

While many epidemiological models were proposed to understand and handle COVID-19 pandemic, too little has been invested to understand human viral replication and the potential use of novel antivirals to tackle the infection. In this work, using a control theoretical approach, validated mathematical models of SARS-CoV-2 in humans are characterized. A complete analysis of the main dynamic characteristic is developed based on the reproduction number. The equilibrium regions of the system are fully characterized, and the stability of such regions is formally established. Mathematical analysis highlights critical conditions to decrease monotonically SARS-CoV-2 in the host, as such conditions are relevant to tailor future antiviral treatments. Simulation results show the aforementioned system characterization.