UNIVERSITY OF INFORMATION TECHNOLOGY AND SCIENCES

Project Proposal

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Simulating the Spread of an Infectious Disease Using Monte Carlo Methods

Introduction

The outbreak of infectious diseases is a global concern that requires efficient modeling and analysis to understand their dynamics. This project uses the Susceptible-Infected-Recovered (SIR) model, a mathematical framework widely used in epidemiology, to simulate and analyze the spread of diseases. By incorporating Monte Carlo techniques, this project introduces stochastic variability to account for real-world randomness, offering insights into epidemic trends across different regions.

Objectives

1. To simulate the spread of an epidemic across multiple regions using the SIR model.
2. To incorporate Monte Carlo methods to account for stochastic variability in disease transmission and recovery.
3. To analyze the progression of the epidemic over time for each region, highlighting key metrics such as peak infections and total recoveries.
4. To visualize the dynamics of disease compartments (Susceptible, Infected, and Recovered populations) over time using time-series plots.

Scope

The project focuses on simulating and analyzing the spread of an epidemic based on a dataset containing regional information. It will provide:

- Region-specific epidemic progression over a fixed time period.
- Visualizations of compartmental changes (S, I, R).
- Quantitative analysis of the epidemic, including peak infection rates and total recoveries.

Methodology

1. **Data Collection**:
    - Use a dataset containing regional data, including:
        - Region name.
        - Population size.

        - Initial number of infected individuals.
        - Infection rate and recovery rate.

2. **Simulation Model**:
    - Implement the SIR model with compartments:
        - **S (Susceptible)**: People who can be infected.
        - **I (Infected)**: People currently infected and infectious.
        - **R (Recovered)**: People who have recovered and are immune.
    - Incorporate Monte Carlo binomial sampling to simulate randomness in infection and recovery events.
3. **Algorithm**:
    - Iterate over the dataset to simulate the epidemic progression for each region.
    - For each time step, compute:
        - New infections: Randomly determined based on the infection rate and current infected individuals.
        - New recoveries: Randomly determined based on the recovery rate and current infected individuals.
4. **Visualization**:
    - Generate time-series plots for each region, showing the progression of S, I, and R populations over time.
5. **Analysis**:
    - Calculate key metrics for each region:
        - Peak number of infected individuals.
        - Total number of recoveries.

Expected Outcomes

1. **Simulations**:

    Accurate and stochastic simulations of epidemic spread for each region.

2. **Visualizations**:

    Informative graphs illustrating changes in Susceptible, Infected, and Recovered populations over time.

3. **Metrics**:

   Insights into regional epidemic behavior, including peak infections and final recovery counts.

4. **Usability**:

   A practical tool for understanding disease dynamics and potential epidemic interventions.

Applications

1. **Epidemic Planning**:

   Helps policymakers understand regional variations in epidemic progression and plan interventions.

2. **Educational Purposes**:

   Demonstrates the application of stochastic modeling in epidemiology.

3. **Research Enhancement**:

   Provides a foundation for exploring advanced epidemic models, such as SEIR (Susceptible-Exposed-Infected-Recovered).

Potential Challenges

1. **Data Availability**: Ensuring the dataset contains accurate and relevant regional data.
2. **Model Assumptions**: Simplifications in the SIR model might not capture all real-world complexities (e.g., vaccination or external interventions).
3. **Parameter Tuning**: Choosing realistic infection and recovery rates for accurate simulations.

Conclusion

This project aims to provide a comprehensive simulation tool for understanding epidemic dynamics in various regions. By leveraging the SIR model and Monte Carlo techniques, it combines mathematical rigor with stochastic variability, delivering insights useful for policymakers, educators, and researchers.