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## Information Entropy in Mutating Viruses

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A large amount of information about the singular type of virus caused by SARS-CoV-2 during the COVID-19 pandemic has provided unique insights into the stochastic processes connected to mutations at the DNA level and changes in system entropy. Predictions made by biophysical Single Hit Target Models associate DNA damage with an increase in system entropy. However, it turns out that not all mutations exhibit the same nature. Using real-world data provided by the National Center for Biotechnology Information, it is evident that viruses, as complex systems, are capable of decreasing Shannon's entropy in the context of their DNA. The analysis of mutating viruses offers unique insights into evolving and self-adapting systems that are far from thermodynamic equilibrium. Naïve simulation methods, which assume complete randomness in the processes of mutation and selection, are not compatible with the observed phenomena. The existence of bifurcations, local maxima, and visible "flares" calls for the development of new and more complex models. With multiple examples demonstrating this observed trend (such as COVID-19, HIV, and influenza), and with both classical statistical methods and Bayesian robust regression confirming the existence of this trend, this could represent a significant step toward developing methods for predicting future mutations and the directions of viral evolution.

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