## Algorithmic issues in (co)phylogenetic analysis

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## Motivation

## Different systems "coevolve"

- hosts and their parasites or pathogens
- whole organisms and their genes
- geographical areas and the species which inhabit them.
- cultural traditions and populations


## Host-Parasite associations

- about $75 \%$ of emergent human diseases are zoonoses, that is, they switched hosts from other species into humans
- determine the rates of evolution in hosts and parasite
- determine how long is the association between host and parasite



## The instance of the problem



## Reconciliation method

## Co-phylogeny reconstruction problem



## State-of-art: reconciliation method



Two trees and the association function between their leaves.


## The mapping function



Selecting the best solution: assign a cost to each of the four types of events and then minimize the total cost.

## Modeling the events

The mapping $f$ induces a partition of $V(P)$ into three sets:

- $\Sigma \rightarrow$ co-speciations
- $\Delta \rightarrow$ duplications
- $\Theta \rightarrow$ host-switches


## Modeling the events

The mapping $f$ induces a partition of $V(P)$ into three sets:

- $\Sigma \rightarrow$ co-speciations
- $\Delta \rightarrow$ duplications
- $\Theta \rightarrow$ host-switches
- Co-speciation

$\operatorname{lca}\left(f\left(p_{1}\right), f\left(p_{2}\right)\right)=f(p)$ and $f\left(p_{1}\right)$ and $f\left(p_{2}\right)$ are incomparable.


## Modeling the events

The mapping $f$ induces a partition of $V(P)$ into three sets:

- $\Sigma \rightarrow$ co-speciations
- $\Delta \rightarrow$ duplications
- $\Theta \rightarrow$ host-switches
- Duplication



## Modeling the events

The mapping $f$ induces a partition of $V(P)$ into three sets:

- $\Sigma \rightarrow$ co-speciations
- $\Delta \rightarrow$ duplications
- $\Theta \rightarrow$ host-switches
- Host-switch



## Modeling the events

We can define a function $\boldsymbol{\alpha}(f)$ that gives the number losses induced by the mapping $f$.

- Loss

the edge ( $p, p_{1}$ ) contributes with 1 loss.

Everything is against us.


## Everything is against us.....



Everything is against us.


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Finding an optimal reconciliation is NP-hard.

The complexity arises from the difficulty of separating possible from impossible host switches combinations.

## Everything is against us.....

## Generate all the optimal reconciliations.

- The number of optimal reconciliations increases rapidly even for small trees.
- The size of the trees can be large.


## Real data

A sample with hundreds of arthropods and the Wolbachia infecting them. Data from Patricia Simões, collected in Tahiti, Moorea, Raiatea.


Wolbachia in Moorea

## Our contribution so far

A polynomial delay algorithm for generating all the optimal reconciliations.

Basic idea:

- Fill a dynamic programming matrix with additional information for the exhaustive traceback.

Problems

- No time-feasible solutions
- Too many time-feasible solutions


## Bounded switch problem

## k-switch Problem:

Given $H, P, \varphi, \underline{c}$, and an integer $k$ find an optimal reconcilation in which all the host switches have a distance bounded by $k$.


## Bounded switch problem

## k-switch Problem:

Given $H, P, \varphi, \underline{\boldsymbol{c}}$, and an integer k find an optimal reconcilation in which all the host switches have a distance bounded by $k$.

- host-switches only between closely related species.
- No time-feasible solutions $\Rightarrow$ decrease $k$.
- Too many time-feasible solutions $\Rightarrow$ decrease k maintaining the same optimal cost.


## Open Problem

What is the complexity of the k -switch problem in the acyclic case?

## Exercise 2

- Given two phylogenetic trees is it possible to find a reconciliation without host-switches? Without duplications?


## Current work

Other types of events

- Failure to diverge

- Spread



## Open Problems

More realistic models

- the cost values influence the optimal solution
- multiple hosts - multiple parasites (communities)


## Sequential speciation

Leaf cutter ants



## phylogenetic forests

## Sequential speciation

## Leaf cutter ants



