12.13.24

CS 5990 Final: Epidemiology

Aumkaareshwar
Jeremy Anunwah
Yurii Lebid
Bill Kim

Methodology

- Three network types
  - Fully-Mixed (complete)
  - Small-World (Watts-Strogatz)
  - Barabasi-Albert
  - Simulated networks generated using same strategy from Group Assignment #1
- Tested three values for the interesting parameter for each network
  - Fully-Mixed: population size
  - Small-World: rewiring parameter (degree held constant)
  - Barabasi-Albert: new edge degree (core size held constant)
- Avoids large number of possibilities given all parameters
- Within each network's three value tests
  - Two β values
  - Three γ values
- 18 total simulations per network type

Methodology

- Stop conditions, whichever comes first
  - SI: all infected (I = N)
  - SIR: all infected (I = N) or all non-infected (S + R = N, S < N, R > 0)
  - 2000 ticks

Source Code

```
public void step() {
    if (this.state == Human.STATE_INFECTED && this.tick > this.infectedTick) {
        for (Object human : this.network.getAdjacent(this)) {
            if (Human.random.nextDouble() < this.beta) {
                ((Human)human).tryBecomeInfected();
            }
        }

        if (Human.random.nextDouble() < this.gamma) {
            this.recover();
        }
    }

    ++this.tick;
}
```

Parameter Summary

	SIR Parameters	Fixed Parameters	Tested Parameters
Fully-Mixed	β = 0.001, 0.002 γ = 0.00, 0.10, 0.20	I_0 / n = 0.01 S_0 / n = 0.99	n = 100, 500, 1000
Small-World	β = 0.001, 0.002 γ = 0.00, 0.10, 0.20	I_0 = 5 S_0 = 495 d = 6	B = 0.05, 0.10, 0.20
Barabasi-Albert	β = 0.001, 0.002 γ = 0.00, 0.10, 0.20	I_0 = 5 S_0 = 495 n_0 = 25	m = 5, 10, 20

Note: γ = 0.00 corresponds to an SI simulation, γ > 0.00 corresponds to an SIR simulation

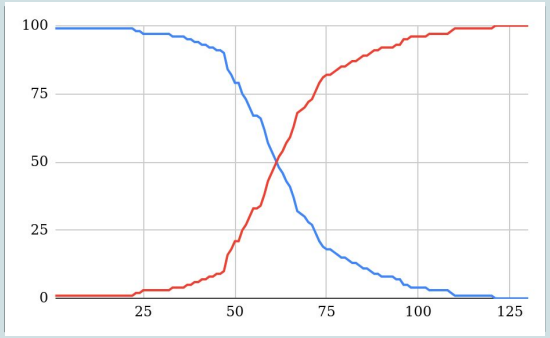
Graph Info

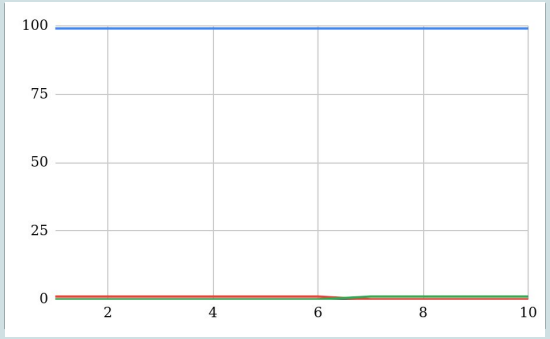
- Legend
  - Blue: Susceptible
  - Red: Infected
  - Green: Recovered
- Horizontal axis: simulation ticks
- Vertical axis: number of agents

