ResistoMeter: Interactive Simulation for Antibiotic-Resistant and Normal Bacterial Strains in Pakistan

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INTRODUCTION

Bacterial resistance to antibiotics is a significant public health concern in Pakistan. The misuse and overuse of antibiotics have led to the emergence of resistant strains, making infections harder to treat. Understanding the growth patterns of both normal and resistant bacterial strains under antibiotic exposure is crucial for researchers, healthcare professionals, and policymakers. This project aims to develop an interactive simulation called ResistoMeter [1] that models bacterial growth under different antibiotics commonly used in Pakistan, allowing users to explore how dosage and treatment intervals affect bacterial survival.

OBJECTIVES

- To design and implement an interactive simulation interface that visually represents bacterial behavior and interaction with antibiotic agents using a dynamic canvas-based rendering system.
- To evaluate the impact of different antibiotics on simulated bacterial populations by enabling real-time visualization and comparative analysis, supporting foundational understanding of antimicrobial effectiveness and resistance development.

METHODOLOGY

- ResistoMeter simulates antibiotic resistance using a logistic growth model with dynamic dosing effects. Bacteria grow logistically but are suppressed by antibiotic concentration, which decays exponentially between doses. Sensitive strains die when drug levels exceed the minimum inhibitory concentration (MIC), while resistant strains (with 90% reduced drug susceptibility) survive and multiply. The model tracks population changes hourly, incorporating:
  - Growth – Limited by carrying capacity
  - Drug effect – Concentration-dependent killing
  - Resistance emergence – Random mutations convert sensitive bacteria
  - Dosing schedule – User-defined intervals control drug peaks
- The simulation visualizes how irregular dosing allows resistant subpopulations to dominate over time.
- The model also incorporates pharmacodynamic effects, where bactericidal drugs directly kill bacteria while bacteriostatic drugs inhibit growth. Antibiotic concentration follows first-order decay kinetics between doses. Mutation rates scale with population size, and resistant strains exhibit a fitness cost (slower growth). The simulation accounts for competitive exclusion, where resistant bacteria outcompete sensitive strains under drug pressure but decline when treatment stops. Real-world data on MIC values and resistance frequencies from clinical isolates inform the parameters. Users can adjust dose timing, antibiotic type, and bacterial species to observe different resistance evolution patterns.

RESULTS

Fig. 1: Different Simulation Parameters on ResistoMeter's homepage

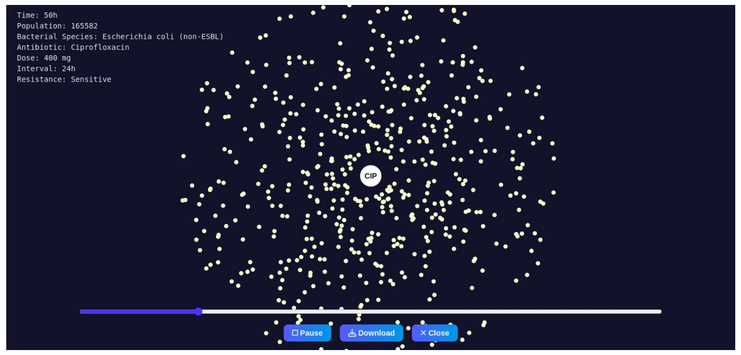

Fig. 2. Real-time simulated population dynamics under 24-hour antibiotic dosing intervals (1 dot ≈ 300 bacterial cells).

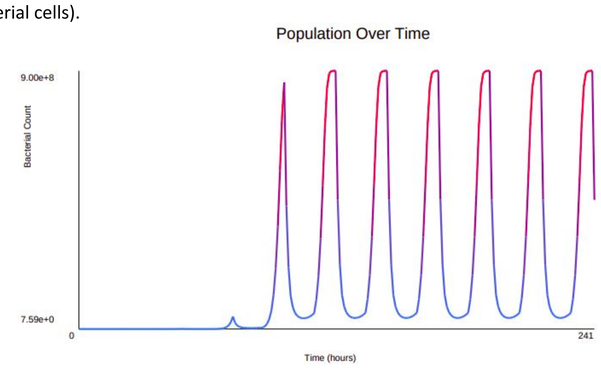

Fig. 3 Temporal dynamics of bacterial population growth, antibiotic-mediated decay, and resistance emergence under sustained pharmacological pressure.

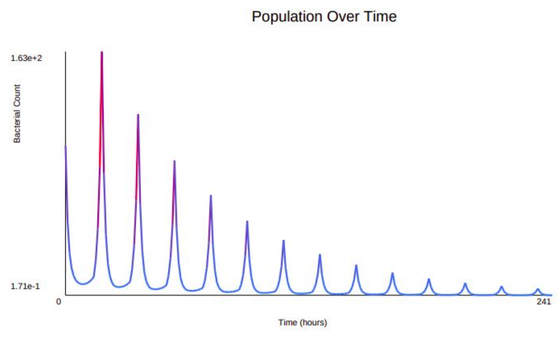

Fig. 4 Pharmacodynamic response to antibiotic interval reduction: enhanced bacterial clearance at higher dosing frequencies.

DISCUSSION

The simulation results effectively illustrate the impact of antibiotic dosing intervals on bacterial population dynamics. Figure 1 presents the initial setup with E. coli, an initial population of 100, and ciprofloxacin administered at 400mg every 24 hours over a 10-day period. The simulation incorporates critical biological parameters such as carrying capacity, mutation probability, and antibiotic efficacy. As shown in Figure 2, the real-time population count enhances user engagement, while the colony's visual representation on an agar plate mimics a susceptibility test, aiding conceptual understanding for students.

Notably, Figure 3 reveals that a 24-hour dosing interval allows the bacterial population to recover between treatments, reducing overall effectiveness. In contrast, Figure 4 demonstrates that reducing the interval to 8 hours significantly suppresses bacterial regrowth. This outcome supports the hypothesis that shorter dosing intervals can enhance treatment efficacy, thereby offering pedagogical value in teaching antibiotic stewardship and resistance mitigation strategies.

CONCLUSION

This study demonstrates the effectiveness of the ResistoMeter simulation in modeling antibiotic resistance dynamics based on real-world parameters from Pakistan. By incorporating logistic bacterial growth, dose-dependent antibiotic action, resistance mutations, and pharmacodynamic effects, the simulation provides an educational yet scientifically grounded platform for understanding how dosage intervals and drug types affect bacterial populations. The results show that improper dosing—especially extended intervals—facilitates the survival and dominance of resistant strains, while optimized schedules can significantly suppress bacterial regrowth. ResistoMeter's interactive design makes it valuable for students, researchers, and healthcare practitioners to visualize complex microbiological concepts, promoting antibiotic stewardship. Ultimately, this tool underscores the need for data-driven policies and informed treatment protocols in combating antibiotic resistance in Pakistan and beyond.

Limitations

1. The model is limited to resistance patterns and bacterial strains commonly found in Pakistan.
2. It does not account for host immune response or pharmacokinetics in different tissues.
3. Only two bacterial phenotypes (sensitive and resistant) are modeled, excluding intermediate resistance.
4. Environmental factors such as temperature or pH are not incorporated, though they can influence bacterial behavior.

REFERENCES

[1] https://m4lf0rm3d.github.io/ResistoMeter/