In-silico simulation of RNA viruses

Authors:

• Pau Reig, Centre de Recerca Matemàtica (preig@crm.cat)

Abstract:

In vivo virology research faces constraints like security, cost, and time. Not all labs can study all viruses, and generating synthetic RNA is expensive and time-consuming. We present an approach to study disease evolution at the microscopic level, simulating RNA replication for any virus quickly. This method uses a probabilistic model for mutations, a dynamic population model, and a diffusion model for disease propagation. As a result, we can efficiently compute these processes, enabling studies on virus evolution, propagation, and potential treatments.

References: