Tree concordance analysis: tree distance measures, clustering techniques, and model selection criteria (working title)

Kevin Gori¹, Nick Goldman¹, and Christophe Dessimoz*1

Email: Christophe Dessimoz - dessimoz@ebi.ac.uk;

Abstract

Text for this section.

Background

- 1. generalities about tree incongruences
- 2. previous approaches & their limitations
 - (a) process specific approaches
 - i. LGT -> cite a bunch of methods
 - ii. Incomplete lineage sorting $-> {\rm e.g.}$ Rannala & Yang 2003
 - iii. BUT: limited to these specific processes and typically on other strong assumptions
 - (b) Bayesian concordance analysis -> Bucky
 - i. BUT: computationally expensive. Cannot go beyond a few taxa
 - (c) Clustering approaches ("Tree of Trees")
 - i. Tom Nye
 - ii. Leigh et al. 2011
 - iii. Darlu and Genoche 2011

¹ EMBL-European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

^{*}Corresponding author

iv. BUT: no statistical framework to work out the optimal distance/clustering method, and no insights into model selection

3. In this work

- (a) introduce a statistical framework for clustering-based concordance analysis
- (b) investigate which combination of distance and clustering method performs best in simulation and real data
- (c) investigate 3 model selection criteria to identify the number topologies (clusters):

Methods

Statistical framework

• show how the traditional ML model (Felsenstein 1981) can be extended to accommodate > 1 tree topology: index tree topologies from 1..K, where K is the number of cluster (or "classes"), the likelihood becomes

$$L_{global} = \prod_{\text{aligned gene } g \in G} L(g|M,T,\theta_g) = \prod_{\text{aligned gene } g \in G} L(g|T_g,\theta)$$

where T is the set of K cluster topologies, M is a map between marker genes and T, and T_g the topology in T corresponding to M(g). Note that $L(T_g, \theta_g)$ is the traditional likelihood formula.

Tree distance measures

• list the various tree distance measures and explain how we computed them

Clustering methods

• list the various clustering methods and explain how we computed

Determining the number of classes

- Permutation analysis
- Goldman-Cox method
- Cluster-based approach (à la Leigh et al. 2011)

Results Discussion and Outlook

Author's contributions

Text for this section \dots

Acknowledgements

Text for this section \dots