Individual-based model highlights the importance of trade-offs in shaping bacteria-phage co-evolutionary dynamics

Fateme Pourhasanzade¹, Swami Iyer², Jesslyn Tjendra³, Selina Våge¹

¹ Department of Biological science, University of Bergen, Norway
² Computer Science Department, University of Massachusetts at Boston, USA

Abstract Number: 3382

Introduction and Motivation

- Understanding the interactions between phage and bacteria can serve as a simple model system for understanding infectious diseases.
- Mathematical and individual based models can be helpful in:
  - analyzing rapid coevolutionary dynamics of phage and bacteria
  - understanding virus-host scenarios depending on the different infection parameters

Method

Evolutionary Individual-based stochastic model for studying phage-bacteria interaction in a chemostat.

Experimental results

The growth curves of bacterium Escherichia coli E28 under bacteriophage T4 infection at different Multiplicity of Infection (MOI). Growth assays (including replicates) were conducted in parallel at 37°C, 150 rpm, using the 2300 EnSpire Multilabel Plate Reader (PerkinElmer) and monitored through automated measurement of optical density at 600 nm (OD600) every 15 min. Dashed line marks the timepoint of T4 infection. Plotted values: mean (n = 8; ncontrol = 11).

Simulation Results

We report population dynamics for hosts (H) and viruses (V) and focused here on:
- **Effect of MOI** (ratio of virus to host numbers)
- **Nutrient concentration** (phosphorous)
- **Constrained vs random phage-bacteria interactions**
  - two virus-host compatibility functions: trade-off based (genotypic) and random
  - two virulence functions: trade-off based (genotypic) and random

Acknowledgment

This work is supported by Trond Mohn Foundation (TMS2018REK02) as well as Meltzers Høyskolefond 2021 (102690132).