Many types of trees: cellular genealogies
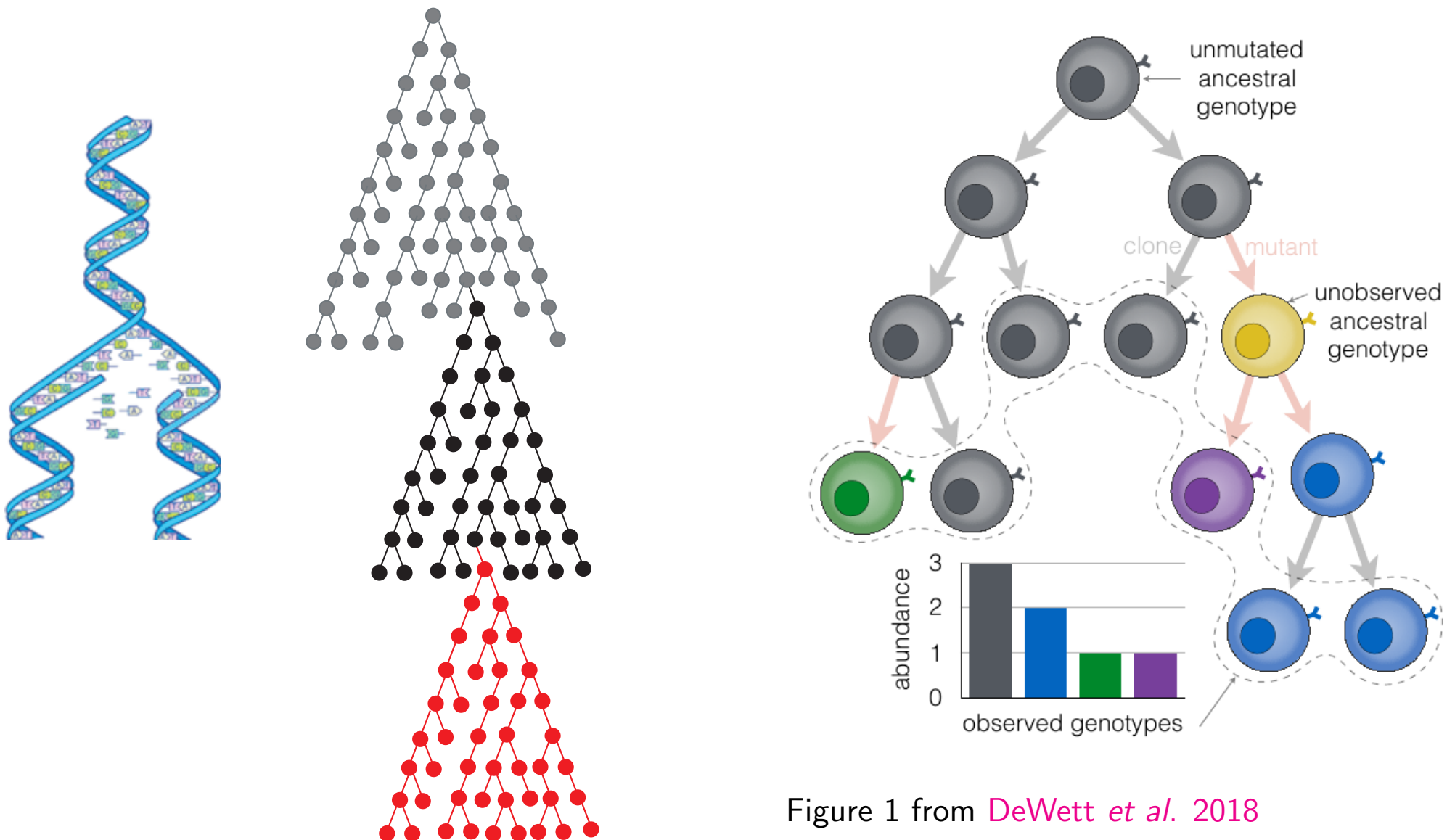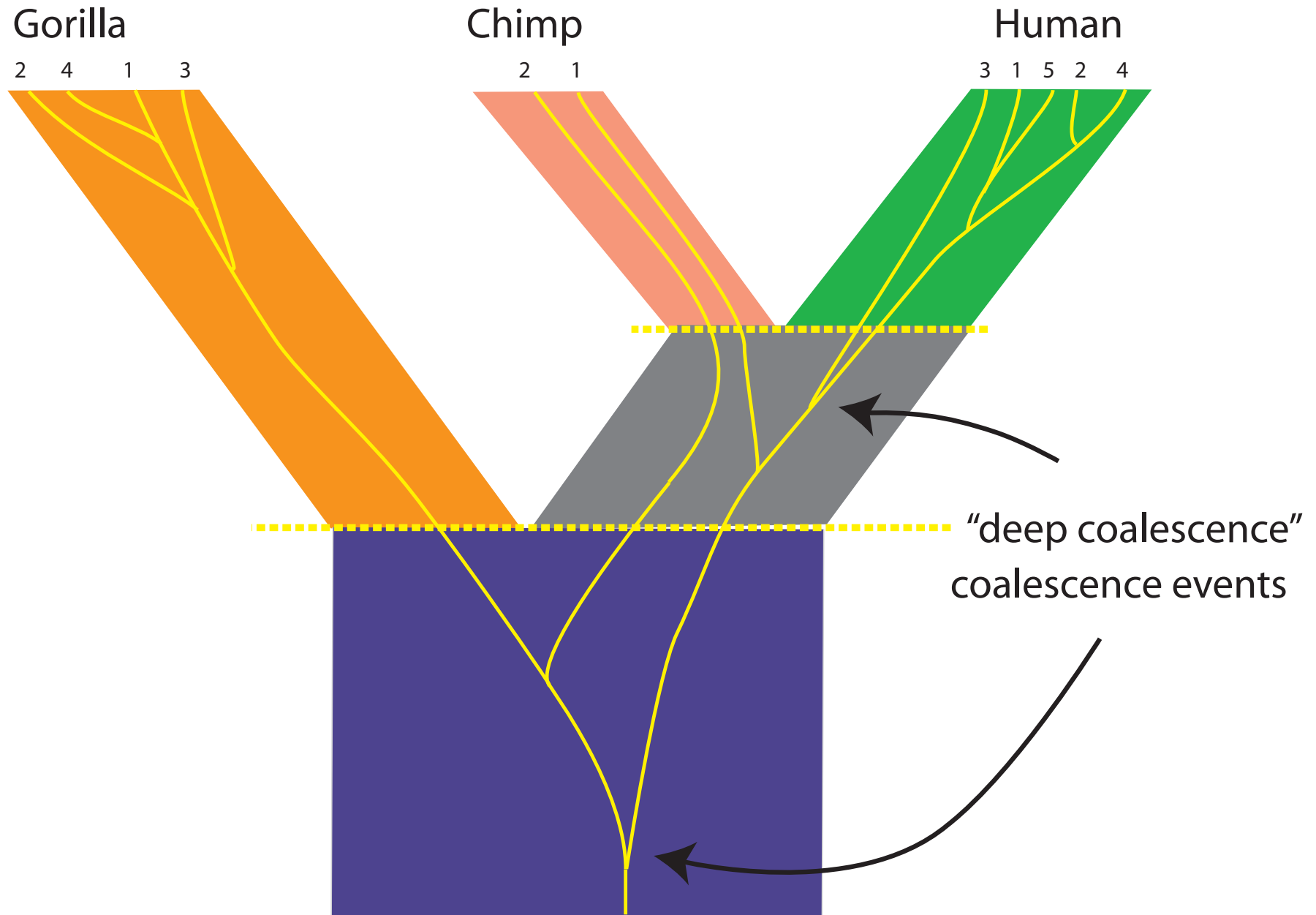

