syst. Biol.* 70, 108–119 (2021).
- Kubatko L.S., Knowles L.L. (eds.), Princeton University Press (2023).
- Olave M., Meyer A., *Syst. Biol.* 69, 848–862 (2020).
- Sánchez K.I. et al. *Syst. Biol.*
- Solís-Lemus C., Ané C., *PLOS Genet.* 12, e1005896 (2016).
- Solís-Lemus C. et al., *Mol. Biol. Evol.* 34, 3292–3298 (2017).
- Yu Y. et al., *Proc. Natl. Acad. Sci. USA.* 111, 16448–16453 (2014).