Krajowa Konferencja Zastosowań Matematyki w Biologii i Medycynie

Jastrzębia Góra, 16th–20th September 2013

CRITICAL CASE STOCHASTIC PHYLOGENETIC TREE MODEL VIA THE LAPLACE TRANSFORM

Krzysztof Bartoszek[1] **and Michał Krzemiński**[2,3]

[1]Mathematical Sciences,
Chalmers University of Technology and the University of Gothenburg
412 96 Göteborg, Sweden,
[2]Department of Probability Theory and Biomathematics, Gdańsk University of Technology,
ul. G. Narutowicza 11/22, 80-233 Gdańsk, Poland
[3]Institute of Mathematics, Polish Academy of Sciences
ul. Śniadeckich 8, 00-956 Warszawa, Poland
[1]krzbar@chalmers.se, [2]mkrzeminski@mif.pg.gda.pl

ABSTRACT

Birth–and–death models are now a common mathematical tool to describe branching patterns observed in real–world phylogenetic trees. Paper [1] is one such example. The authors propose a simple birth–and–death model that is compatible with phylogenetic trees of both influenza and HIV, depending on the birth rate parameter. An interesting special case of this model is the critical case where the birth rate equals the death rate. This is a non–trivial situation and to study its asymptotic behaviour we employed the Laplace transform. With this we correct the proof of [1] in the critical case.

ACKNOWLEDGEMENTS

We are grateful to Wojciech Bartoszek and Joachim Domsta for many helpful comments, insights and suggestions. K.B. was supported by the Centre for Theoretical Biology at the University of Gothenburg, Stiftelsen för Vetenskaplig Forskning och Utbildning i Matematik (Foundation for Scientific Research and Education in Mathematics), Knut and Alice Wallenbergs travel fund, Paul and Marie Berghaus fund, the Royal Swedish Academy of Sciences, Wilhelm and Martina Lundgrens research fund and Östersjösamarbete scholarship from Svenska Institutet (00507/2012).

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