unmutated ancestral genotype

clone   mutant

unobserved ancestral genotype

abundance

observed genotypes

Figure 1 from DeWett *et al.* 2018

Many types of trees: "gene tree" within a species tree

B

Amino terminus

Carboxyl terminus

STAS region

AA position in alignment

Figure 1 from Liu et al. (2010)

A

Yinpterochiroptera

Megachiroptera

Yangochiroptera

Microchiroptera

B

Eidolon helvum

Megaderma lyra

Myotis lucifugus

56.7%

Me. lyra

My. lucifugus

E. helvum

22.3%

E. helvum

My. lucifugus
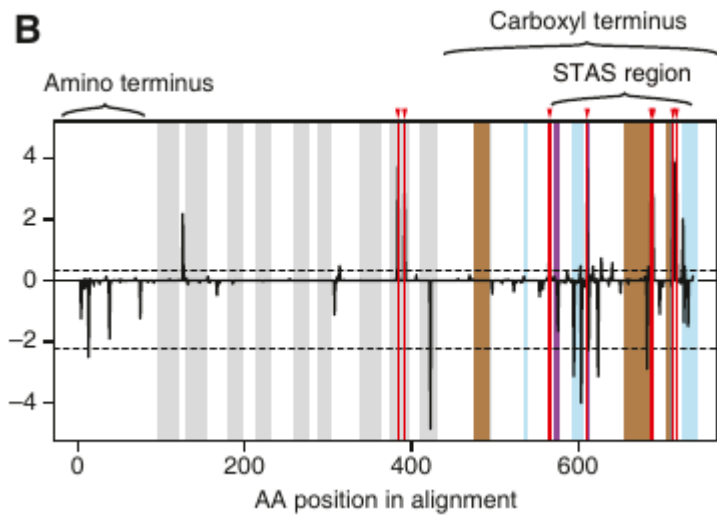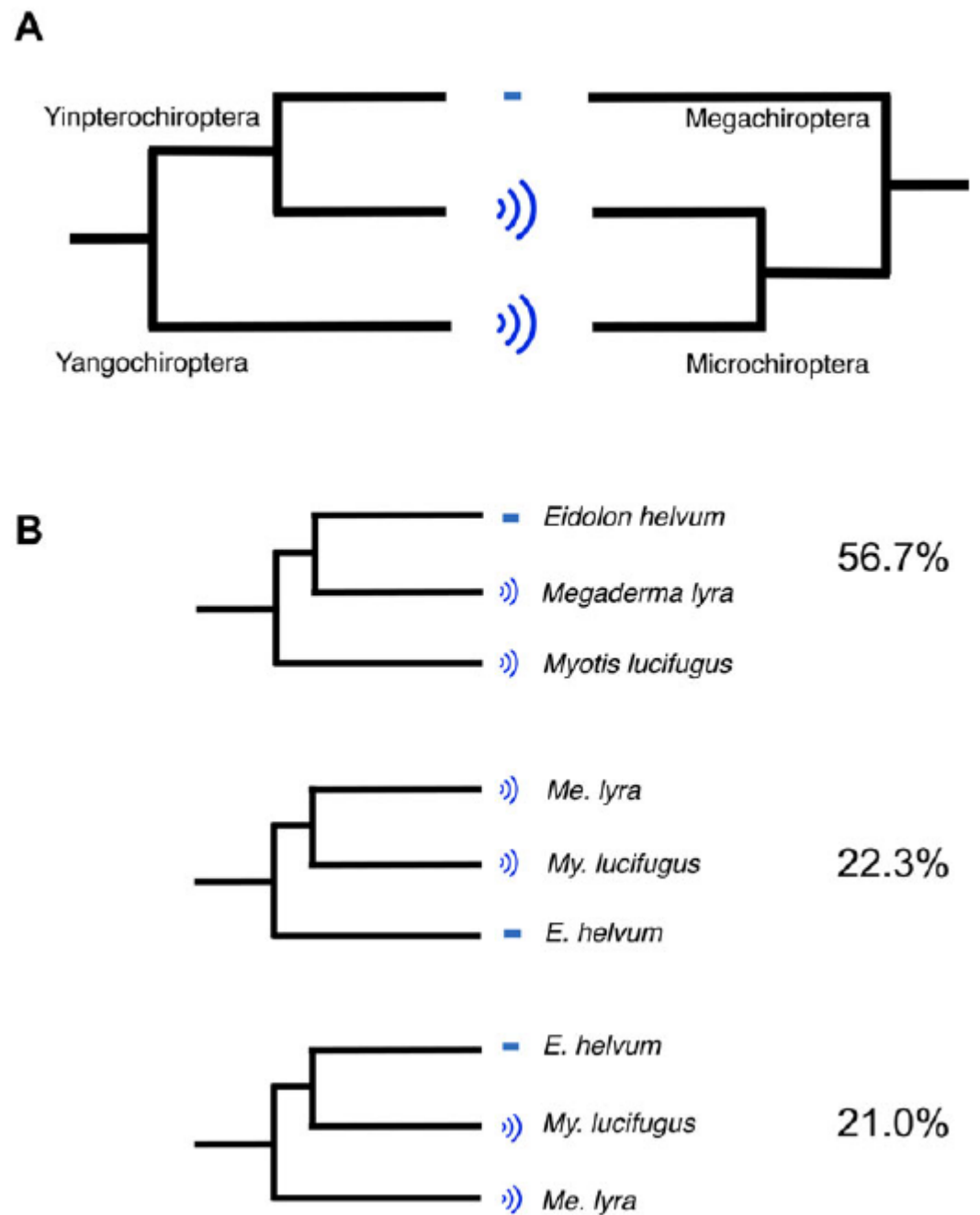
Me. lyra

