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NEXT-GENERATION TOOLS FOR EVOLUTIONARY INVASION ANALYTICS

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Abstract

Evolutionary invasion analysis is a powerful modeling technique in evolutionary biology. It allows us to study when a new mutation or strategy can spread in a population. In the case of resistance evolution, for example, it helps to understand how resistant variants can invade a population of individuals vulnerable to pesticides or other means of control. The Next Generation Theorem (NGT) offers a simpler and more biologically intuitive alternative to traditional stability analysis. The aim of this work is to present the NGT, as well as its tools and how it works, in order to make it more accessible and applicable, especially to evolutionary biology. First, I present a conceptual review of the NGT, explaining its logic with a new interpretation that facilitates its connection with classical techniques for analyzing dynamic models. Subsequently, I apply this approach to specific problems of evolutionary invasion, a fundamental field for understanding how mutations or alternative strategies can spread in a population.

Through progressive examples, I show how next-generation methods not only reduce the mathematical complexity of high-dimensional models, but also allow for clearer biological interpretations, such as the reproduction rate of mutants and the conditions for their persistence.

Although the main focus is on evolutionary analysis, the ideas and applications presented extend to many types of biological modeling, including population ecology, disease dynamics, and life cycle strategies. Thus, this work seeks to broaden the use of these cutting-edge tools, contributing to a better integration between applied mathematics and evolutionary biology.

References

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