On the inference of complex phylogenetic networks by Markov Chain Monte-Carlo

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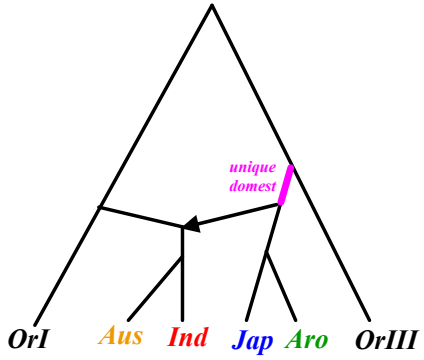
Phylogenetic networks

Phylogenetic networks are Directed Acyclic Graphs (DAG) that allow to detect reticulation events, such as :

- Admixture (e.g. humans)
- Introgressions (e.g. plants and animals)
- Horizontal gene transfers (e.g. bacteria)



Some key points on networks :

- Edge length = evolutionary time
- Reticulation nodes have 2 parents and represent reticulation events
- We want to obtain a probability distribution of networks (uncertainty on clades)
- The more data we have, the more precisely we can infer the network

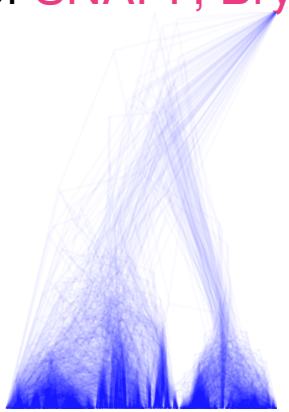
Data in our study :

- A Data matrix containing an alignment of m biallelic markers
- Markers can be SNPs or random sites including invariant sites
- A certain distance must be preserved between genomic sites

Our new Bayesian method, SNAPPNet

- N : phylogenetic network (topology, branch lengths, population sizes)
- X_i : data for marker i
- G_i : locus tree for marker i
- m markers, $Data = (X_1, \ldots, X_m)$
- $\mathbb{P}(Data \mid N)$: likelihood of the data given the network
- P(N) : network prior
  birth hybridization process of Zhang et al. MBE 2018
- Posterior probability distribution (extension of SNAPP, Bryant et al. MBE 2012)

$$\mathbb{P}(N|Data) \propto \left(\prod_{i=1}^{m} \int_{\psi} \mathbb{P}(X_i|G_i)\mathbb{P}(G_i|S)dG_i \right) P(N)$$
$$\propto \mathbb{P}(Data \mid N)\, P(N)$$



$\Rightarrow$ Markov Chain Monte Carlo (MCMC) in order to sample the posterior probability distribution $\mathbb{P}(N|X_1, \ldots, X_m)$ using new algorithms dedicated to networks

SNAPPNet implemented in BEAST

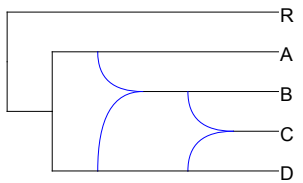
How SNAPPNet computes the likelihood $\mathbb{P}(Data \mid N)$

Contrary to trees, network edges can not be treated independently

- We compute joint probability distributions
- We minimize computing time by minimizing the conditional part in computation

Dataset ID	CPU time	
	SNAPPNet (in minutes)	MCMCBiMarker (in hours)
1	5.559	35.9354
2	5.6763	34.2433
3	5.7351	32.6519
4	5.446	34.2011
5	5.5996	33.2354

SNAPPNet (Us) vs MCMCBiMarker
(Zhu et al., Plos Comp Biol 2018)

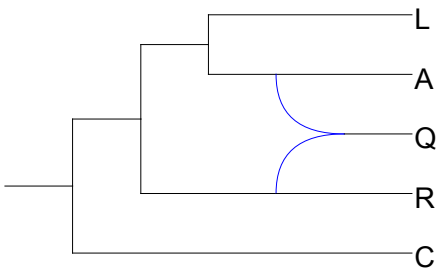


a level-2 network

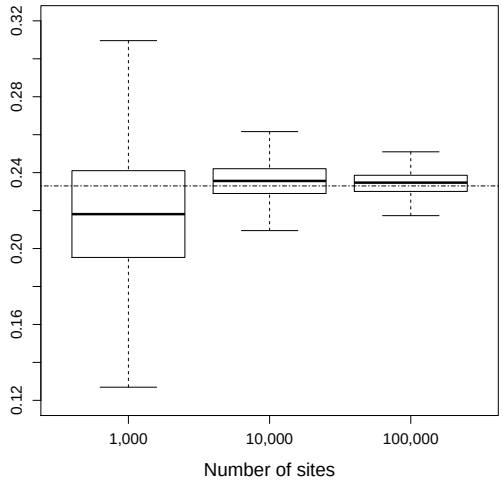
Illustration of SNAPPNet on simulated and real data

- Simulation study

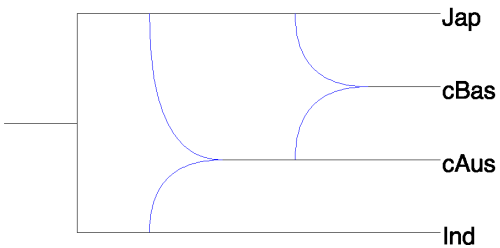
True network



Estimated network length



- Study on rice genome (4 subpopulations ***Ind***ica, ***Jap***onica, circum***Aus*** and circum**Bas**mati using data from *Wang et al., Nature 2018*)



Rice evolution scenario inferred by SNAPPNet

c*Aus* : result of an early(old) combination between the *Ind* and the *Jap* lineages

c*Bas* : a later combination between the c*Aus* and the *Jap* lineages

New scheme that appears compatible within the simpler schemes that have been proposed so far (e.g. *Choi et al, Genome Biology 2020*)