21.0%

Figure 2 from Hahn and Nakhleh (2016)

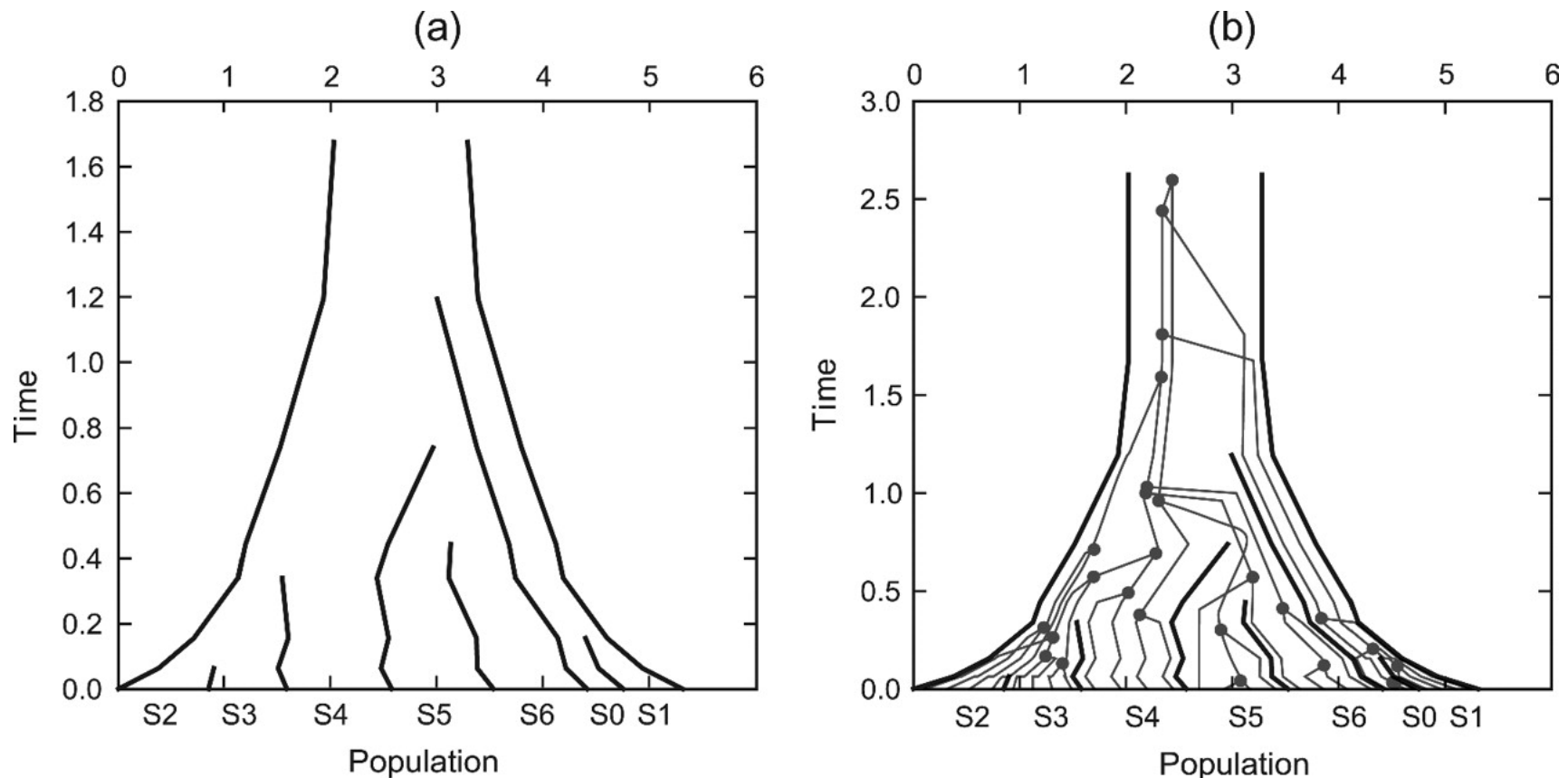# Inferring a species tree while accounting for the coalescent

Figure 2 from Heled and Drummond (2010) *BEAST
See also the recent work by Huw Ogilvie and colleagues on StarBEAST2.

