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Title: Stochastic Processes and Population Genetics

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Keywords: Stochastic Processes

Population Genetics

Issue Date:

Abstract:

28-Jul-2021

Publisher: IISERM

Mathematical models play a crucial role in enhancing our understanding of the intri- cacies of natural phenomena. At the same time the complexity of real-life processes translate into intriguing quantitative questions and on multiple occasions have led to the formulation of new mathematical theories. In this thesis, we outline this two-way interaction between the mathematical theory of stochastic processes and the biological field of population genetics. On one hand, we develop and analyse a stochastic model to understand the effect of mate-limitation on evolutionary rescue, the phenomenon of rapid adaptation of a population to prevent extinction due to a harsh change in the environment. We find that mate limitation reduces the survival probability. For species with distinct males and females, female-biased populations have a higher chance of being rescued when mates are assured but populations with a fisherian sex ratio of 1:1 have a better chance of adapting when mates are limiting. Further, populations where mutant individuals have a higher fecundity are less prone to extinction than those where mutants are more efficient in searching for mates. On the other hand, we study the theory of graphons and a diffusion process on the space, motivated from the moran process of population genetics. An exposition of two papers on graphons is presented with a focus on the convergence of non-random graphs, specific random graphs and random graphs evolving in time. The time-evolving random graphs are motivated from population genetics and at the same time show potential for meaningful application to the field.

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It is under embargo period.odt 9.47 kB OpenDocument Text

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