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The evolution of genealogies

## Abstract

Exchangeable population models of constant size are a focus of interest in mathematical population genetics. They give rise to measure-valued processes as well as random trees describing the genealogy at fixed times. As a matter of fact, genealogies change during the evolution of the population. In this talk I will describe the tree-valued Markov process describing the large-population-limit of the evolution of genealogies. In addition, I will show that the process of total branch lengths of the tree converges to a cadlag process in the limit of large population sizes.