

Probability of Extinction in Metapopulation Models of Infectious Salmon Anemia virus

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Abstract

Infectious Salmon Anemia virus (ISAv) causes Infectious Salmon Anemia in a variety of finfish including Atlantic salmon (*L. Salmo salar*). This disease has impacted most salmon producing countries and has had a devastating effect on the salmon culture industry. In previous work, deterministic models of an ISAv infectious were proposed and studied. Analysis indicated that whenever the basic reproduction number was above the threshold value of 1, the disease would invade and persist if introduced in small numbers. However, in small numbers, individuals in infectious classes are subject to random fluctuations not captured by deterministic models. Markov chain models are proposed that capture these fluctuations, but the complexity of these systems makes analysis difficult. Multitype branching process models are proposed to approximate the probability of extinction of the Markov chain models. Strengths and weaknesses of these approximations are discussed.