

Spectral Signature of Gene Family Trees

Leonardo de Oliveira Martins^{1,2} and Christophe Dessimoz^{1,2,3}

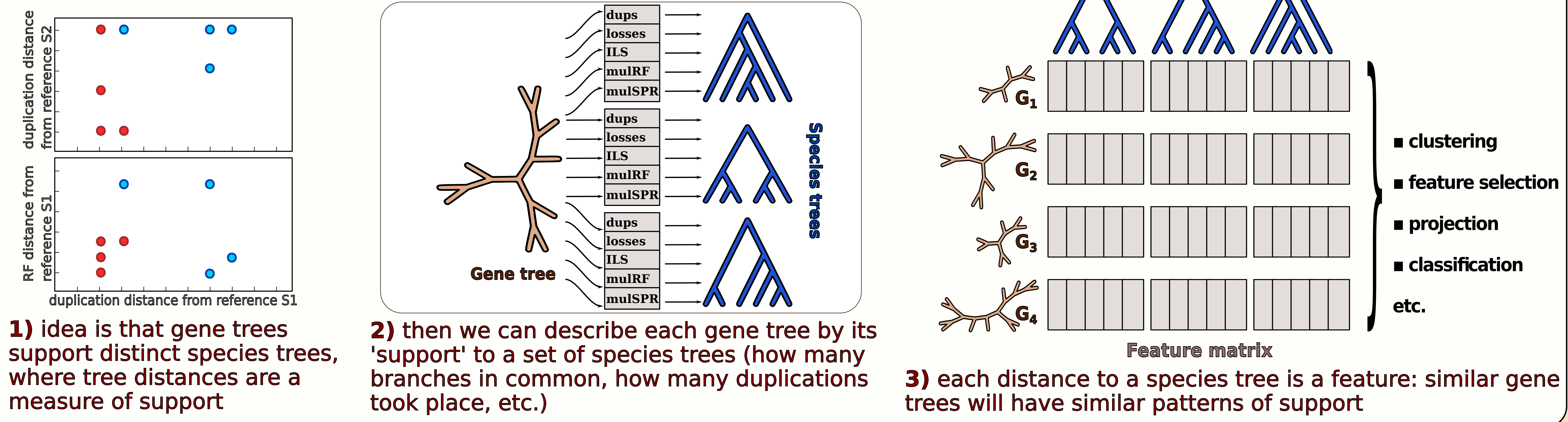
1 University of Lausanne, Lausanne, Switzerland
2 SIB Swiss Institute of Bioinformatics, Switzerland
3 University College London, London, UK



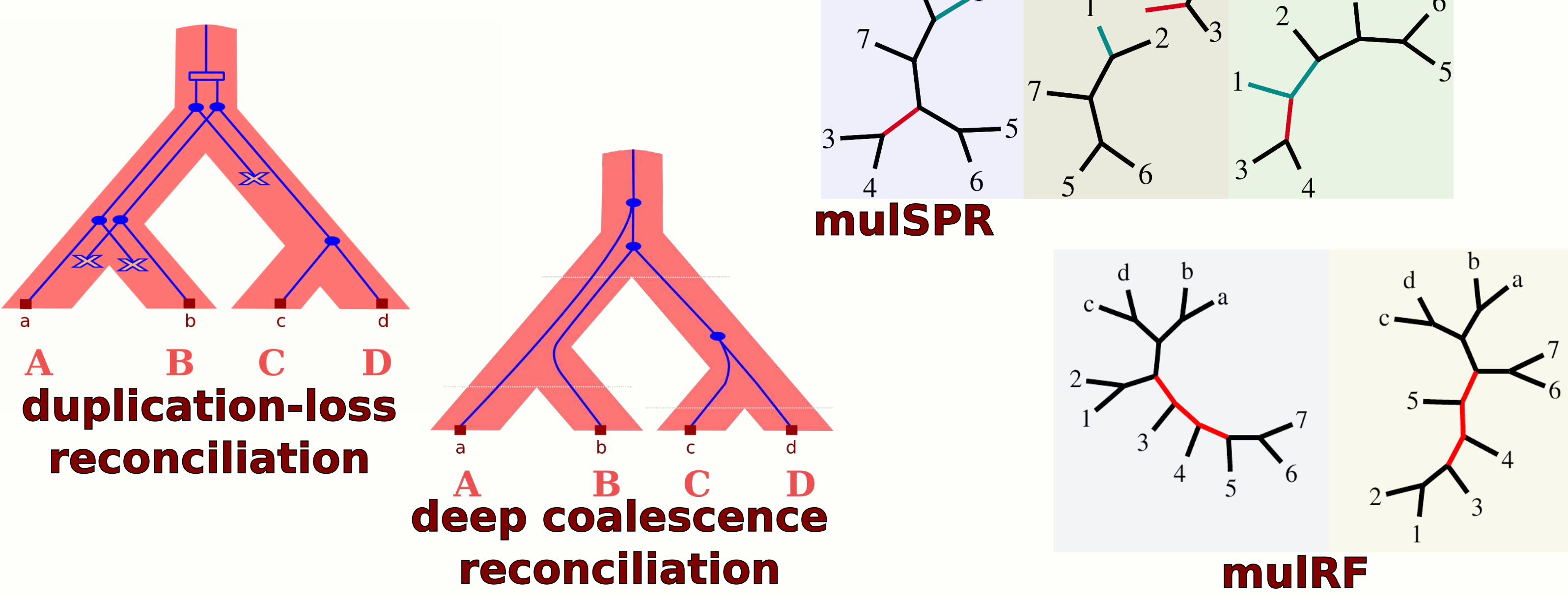
Objective: create a framework for visualisation and comparison of arbitrary gene families (which may include paralogs, populational samples, etc.)

