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Distribution of coalescent histories under the coalescent model with gene flow

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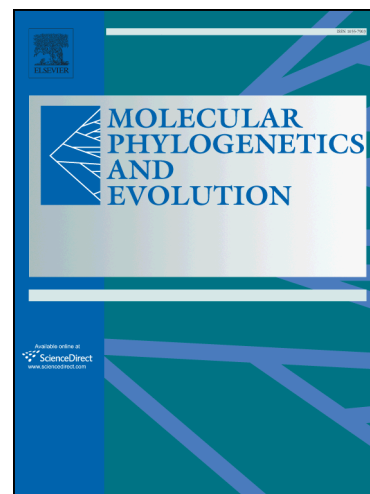
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1 TIAN AND KUBATKO – COALESCENT WITH GENE FLOW

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8 **Abstract**– We propose a coalescent model for three species that allows gene flow between both  
9 pairs of sister populations. The model is designed for multilocus genomic sequence alignments,  
10 with one sequence sampled from each of the three species, and is formulated using a Markov  
11 chain representation that allows use of matrix exponentiation to compute analytical expressions for  
12 the probability density of coalescent histories. The coalescent history distribution as well as the  
13 gene tree topology distribution under this coalescent model with gene flow are then calculated via  
14 numerical integration. We analyze the model to compare the distributions of gene tree topologies  
15 and coalescent histories for species trees with differing effective population sizes and gene flow  
16 rates. Our results suggest conditions under which the species tree and associated parameters are  
17 not identifiable from the gene tree topology distribution when gene flow is present, but indicate that  
18 the coalescent history distribution may identify the species tree and associated parameters. Thus,  
19 the coalescent history distribution can be used to infer parameters such as the ancestral effective  
20 population sizes and the rates of gene flow in a maximum likelihood (ML) framework. We conduct  
21 computer simulations to evaluate the performance of our method in estimating these parameters,  
22 and we apply our method to an Afrotropical mosquito data set (Fontaine et al., 2015).

23 Key words: gene tree, species tree, coalescent model, gene flow, migration, topology, coalescent  
24 history

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