Assessing Virus and Host Encounter Rates with Ordinary Differential Equations and Agent Based Modeling

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Hopeful Monsters

Abstract

Viral lysis of microbes is a leading cause of microbial death. Lysis is commonly modeled using the Mass Action term, where encounters are proportional to the products of host and viral densities, despite it not being validated empirically or theoretically. **To assess the validity of Mass Action in modeling virus-host encounter rates, we implemented dynamical models using ODEs and agent-based models to determine if it accurately estimates virus and host encounters.** Doing so, we found that Mass Action overestimates encounters between virus and host populations by nine orders of magnitude **(i.e.,1,000,000,000 fold)**. Further, we found that implementing models without the Mass Action term leads to stability of both hosts and viral populations while including Mass Action leads to oscillations and collapses within the populations. Altogether, this suggests that the Mass Action term is logically problematic and unrealistic.
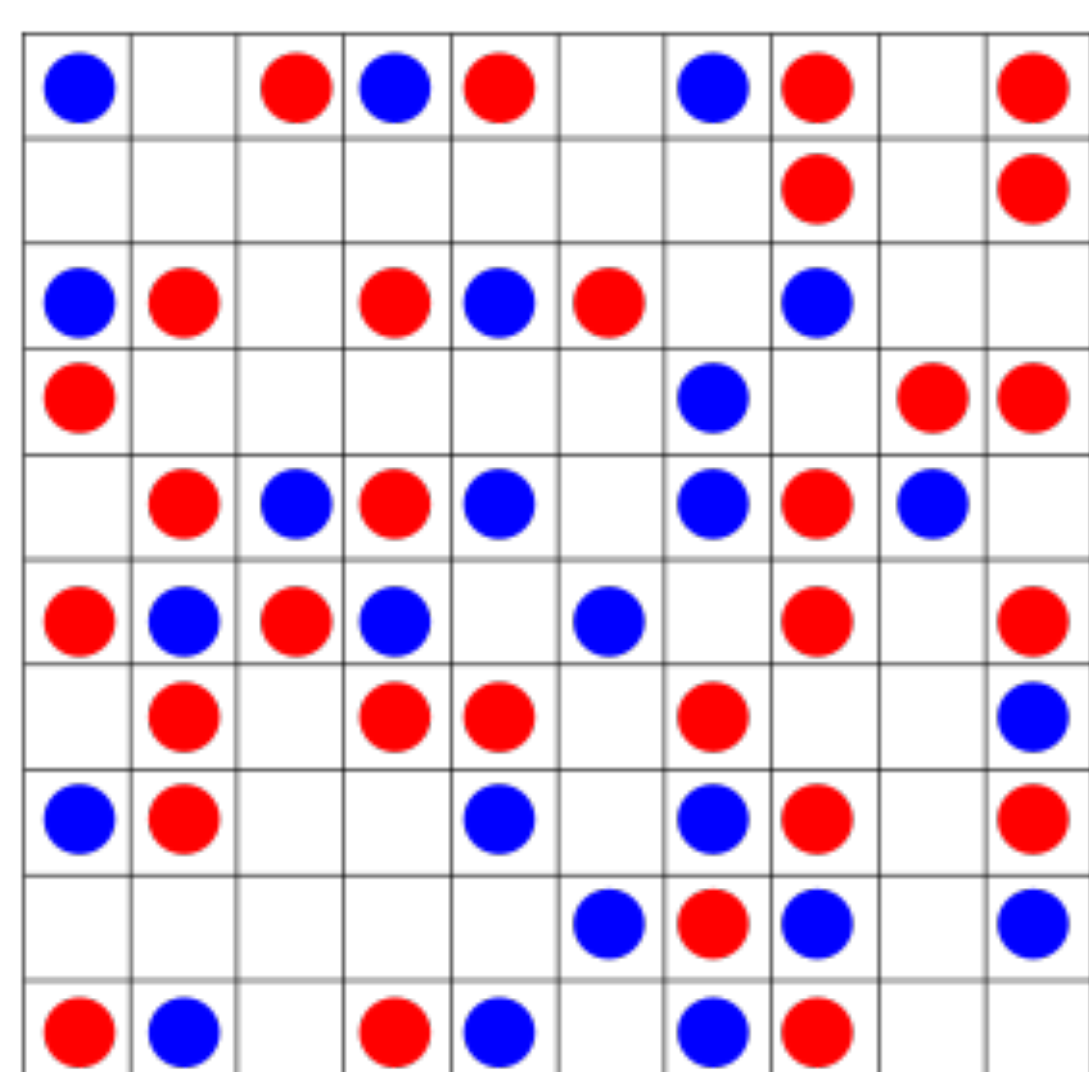
## Building Agent Based Model

