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Inferring rooted species trees from unrooted gene trees using approximate Bayesian computation

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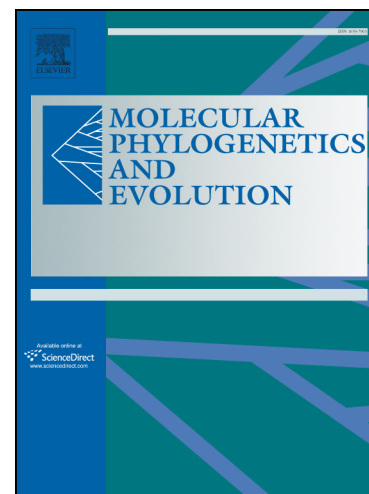
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1 Inferring rooted species trees from unrooted gene trees using approximate
2 Bayesian computation

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13 Abstract.—Methods for inferring species trees from gene trees motivated by incomplete lineage
14 sorting typically use either rooted gene trees to infer a rooted species tree, or use unrooted gene
15 trees to infer an unrooted species tree, which is then typically rooted using one or more outgroups.
16 Theoretically, however, it has been known since 2011 that it is possible to consistently infer the
17 root of the species tree directly from unrooted gene trees without assuming an outgroup. Here,
18 we use approximate Bayesian computation to infer the root of the species tree from unrooted gene
19 trees assuming the multispecies coalescent model. It is hoped that this approach will be useful in
20 cases where an appropriate outgroup is difficult to find and gene trees do not follow a molecular
21 clock. We use approximate Bayesian computation to infer the root of the species tree from unrooted
22 gene trees. This approach could also be useful when there is prior information that makes a small
23 number of root locations plausible in an unrooted species tree.

24
25 Keywords: multispecies coalescent, outgroup, midpoint rooting, molecular clock, identifiability,
26 sufficiency

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