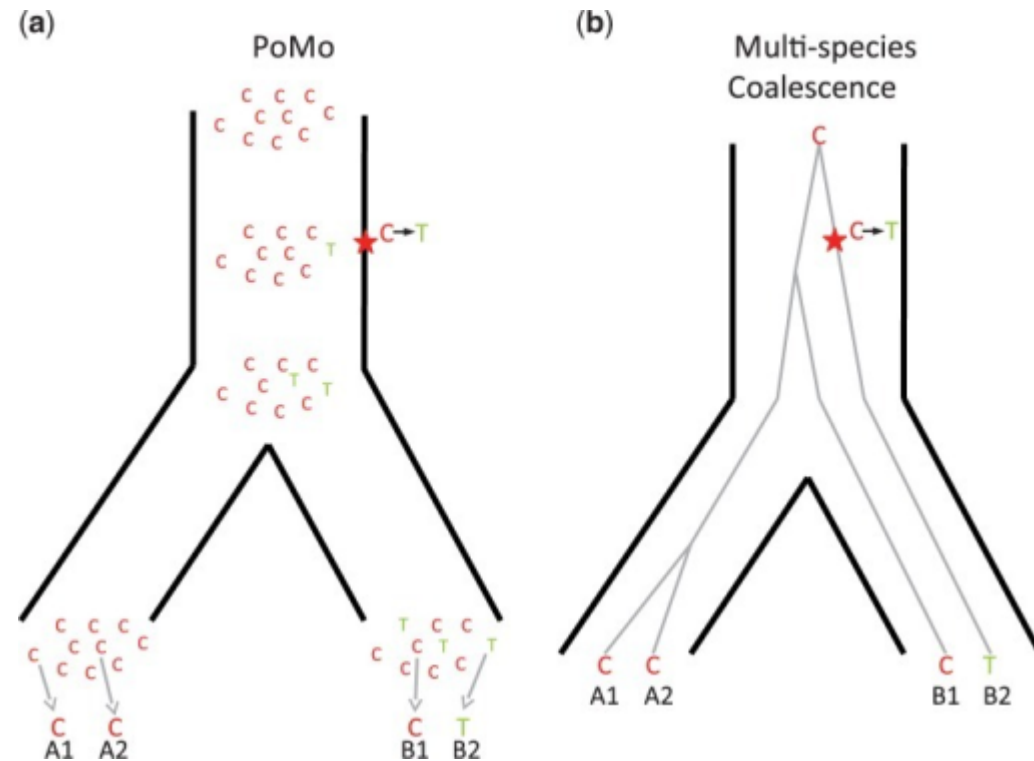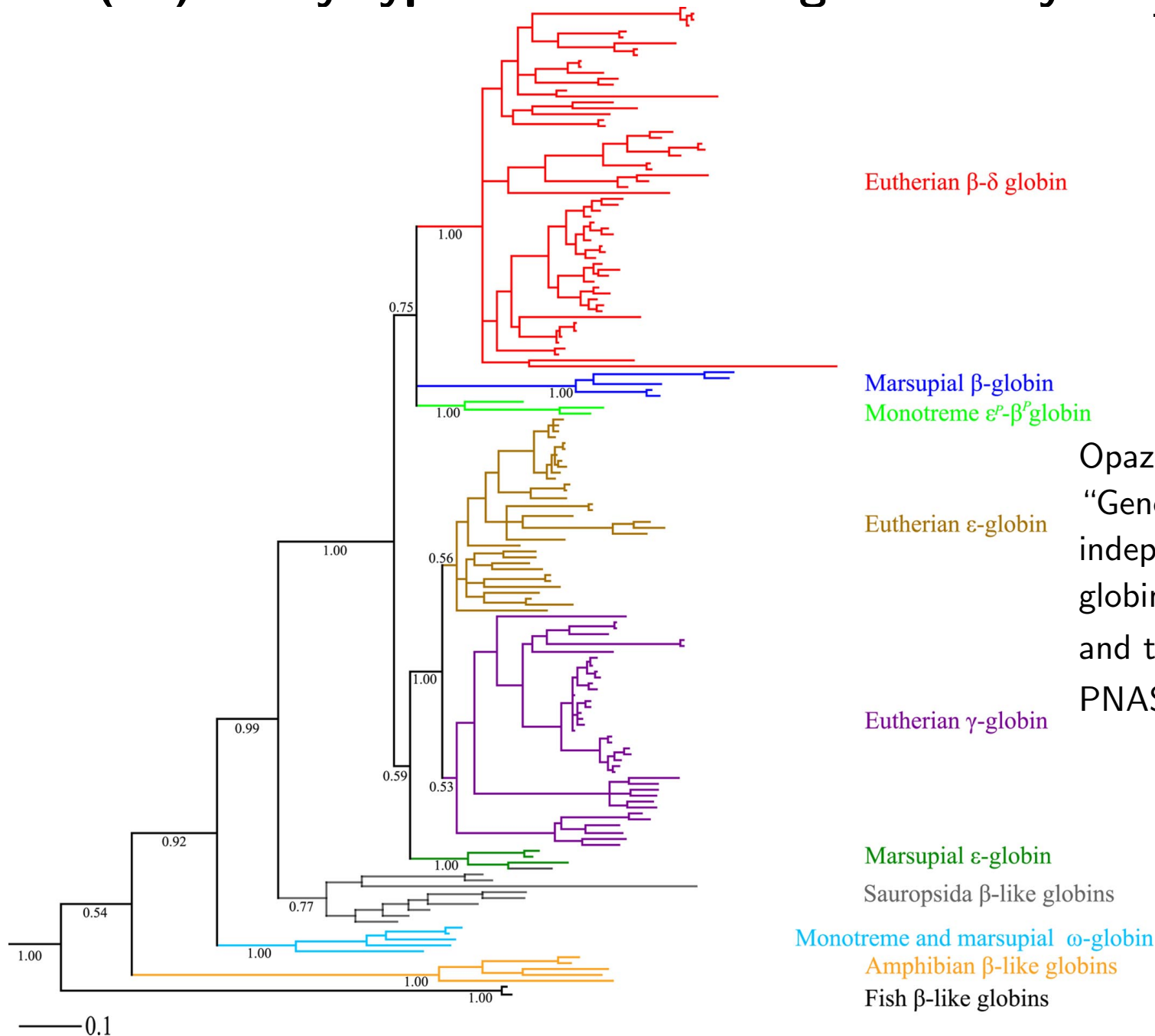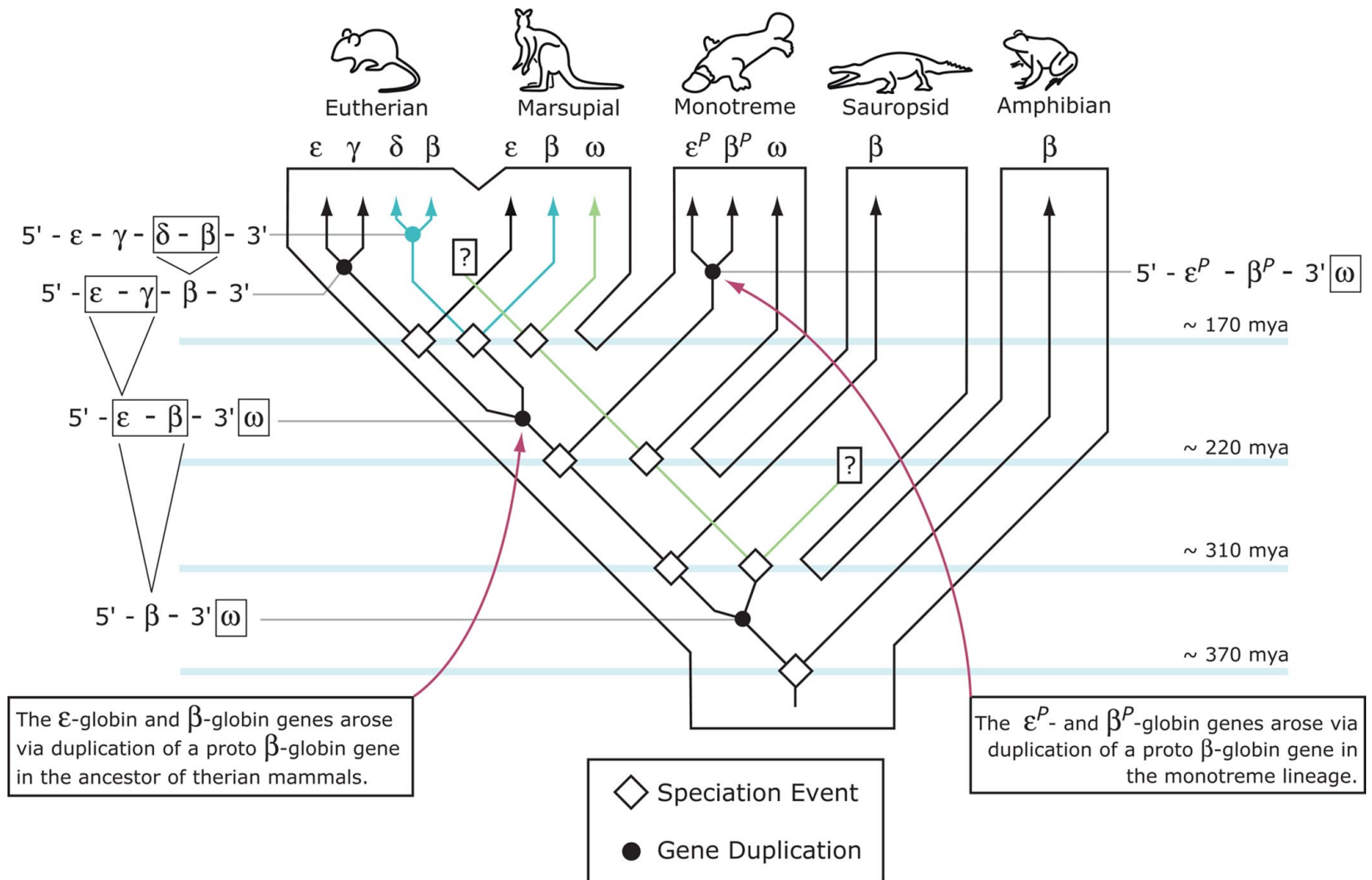# Considering ILS effects without modeling gene trees

