**Project Proposal: Epidemic Spread Simulation Across Regions**

**Project Overview**

The goal of this project is to simulate the spread of an epidemic across multiple regions over a series of discrete time periods. The simulation will model how a disease propagates through different populations, taking into account factors like infection rates and recovery rates. This project aims to provide insights into how an epidemic can evolve over time and how it affects various regions differently.

**Implementation**

**Data Structures:**

First I'll set up a specific data structure using a std::map to track each region's population and their disease states. In this structure, each region’s name serves as a key, while the value is an array containing three lists for individuals in different disease states: susceptible, infected, and recovered. This organization allows me to easily access and update the state of each individual in each region, enabling efficient tracking throughout the simulation.

**External Data File:**

Next, I'll pull initial data from an external file called population\_data.txt, which includes details on at least 100 individuals. Each line will specify an individual’s ID, region, and initial disease state. This data helps establish an accurate starting point for each region, ensuring that the simulation begins with a realistic distribution of susceptible, infected, and recovered individuals.

**Simulation Mechanics:**

Then, I'll run the simulation across 25 discrete time periods, going through two main phases in each period: the infection phase and the recovery phase. During the infection phase, infected individuals have a set probability (e.g., 30%) of infecting susceptible neighbors within their region. In the recovery phase, infected individuals have a chance (e.g., 10%) of recovering from the disease. I'll update each individual's state based on these probabilities, moving individuals from the susceptible to the infected list when infected and from infected to recovered as they recover.

**Functions:**

I'll create a function, simulateDiseaseSpread, which will carry out the disease spread across the specified time periods. This function will operate on the regions map, updating each individual’s state over the course of the simulation. This central function will manage all changes, enabling a structured and clear progression of the disease within each region.

**Simulation Display**

To visualize the simulation, I’ll start by displaying the initial state of each region, showing the counts of susceptible, infected, and recovered individuals. After each time period, I’ll update this display to show how each region’s state has changed. This regular update will help me observe the disease's progression, allowing me to monitor how the epidemic spreads and evolves.

**Time Periods**

Finally, at the end of the 25 time periods, I’ll present a comprehensive summary that shows the overall impact of the epidemic on each region. This summary will provide valuable insights into how the epidemic affected different populations and will highlight any significant trends or variations observed across the regions.