and their duration. There has been considerable effort in employing various useful control strategies for a variety of diseases and illnesses. Some control strategies have been developed for the hepatitis B virus (HBV). For instance, Sheikhan et al. [13] compared three strategies (nonlinear feedback neural-type sigmoid, open-loop time-based fuzzy and closed-loop fuzzy) to achieve the optimum performance of the HBV control. Laarabi et al. [14] proved the existence of an optimal control method by combining two control laws to reduce the therapy cost and maximize the number of healthy cells in HBV infection. In another work [15], a fuzzy logic structure was used to solve an HBV optimal control problem. Two other control inputs were designed to have efficient drug therapy considering both hindering viral production and inhibiting new infection of HBV based on a robust adaptive Lyapunov-based control theory [16]. Hepatitis C virus (HCV) has also attracted the attention of researchers in recent years. Zhang et al. [17] developed an epidemiological model of HCV and used numerical simulations to study the influence of the model parameters based on available data obtained from China. In another study [18], the performance of an optimal controller was investigated based on an HCV model having acute-infected and chronic-infected individuals as its compartments. After that, Zhang et al. [19] utilized an optimal control measure to inhibit the prevalence of HCV while minimizing the cost and population of infected individuals. A novel optimal adaptive neuro-fuzzy controller was developed to decrease the number of HCV infected individuals using an additional genetic algorithm optimization [20]. Cancer tumor modeling and control have also been studied in this field of research. In 2001, a four-population model containing tumor and host cells, drug therapy and immune response was presented [21]. Accordingly, Babaei et al. [22] proposed a model reference adaptive control method to determine a personalized drug administration to treat cancer with parametric uncertainty. Moradi et al. [23] also developed an adaptive robust control method for three nonlinear mathematical cell-kill models of cancer in the presence of parameter uncertainties. They have extended the previous study [23] by enhancing their strategy to a modern composite adaptive control in which the model parameters were precisely identified online during the cancer chemotherapy [24]. Moreover, Khalili et al. [25] suggested an optimal open-loop control strategy for drug delivery in chemotherapy considering the human obesity effects.

Moradi and Sharifi [26] also proposed a nonlinear robust adaptive sliding mode control method to reduce the number of susceptible and infected humans to zero in an influenza outbreak regarding a five-state compartmental model of this disease. The employed model of influenza was developed by Arino et al. [27] with five state variables known as SEAIR (Susceptible-Exposed-Asymptomatic-Infectious-Recovered). That model was enhanced in Ref. [28] by defining the vaccination, social distancing and antiviral rates as three possible control inputs. In this modern era, HIV prevention and treatment is also of pivotal importance. Ngina et al. [29] presented an in vivo deterministic model of HIV and presented an optimal control scheme based on that. In a new study [30], a robust sliding mode controller was formulated to reduce the population of infected $CD4^+$ T cells with antiviral therapy according to the acquired output information. In 2000, a differential SEIR model of malaria, containing both humans' and mosquitos' populations and their interaction was taken into account [31]. Another epidemiological model of malaria was formulated to consider personal protection, possible treatment and vaccination strategies in two latent periods [32]. After that, Rafikov et al. [33] employed an optimal control method for a mathematical malaria model by placing genetically modified mosquitos in the environment. Furthermore, a robust nonlinear controller with adaptive gains was proposed to inhibit the prevalence of malaria with seven variables for human and mesquite compartments [34].

To study the immune response of renal transplant recipients, there has been made considerable effort to predict, model and optimally control the HCMV infection in both primary and latent cases. Flechet et al. [35] analyzed AKI-predictor as an online machine learning-based prediction tool and compared it to physicians' ability to predict AKI in clinical uses. Based on the obtained results, it was emphasized that AKI-predictor was beneficial in terms of successfully removing false HCMV positives (error in determining a patient at high risk) and reducing clinical costs. In addition, Parreco et al. [36] compared different machine learning algorithms for predicting AKI. Wodarz et al. [37] presented a model based on mice infected with murine cytomegalovirus (MCVM), which introduced important knowledge for explaining the growth of CMV specific $CD8^+$ T cells in human by getting older. Kepler et al. [38] formulated a fifth-order state-space model for HCMV infection that was extended by Banks et al. [39] to six-order one, considering serum creatinine of the blood as a measure of the kidney performance. Their model contained antiviral and immunosuppressive drugs as two control inputs. Then, Kwon et al. [40] simplified the model in [39], considering immunosuppressive drug as the only control input, proved the local stability of the dynamics