Rapidly mutating RNA viruses, such as SARS-CoV-2, do not follow a simple or constant evolutionary pace. Large-scale analysis of genome sequences reveals that mutation rates shift over time, often accelerating when new variants emerge. These patterns defy traditional molecular clock models and call for more flexible, dynamic approaches.

By combining stochastic modeling with tools from statistical physics and data science, this work uncovers variantspecific evolutionary behaviors and introduces a framework based on anomalous diffusion. The result is a deeper understanding of how viral genomes evolve—and how complexity and randomness shape their path.







