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Numerical modeling for transmission dynamics of hepatitis B virus disease

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Numerical modeling of communicable disease is a device to appreciate the instrument in what way syndrome pushovers and in what way stately. we have studied numerically the dynamics of HBV. We frame an entirely constant Non-Standard Finite Difference (NSFD) structure for a mathematical model of HBV. The introduce numerical array is bounded, dynamically designate and contain the positivity of the solution, which is one of the important requirements when modeling a prevalent contagious.

The comparison between the innovative Non-Standard Finite Alteration structure, Euler method and Runge-Kutta scheme of order four (RK-4) displays the usefulness of the suggested Non-Standard Finite Alteration scheme. NSFD scheme shows convergence to the exact equilibrium facts of the model for any time steps used but Euler and RK-4 fail for large time steps.

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