Phylogenetics + Phylogenomics = Cophylogen_what? (part II)

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On the Reconstruction of the Evolutionary History of Gene Families
Phylogenetics

The study of the evolution of various groups of related organisms
Gene Tree vs Species Tree

Godmann et. al. 1979
Mapping GT onto ST

Guigó et al. 1996
Reconciliation Tree
Evolutionary history of Gene Families

A group of genes that are related by sequence or function similarity

A set of genes originated by duplications from some ancestral gene
Our Reconstruction Algorithm: the data
1st step: Lowest Common Ancestor
1\textsuperscript{st} step: Lowest Common Ancestor

Gene Duplication: $c_1 \rightarrow c_2$

Gene Loss: $b_3$
Our Reconstruction Algorithm: the data
1st step: Lowest Common Ancestor
2\textsuperscript{nd} step: Duplications and Losses
Algorithm

For each gene family
Map each node of the gene tree onto a node in the species tree according to the LCA
Infer Gene Losses and Gene Duplications

Identify Multiple Gene Duplications: cluster duplications and genome duplications
Correct gene trees and/or matrix of synteny when inconsistencies
Conclusions

Synteny information: paralogy and orthology can help to improve reconstruction

Allow duplication events at the leaves of the species tree

More than one gene per species leads to a better clue on the gene family evolutionary history, reduces the number of introduced duplications and thus losses

Allow imperfect data leads to correct the provided information
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SALUD!!