PoMo model

Figure 1 from De Maio et al. (2015)

(3a) Many types of trees: A "gene family tree"

Eutherian β-δ globin

Marsupial β-globin
Monotreme ε^P-β^P globin

Opazo, Hoffmann and Storz "Genomic evidence for independent origins of β-like globin genes in monotremes and therian mammals"
PNAS **105(5)** 2008

Eutherian ε-globin

Eutherian γ-globin

Marsupial ε-globin

Sauropsida β-like globins

Monotreme and marsupial ω-globin
Amphibian β-like globins
Fish β-like globins

Opazo, Hoffmann and Storz "Genomic evidence for independent origins of β-like globin genes in monotremes and therian mammals" PNAS **105(5)** 2008

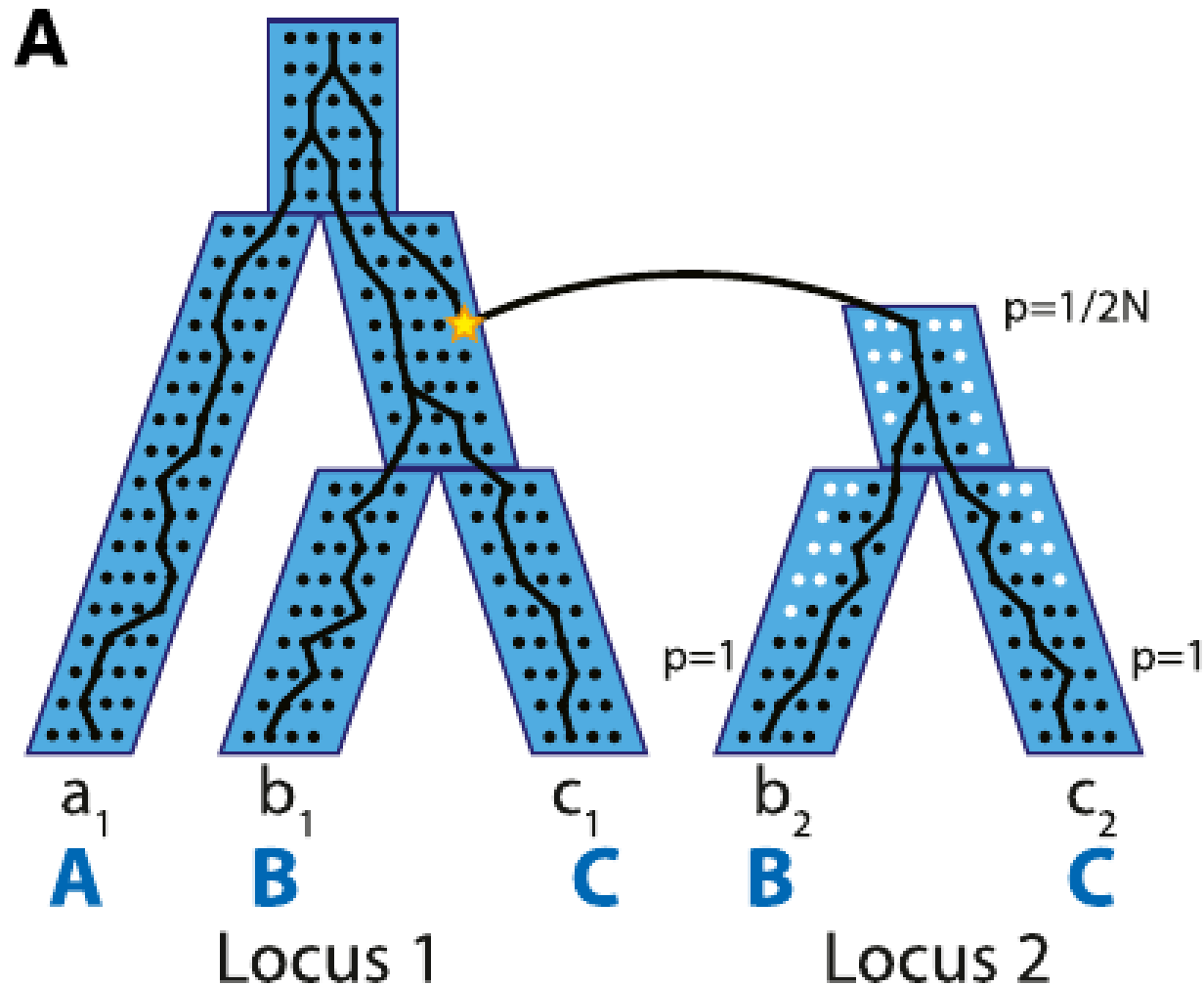# Joint estimation of gene duplication, loss, and coalescence with DLCoalRecon