One Time Step
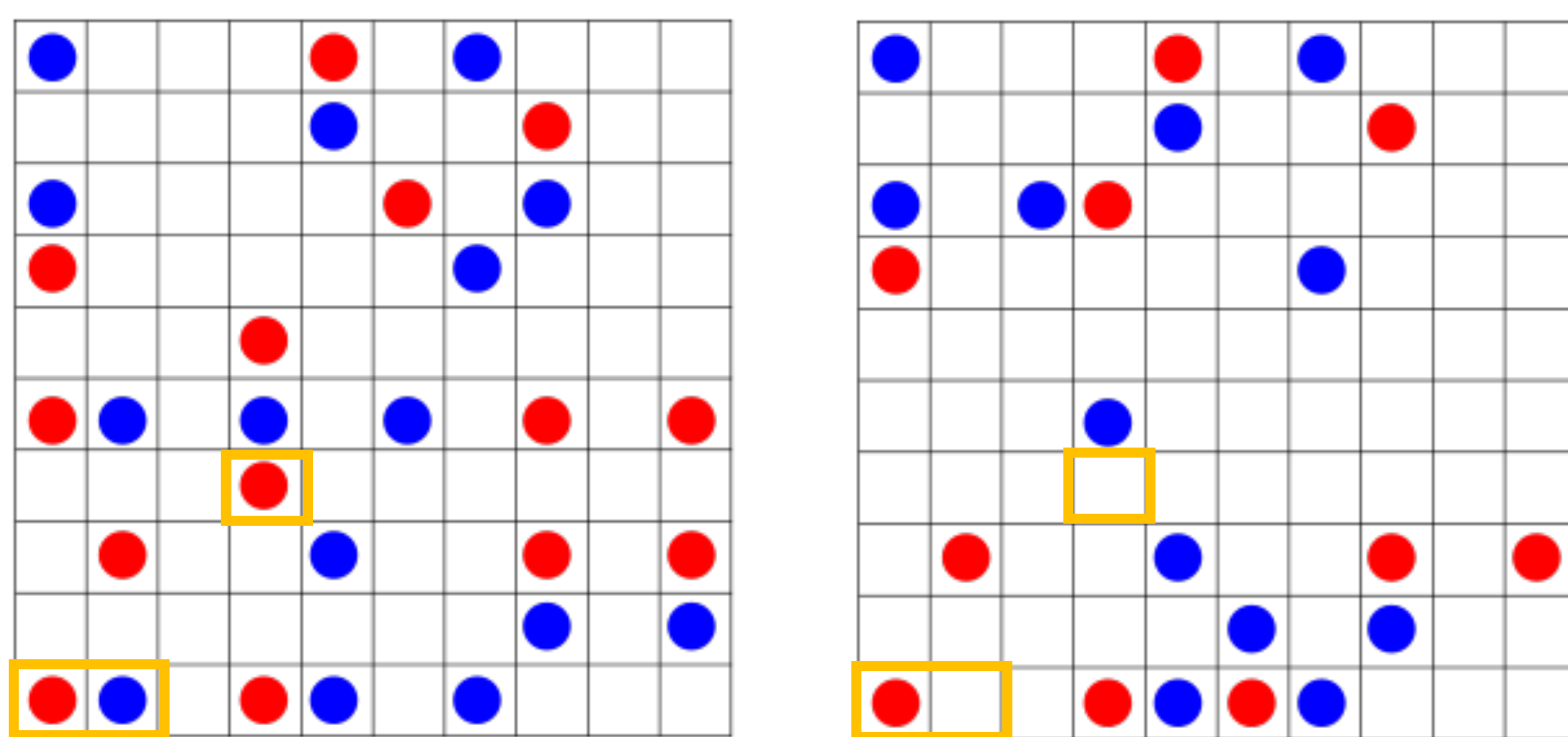
- Randomly populate the spatial grid with viral and host agents.
- Implement stochastic rules about viral and host interactions.
- Track agents over time.

Dynamical Virus-Host Encounters:

Mass Action= Predator Densities * Prey Densities = encounter rate ?

