INTERNATIONAL JOURNAL OF
NUMERICAL ANALYSIS AND MODELING
Volume 1, Number 2, Pages 173–187

JUMP-DIFFUSION MODEL FOR THE GLOBAL SPREAD OF AN AMPHIBIAN DISEASE

EDWARD J. ALLEN

Abstract. A system of jump-diffusion stochastic differential equations is considered for modelling the dynamics of the spread of an amphibian disease. In this investigation, it is assumed that the amphibians are located in M regions which are widely and uniformly spaced on the surface of the earth and that the disease is present initially in only one region. Within each region, the amphibians live in N separate patches. A jump-diffusion stochastic system is derived for the number of infected patches in each of the M regions. Computational simulations are performed and compared with results predicted by a deterministic SIS model, a continuous-trajectory stochastic differential equation model, and Monte Carlo calculations. It is seen that the rate of spread predicted by the jump-diffusion model agrees well with that predicted by Monte Carlo calculations. Indeed, if there is a step increase in the transmission rates or a step decrease in the recovery rates, then the disease can spread globally from region to region at an exponential rate.

Key Words. amphibian disease, stochastic differential equation, jump diffusion, chytridiomycosis

1. Introduction

Since the 1970's, populations of amphibians have declined or vanished worldwide (see, e.g., Berger et al., 1998, Carey et al., 1999, Daszak et al., 1999, Morell, 1999). Mass mortalities have been reported in North America, Central America, South America, Europe, and Australia. The severity, the rapid rate, and the abruptness of the amphibian population declines have led to much scientific interest and several hypotheses for the causes of the population declines have been proposed. It was hypothesized that changes in the global environment, such as increased ultraviolet light, global warming, and pollutants, were responsible (see, e.g. Alexander and Eisched, 2001, Corn and Muths, 2002, Stallard 2001). After the amphibian chytrid fungus (*Batrachochytrium dendrobatidis*) was found at sites of mass mortality in Australia and Central America (Daszak et al., 2001), it was hypothesized that emerging infectious diseases (EIDs) were responsible for the amphibian die-offs. In addition, it has been hypothesized that a combination of factors is responsible (Daszak, et al., 2001, Rollins-Smith, et al., 2002). For example, global warming may

Received by the editors January 10, 2004.
2000 *Mathematics Subject Classification.* 60H10, 92D25, 65C30, 34F05.
Financial support for this investigation was provided by the National Science Foundation grant DMS-0201105. The author is grateful to L. J. S. Allen for helpful comments and suggestions on this research.

have changed the behavior of montane amphibians resulting in increased transmission rates of a disease or, possibly, increased ultraviolet light has decreased the resistance of the amphibians to infections (Daszak et al., 2001).

Of particular interest has been the global spread of chytrid fungus with the fungus recorded in the United States in the 1970's, Australia, Central America, and South America in the 1980's, and Europe and Africa in the 1990's (Berger et al., 1999, Speare and Berger, 2000). Chytrid fungus is interesting as it has emerged in pristine sites, infected a wide variety of hosts, and has caused severe population declines in disparate regions (Daszak et al., 1999, 2000). Chytrid fungus spreads through waterborne zoospores and apparently prefers cool temperatures for optimal growth (Daszak et al., 2001, Sparrow, 1968). As a result, montane amphibians have been the most susceptible to the disease (Berger et al., 1999, Bosch, et al., 2001) even though the populations are generally located at widely separated regions on the earth. The international trade in amphibians, which has undoubtedly increased since the 1970's, has been a possible mechanism for the introduction of chytrid fungus (Daszak et al., 2001).

In the present investigation, the dynamics of the global spread of an amphibian disease are studied. Of particular interest is determining how increased transmission rates or increased susceptibility affect the rate of global spread of a disease. To study these effects, the assumption is made that the disease initially is present at only one location on the earth's surface. (For example, a virulent strain may evolve at a certain location.) Unfortunately, with regard to a particular disease such as chytrid fungus, appropriate data may never be obtained to support or disprove such an assumption. For example, one may argue that chytrid fungus has been distributed worldwide for thousands of years and we have just recently begun to identify the effects of the fungus.

In addition to the assumption that the disease originates at one location, it is also assumed that the amphibian populations susceptible to the disease are located at disparate regions on the surface of the earth. With these assumptions, a stochastic model is formulated for the global spread of an amphibian disease, in particular, a jump-diffusion model is introduced and studied. Often, in mathematical models for dispersal and growth, small fractions of the population can immediately diffuse with the result that migrated populations can quickly increase. However, a jump-diffusion model realizes that the populations are discrete and that migrated populations cannot undergo growth unless at least one individual has moved. Jump-diffusion models have recently become popular in mathematical finance in order to account for random discrete jumps in prices (see, e.g., Hanson and Westman, 2002, Runggaldier, 2003). In the present investigation, a jump-diffusion model is considered for modelling the spread of amphibian infections. (In addition, it is worthwhile to note that the mathematical model developed here is not a small-world network (Collins and Chow, 1998, Watts and Strogatz, 1998) as all regions are interconnected. However, the problem studied may be considered as a metapopulation since a collection of amphibian subpopulations exist on a system of habitat patches (Hanski, 1999, Marsh and Trenham, 2001).) The purpose of the investigation is to assess the impact of increased transmission coefficients and decreased recovery coefficients on the rate that an amphibian disease can spread globally. The model may help improve our understanding of how a disease spreads rapidly through widely separated populations and whether changing global conditions are partly responsible for the amphibian population declines.