Simulation of the SI and SIR Epidemiological Models
(Final Exam)

- This is group work.

  Due Date: **check** Canvas

Software and Computational resource: You will use the JAVA (or python) based Agent simulation software Repast Simphony [1] for the project. You may use the cluster resource provided for this class and/or personal computer. However, note that that the HPC cluster does not come installed with Repast.

PROJECT DESCRIPTION

Part A: Traditional Fully Mixed Modeling

- You will simulate a disease spread scenario with n number of individuals using **an agent based model (ABM) using Repast Simphony**. You will use the traditional fully mixed SI and SIR models (these models are covered in class). Assume that the agents are stationary and each agent has the potential to infect all susceptible individuals in the group.
- The goals of this simulation is to trace the changes in the number of susceptible (S), infected (I) and recovered (R) over time and analyze the spread with different values of β and γ model parameters.
- As deliverable, you will provide the code and an analysis of disease spread for different values of n (n=100, 250, 500, 750 etc.) and model parameters over time (ticks). Provide appropriate tables, figures and plots for the results.

Part B: Social Network based SI and SIR models

- A key drawback of fully mixed models of Part A is that each individual has the potential to infect any other individual which is not realistic. In reality, each individual only infect those he/she is in contact with. In Part B, you will include a synthetic social network that

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[1] https://repast.github.io/repast_simphony.html

will serve as the contact network for the ABM based simulation of SI and SIR models. In these modified models, an individual has the potential to only infect those individual it is directly connected to on the contact network. The agents in the simulation should be considered to be stationary.

- You will generate a <u>synthetic social network using both Small World and Barabasi-Albert models</u> to be used as the contact network in the simulation. Leverage the work from Group Assignment 1.

- The goals of this simulation is to trace the changes in the number of susceptible (S), infected (I) and recovered (R) over time and analyze the spread with different values of β and γ model parameters using the synthetic networks.

- As deliverable, you will provide the code used in the implementation and an analysis of the disease spread for different values of n (n=100, 250, 500, 750 etc.), synthetic networks and model parameters over time (ticks). Provide appropriate tables, figures, and plots for the results.

- A PowerPoint file that provides a description of your modeling and simulation with code, results and analysis. This ppt represents your report You may use flowcharts, UML etc. to provide details of your implementation.
- The source code files.
- The compiled files

You will schedule a presentation with the instructor (Dec 11 - 13). Your presentation will last about 20 minutes. The instructor will email you to set up the presentations.

<mark>**Anyone who misses the final presentation will not receive a grade.**</mark>