A

p=1/2N

p=1

p=1

a₁
A

b₁
B

c₁
C

b₂
B

c₂
C

Locus 1

Locus 2

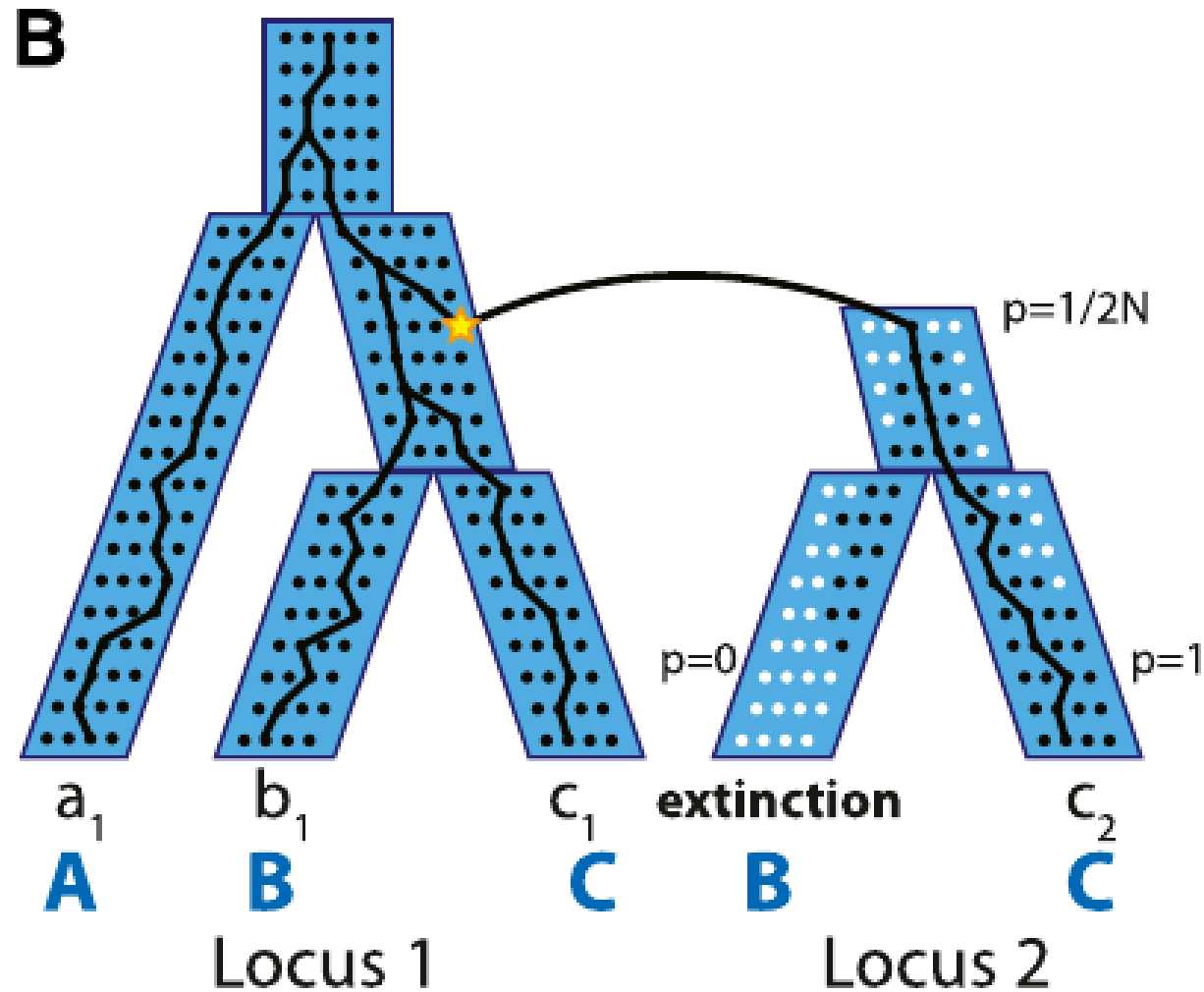Figure 2A from Rasmussen and Kellis (2012)

DL models and coalescence

Figure 2B from Rasmussen and Kellis (2012)

