



## Coalescence 2.0: a multiple branching of recent theoretical developments and their applications

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Titre	Coalescence 2.0: a multiple branching of recent theoretical developments and their applications
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Auteur	Tellier, Aurélien [1], Lemaire, Christophe [2]
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Mots-clés	genetic drift [3], natural selection [4], parasite evolution [5], rapid evolution [6]
Résumé en anglais	<p>Population genetics theory has laid the foundations for genomic analyses including the recent burst in genome scans for selection and statistical inference of past demographic events in many prokaryote, animal and plant species. Identifying SNPs under natural selection and underpinning species adaptation relies on disentangling the respective contribution of random processes (mutation, drift, migration) from that of selection on nucleotide variability. Most theory and statistical tests have been developed using the Kingman coalescent theory based on the Wright-Fisher population model. However, these theoretical models rely on biological and life history assumptions which may be violated in many prokaryote, fungal, animal or plant species. Recent theoretical developments of the so-called multiple merger coalescent models are reviewed here (<math>\Lambda</math>-coalescent, beta-coalescent, Bolthausen-Sznitman, <math>\Xi</math>-coalescent). We explain how these new models take into account various pervasive ecological and biological characteristics, life history traits or life cycles which were not accounted in previous theories such as (i) the skew in offspring production typical of marine species, (ii) fast adapting microparasites (virus, bacteria and fungi) exhibiting large variation in population sizes during epidemics, (iii) the peculiar life cycles of fungi and bacteria alternating sexual and asexual cycles and (iv) the high rates of extinction-recolonization in spatially structured populations. We finally discuss the relevance of multiple merger models for the detection of SNPs under selection in these species, for population genomics of very large sample size and advocate to potentially examine the conclusion of previous population genetics studies.</p>
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### **Liens**

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