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Distribution of branch lengths and phylogenetic diversity under homogeneous speciation models

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(Submitted on 29 Jul 2011)

The constant rate birth--death process is a popular null model for speciation and extinction. If one removes extinct and non-sampled lineages, this process induces `reconstructed trees' which describe the relationship between extant lineages. We derive the probability density of the length of a randomly chosen pendant edge in a reconstructed tree. For the special case of a pure-birth process with complete sampling, we also provide the probability density of the length of an interior edge, of the length of an edge descending from the root, and of the diversity (which is the sum of all edge lengths). We show that the results depend on whether the reconstructed trees are conditioned on the number of leaves, the age, or both.

Subjects: **Probability (math.PR)**

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