Many types of trees: Lateral Gene Transfer

tree - a graph without cycles (loops)
network - general graph; cycles allowed

Cycles can represent

- lateral ("horizontal") gene transfer ,
- hybridization between species,
- introgression between populations.
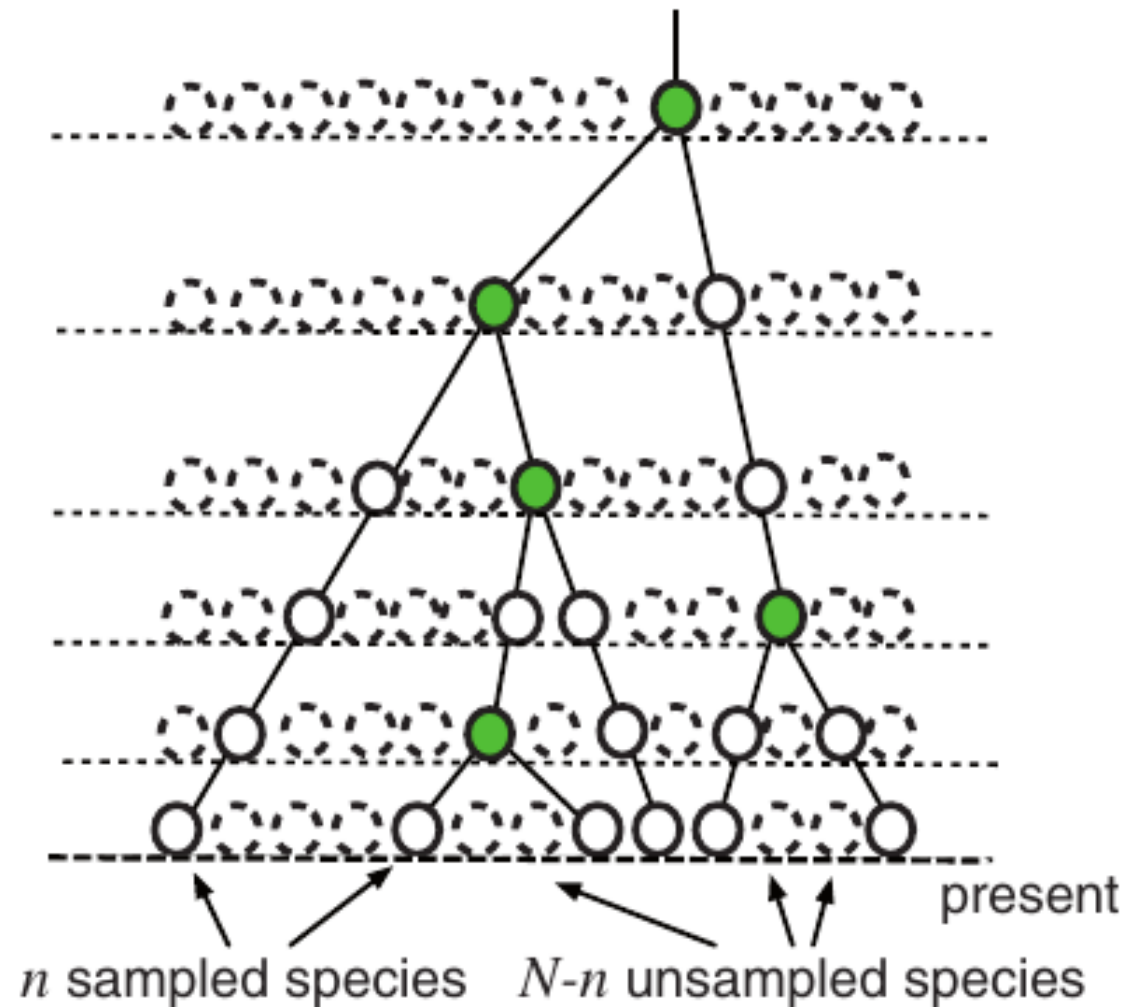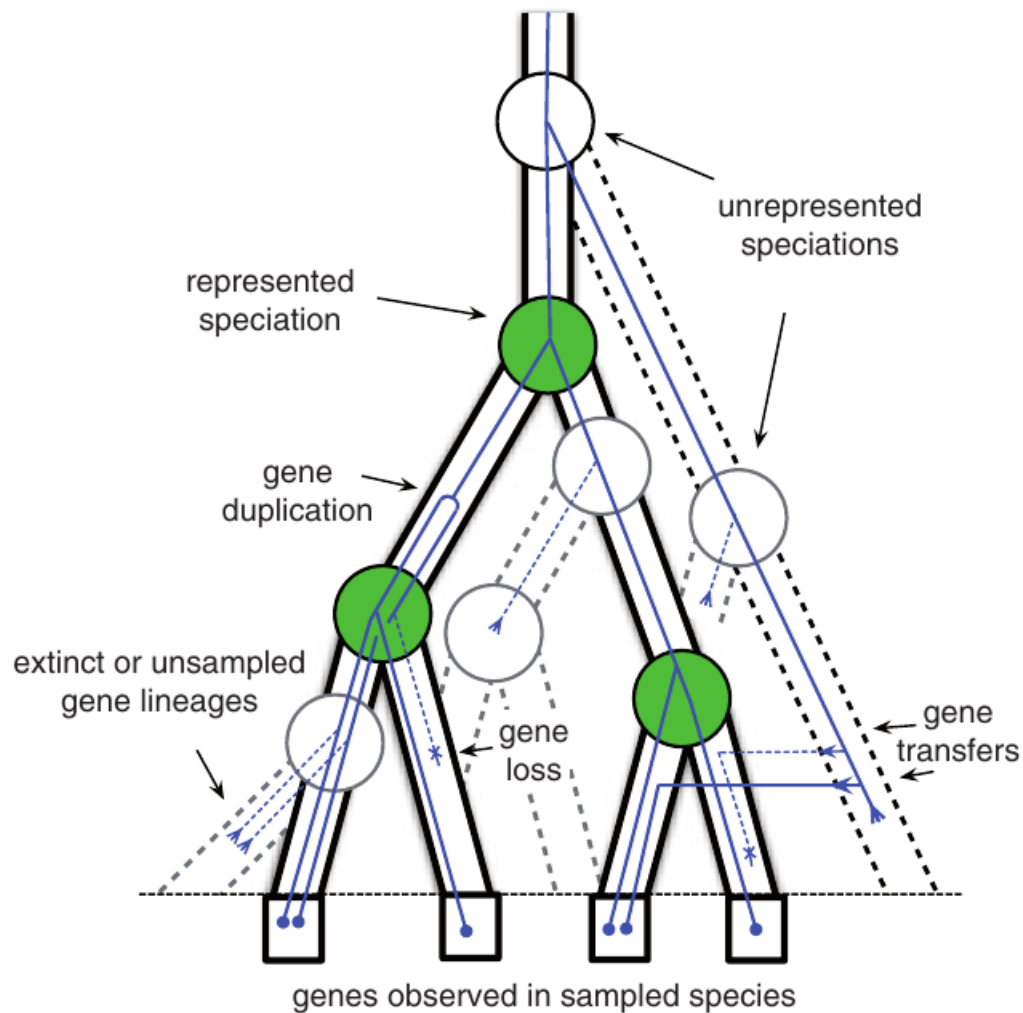
Many types of trees: Lateral Gene Transfer

present

n sampled species $N\text{-}n$ unsampled species

Figure 2c from Szöllősi et al. (2013)

a)

evolutionary scenario along complete phylogeny

represented speciation

gene duplication

extinct or unsampled gene lineages

unrepresented speciations

gene loss

gene transfers

genes observed in sampled species

Figure 3 from Szöllősi et al. (2013)

They used 423 single-copy genes

in ≥ 34 of 36 cyanobacteria

They estimate:

