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Dynamics of Bacteria and antibiotic

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Abstract

1 Introduction

The human digestive tract hosts a vast consortium of bacteria. They form a dynamic ecosystem throughout the host's lifetime. While some microbes are host-specific, others are shared within communities and they are collectively called the **gut microbiome**. Compelling evidence indicates that this microbiome directly influences not only digestive processes but also the host's nervous system—a bidirectional relationship termed the **gut-brain axis** Schlomann and Parthasarathy [2019]. For instance, stress can trigger nausea and alter gut conditions, stimulating specific bacterial populations whose metabolites then signal back to the nervous system Magnúsdóttir and Thiele [2018].

This microbiome is inherently **alive and reactive**, dynamically responding to host diet and lifestyle. Its composition fluctuates through microbial competition, cooperation, and mutation, making rigid species-level identification impractical; instead, we focus on functional *strains* and *lineages*, often inferred via their metabolic byproducts Rios Garza et al. [2023]. Capturing the population dynamics of these lineages is crucial to decoding the gut-brain axis. However, the system's complexity—with thousands of interacting taxa and host interactions—demands a tractable theoretical framework.

To this end, we derive a **minimal yet essential dynamic model** of gut microbiome populations, distilling key interactions into a mathematically analyzable form. By abstracting lineage competition and host-mediated feedback into a parsimonious system of equations Murray [2002], we enable rigorous exploration of stability and critical transitions. Though simplified, this model serves as a foundational scaffold for identifying core principles

governing microbiome dynamics.

2 Litrature Review

3 Our Model

We are going to find an equation that shows the rate of population change of bacterias.

We take the growth rate of their population considering limits like their lifespan and limited resources. in this case logistic equation could give us an an acceptable model.

then we are going to consider the factors that decrease their population. the factors that we are going to take in consideration are immune system cells, antibiotics and the natural clearance of body. for the first two we generalize Lotka-Volterra predator-prey model and for the last one we can simplify our model and take the clearance rate of the body as a constant coefficient of population.

with all the considerations above given we get these equations:

$$\dot{B} = rB(1 - \frac{B}{K}) - \lambda.I - \zeta.A - \gamma.B$$

$$\dot{I} = \theta.B - \mu.I$$

$$\dot{A} = \eta - \beta.B.A - \psi.A$$

where B represents bacterial population, A represents the antibiotic concentration and I represents immune cells.

4 Computation & Analysis

5 Results

References

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