Number of Hosts: 24
Number of Viruses: 30
Mass Action Encounters: 720
ABM Encounters: 24
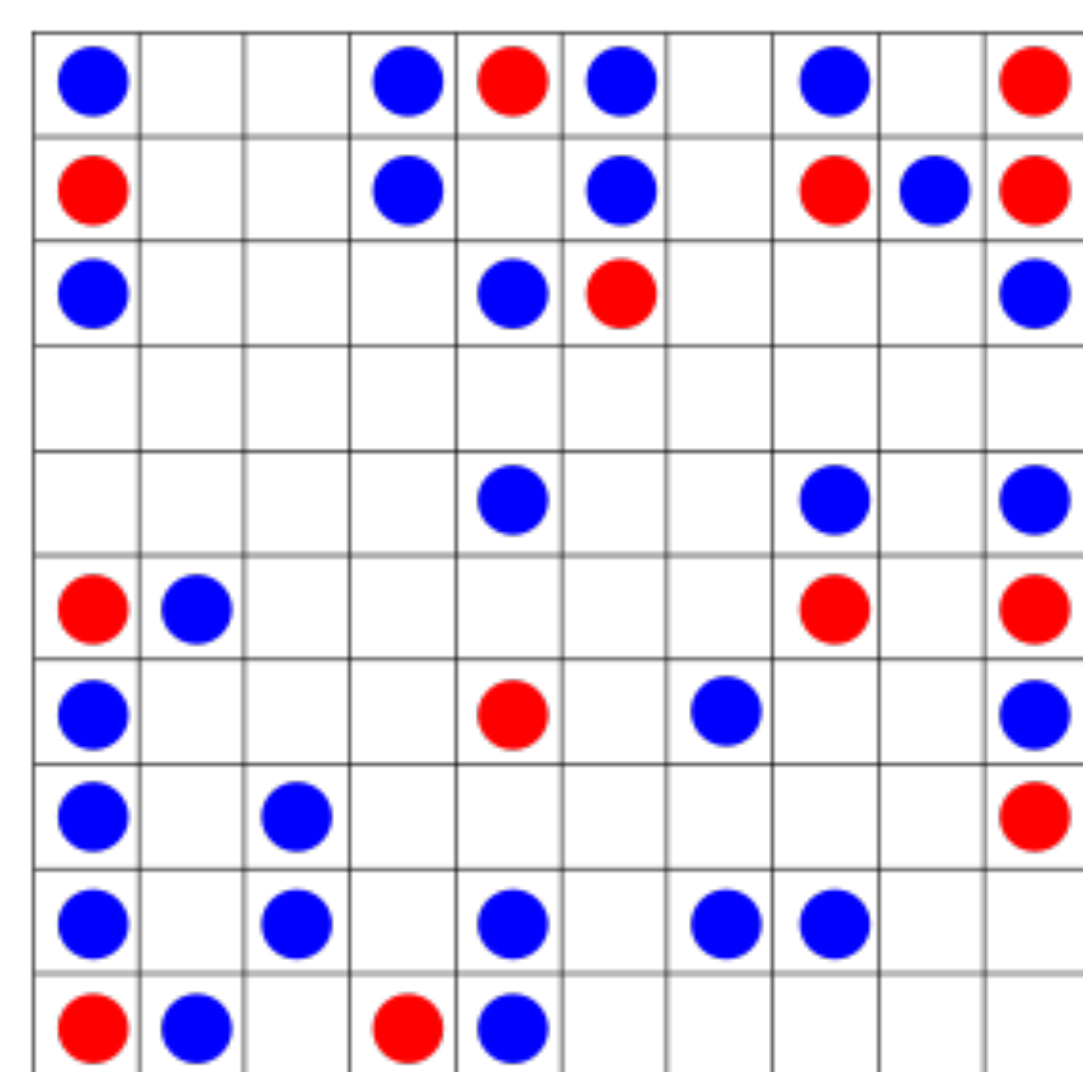