Challenge: many gene families cannot be directly compared (e.g. few species in common etc.)

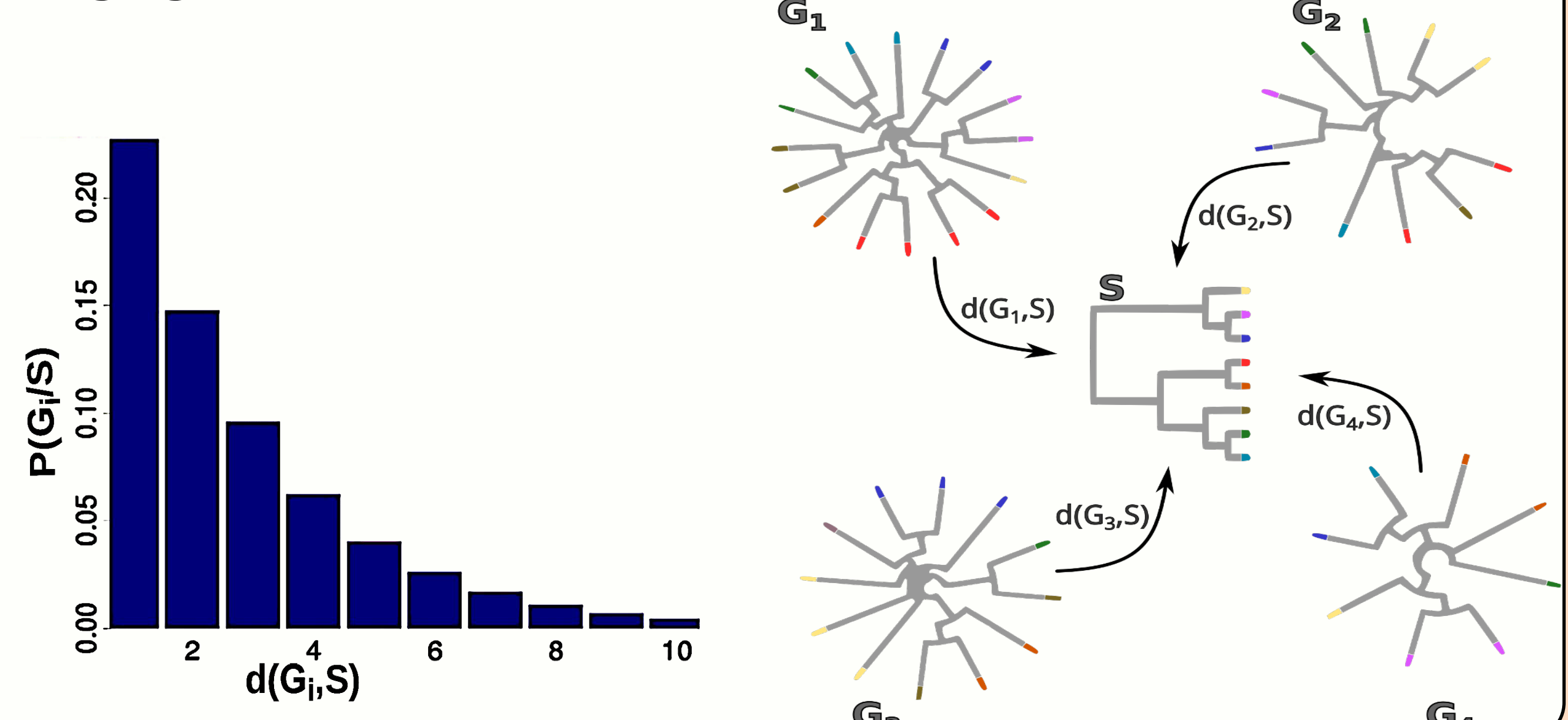
Solution: comparing them in relation to a fixed set of reference species trees



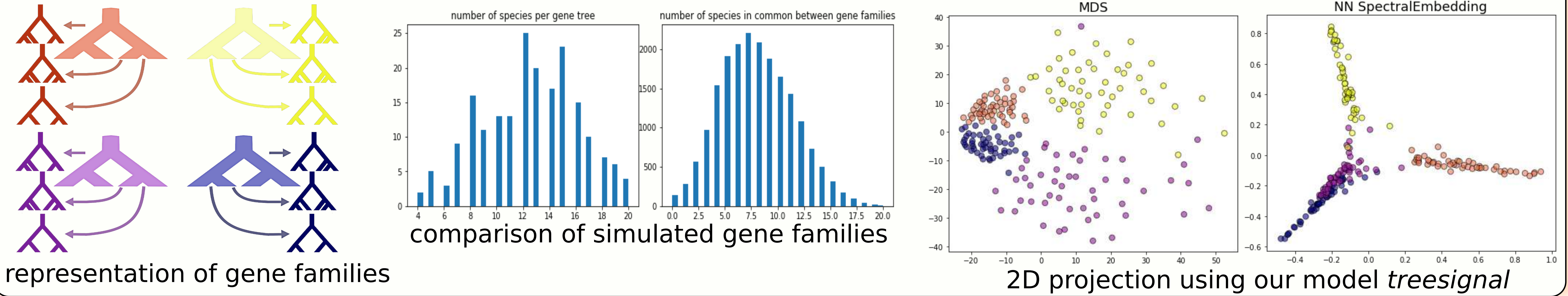
Tree distances: must handle multi-labelled gene trees, can have biological interpretation



Reference trees: local species tree estimates (e.g. *guenomu* software)



Results on simulated data: gene families from four distinct species trees using *simphy*



Preliminary results on real data: fungal gene families from OMA database

