Radcliffe, J.; **Rass, L.**
Discrete time spatial models arising in genetics, evolutionary game theory, and branching processes. (English) ⟦Zbl 0882.92022⟧
Math. Biosci. 140, No. 2, 101-129 (1997).

Summary: A saddle point method is used to obtain the speed of first spread of new genotypes in genetic models and of new strategies in game theoretic models. It is also used to obtain the speed of the forward tail of the distribution of farthest spread for branching process models. The technique is applicable to a wide range of models. They include multiple allele and sex-linked models in genetics, multistrategy and bimatrix evolutionary games, and multitype and demographic branching processes. The speed of propagation has been obtained for genetic models (in simple cases only) by *H. F. Weinberger* [Lect. Notes Math. 648, 47-98 (1978; Zbl 0383.35034); SIAM J. Math. Anal. 13, 353-396 (1982; Zbl 0529.92010)] and *R. Lui* [SIAM J. Math. Anal. 13, No. 6, 913-953 (1982; Zbl 0508.45006 and 007); J. Math. Biol. 16, 199-220 (1983; Zbl 0514.45006); Math. Biosci. 93, No.2, 269-312 (1989; Zbl 0706.92014 and 015)], using exact analytical methods. The exact results were obtained only for two-allele, single-locus genetic models. The saddle point method agrees in these very simple cases with the results obtained by using the exact analytic methods. Of course, it can also be used in much more general situations far less tractable to exact analysis. The connection between genetic and game theoretic models is also briefly considered, as is the extent to which the exact analytic methods yield results for simple models in game theory.

Reviewer: Reviewer (Berlin)

MSC:

92D10	Genetics and epigenetics
91A40	Other game-theoretic models
60J80	Branching processes (Galton-Watson, birth-and-death, etc.)

Cited in **5** Documents

Keywords:

saddle point method; sex-linked models; bimatrix evolutionary games

Full Text: DOI

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