Number of Hosts: 27
Number of Viruses: 13
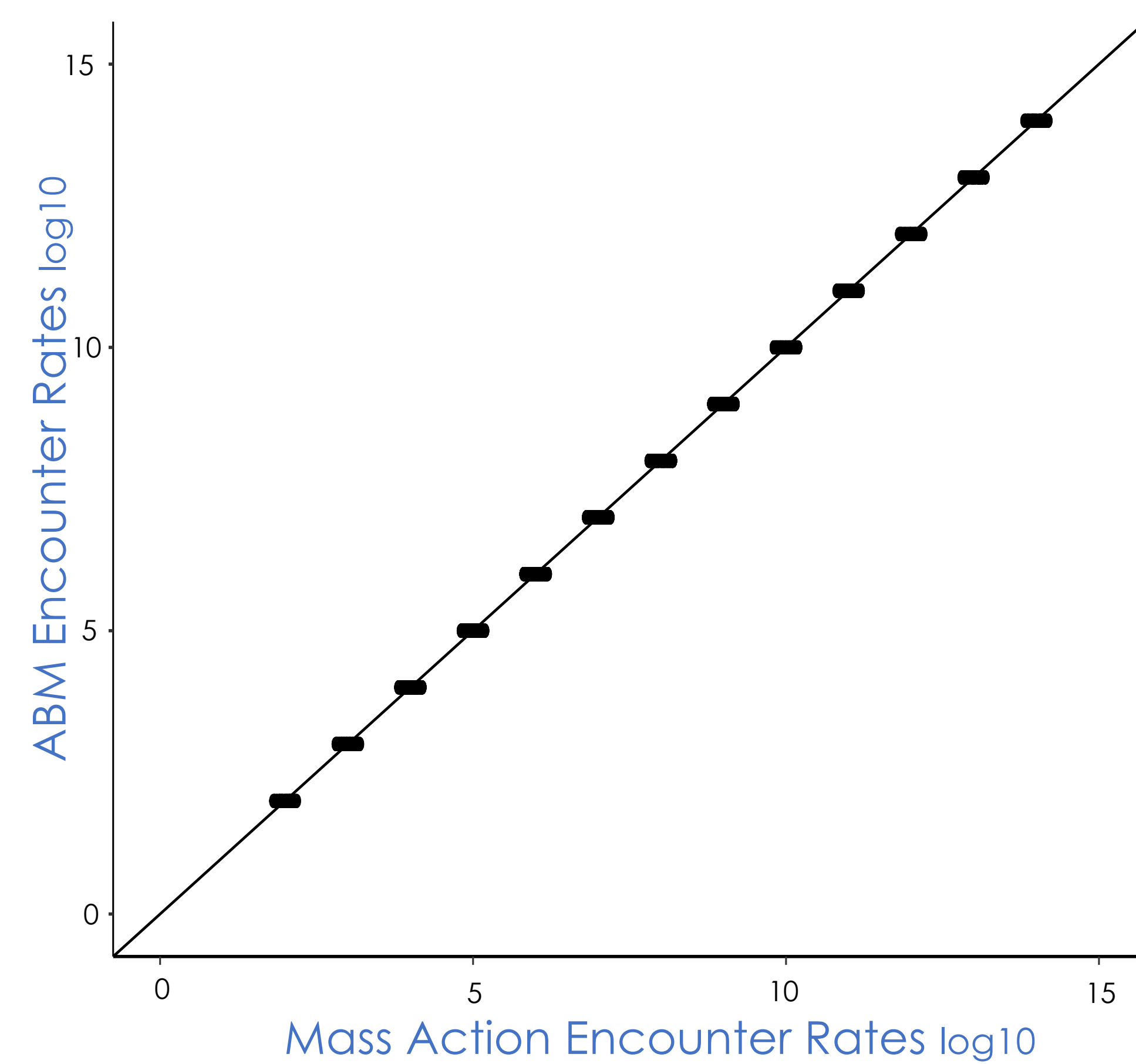Mass Action Encounters: 351
ABM Encounters: 21