2.56 losses/family

2.15 transfers/family

$\approx 28\%$ of transfers between
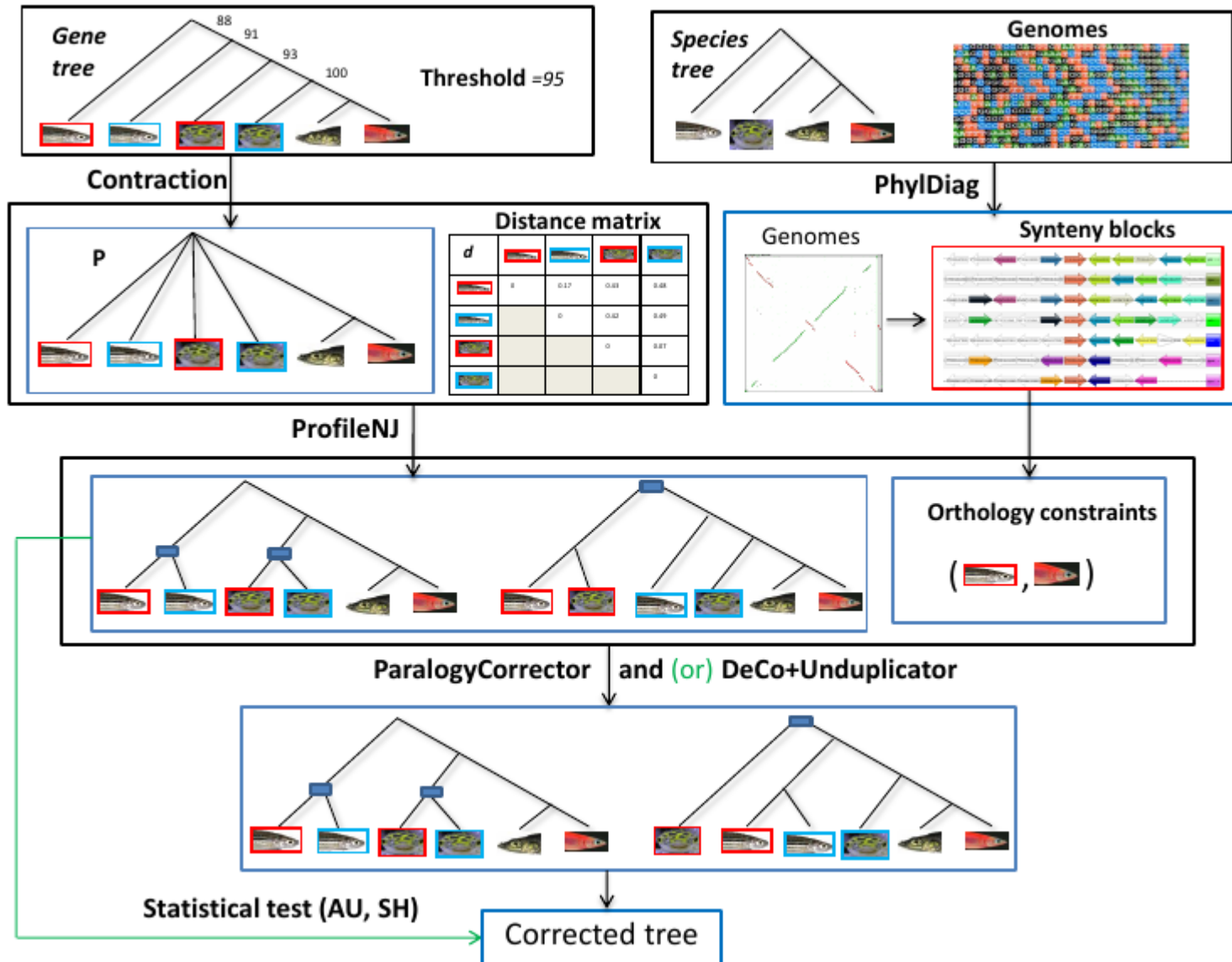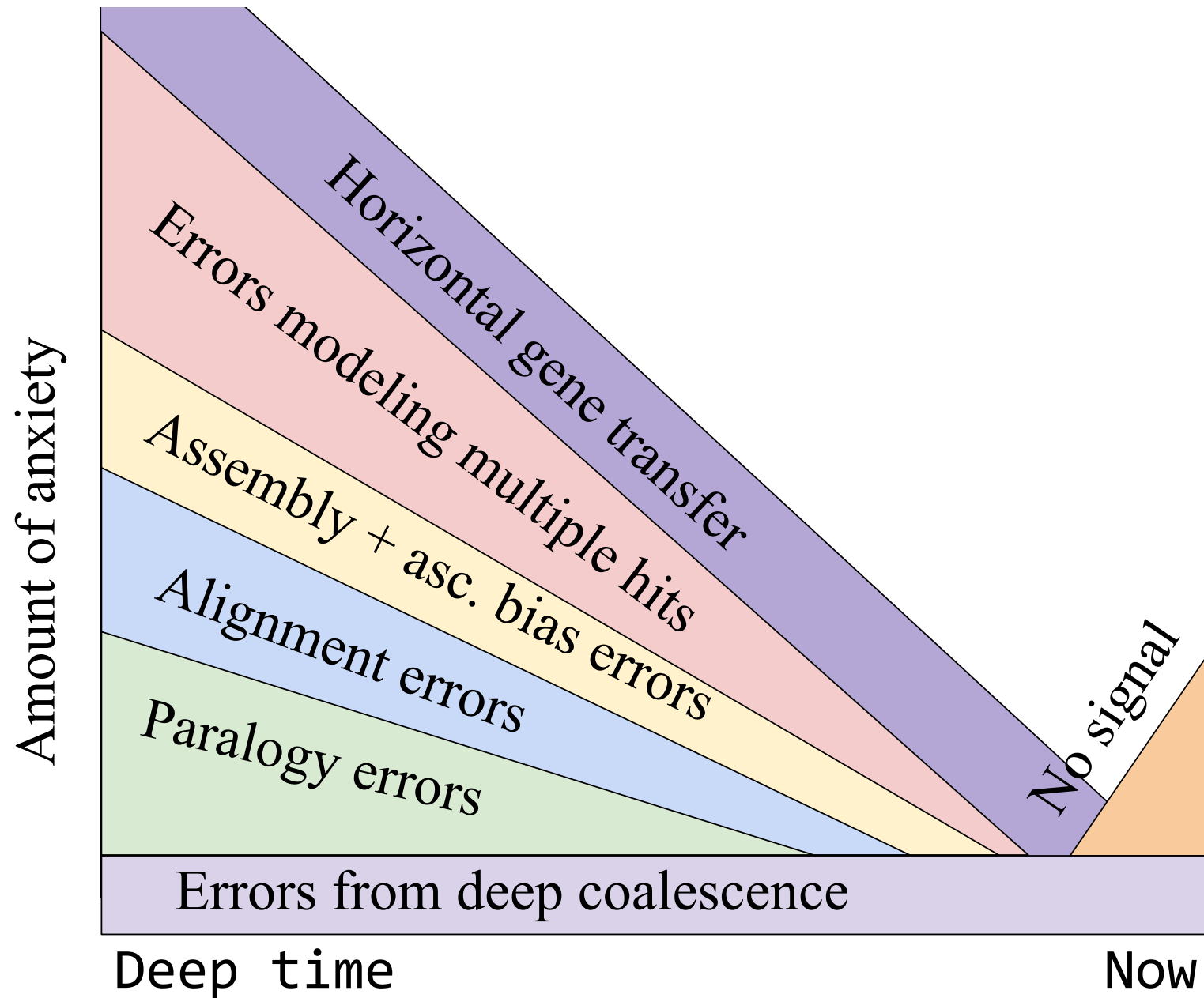
non-overlapping branches

Figure 4 from Noutahi et al. (2016)

(3b) sources of error cartoon

References

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Noutahi, E., Semeria, M., Lafond, M., Seguin, J., Boussau, B., Guéguen, L., El-Mabrouk, N., and Tannier, E. (2016). Efficient gene tree correction guided by species and synteny evolution. *PLoS One*.

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