

MATHEMATICAL ANALYSIS OF A BASIC VIRUS INFECTION MODEL WITH APPLICATION TO HBV INFECTION

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ABSTRACT. The basic virus infection model (BVIM) is widely used in the studies of hepatitis B virus (HBV) infection dynamics. This model assumes that the infection process follows a mass action law. The basic infection reproductive number of the model is proportional to the number of all cells of the host's organa prior to the infection. This suggests that the BVIM may not be a reasonable model for describing the HBV virus infection since it implies that an individual with a smaller liver may be more resistant to virus infections than an individual with a larger one. In this paper, we formulate a standard incidence based model that amends the BVIM (we shall call it ABVIM below) which will correct this mass action induced model artifact. If its basic infection reproductive number is less than 1, then every positive solution will converge to the infection-free steady state. We also present an application of ABVIM to some clinic HBV infection data.

1. Introduction. Hepatitis B is one of the major diseases in the world. The WHO has reported that over one-third of the world's population (more than 2 billion people) has been or is actively infected by HBV, more than 350 million have chronic (lifelong) infections [12], 25-40 percent of these chronic infection carriers will die from liver cirrhosis or primary hepatocellular carcinoma [10]. The HBV carrier rate varies from 0.1 percent to 20 percent in different areas of the world [4]. Chronic HBV infection is often the result of exposure early in life, leading to viral persistence in the absence of strong antibody or cellular immune responses [9].

The study of anti-HBV infection treatment may benefit from the use of mathematical modeling. Several models have been introduced for

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