Mass Action vs ABM Encounter Rates

Predicted Encounter Rates: Mass Action vs ABM Encounter Rates

ABM Encounter Rates $log10$

Mass Action Encounter Rates $log10$
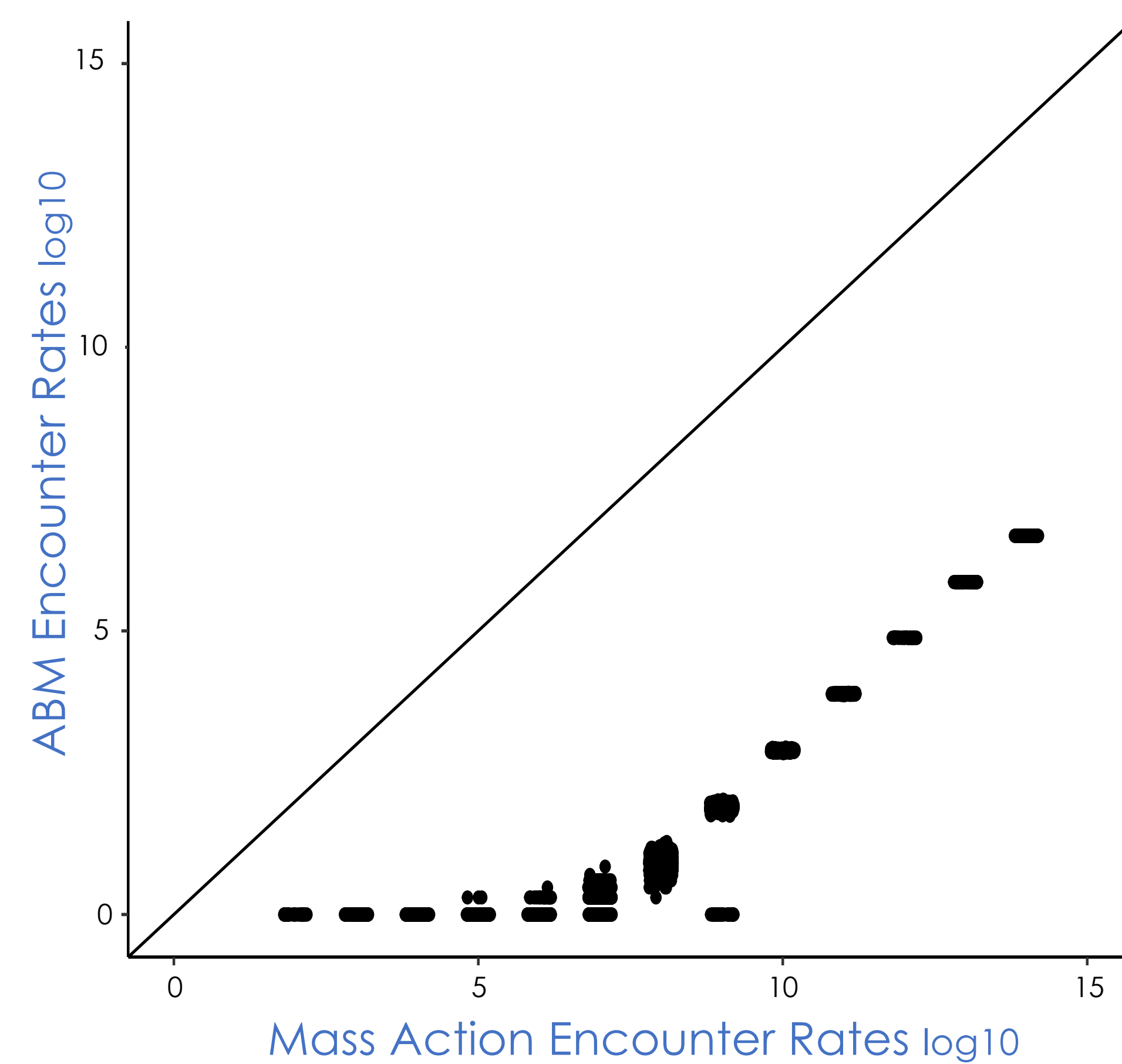
ABM Encounter Rates **<<<<** Mass Action Encounter Rates

Δ ABM Encounter Rates vs Mass Action Encounter Rates

ABM Encounter Rates $log10$

Mass Action Encounter Rates $log10$

- Mass Action over predicts encounter rates by a magnitude up to the **1,000,000,000–fold.**
- Mass Action significantly over predicts encounter rates between host and viruses and by doing so it over predicts the number of lysis events occurring.

Stochastic Agent Based Model

Lytic Model

Lysis — Poisson Distribution with Mean 6

Mortality — Normal Distribution with Mean 0.3

Host Agents   Virus Agents

Temperate Model

Lysis — Poisson Distribution with Mean 3

Mortality — Normal Distribution with Mean 0.3

Host Agents   Virus Agents

Non-Oscillatory Pattern

Lysis — Poisson Distribution with Mean 5

Mortality — Normal Distribution with Mean 0.475

Host Agents   Virus Agents