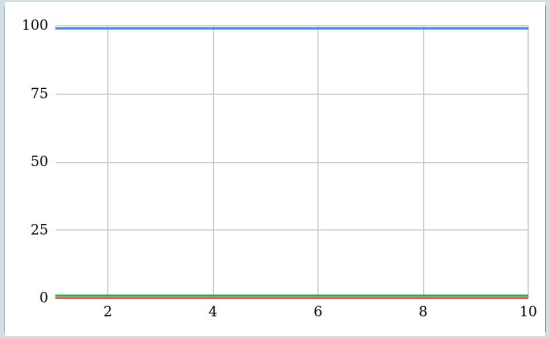
Fully-Mixed Model: n = 100

γ = 0.00 | γ = 0.10 | γ = 0.20

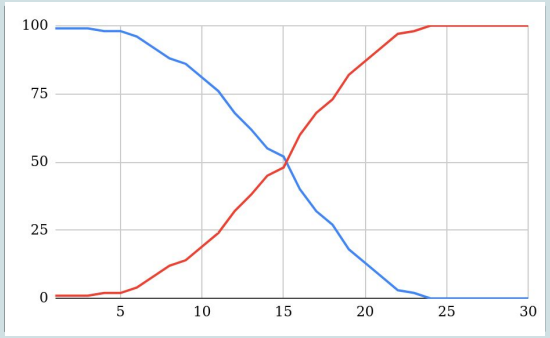
β = 0.001

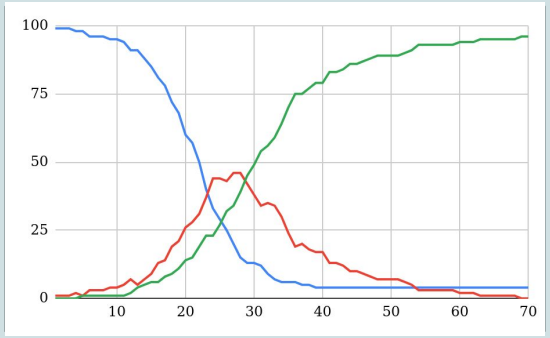


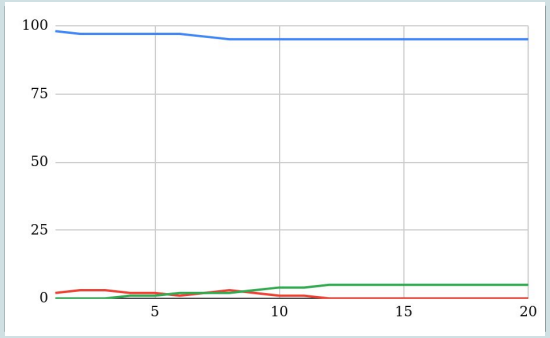




β = 0.002



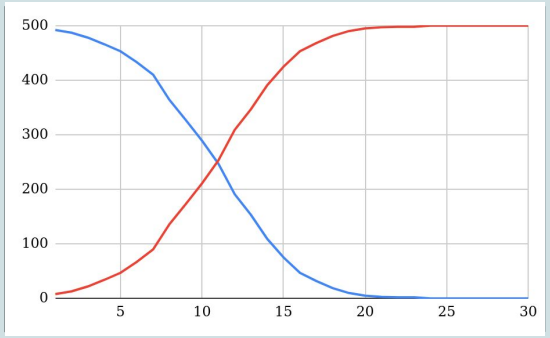


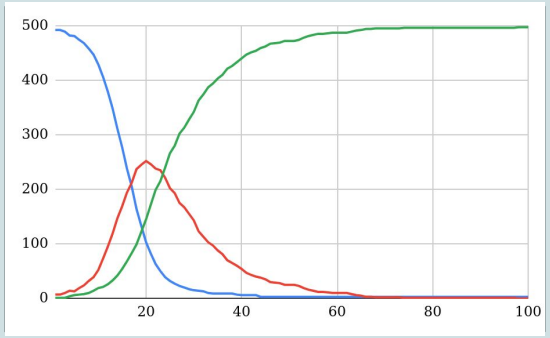


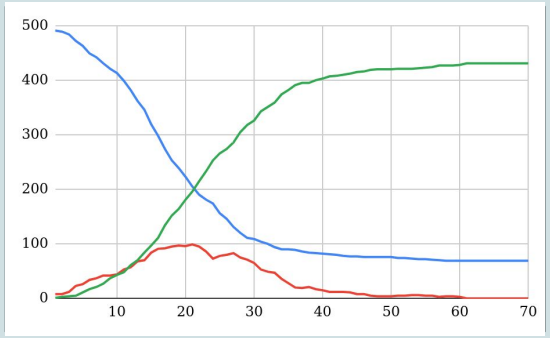
Fully-Mixed Model: n = 500

γ = 0.00 | γ = 0.10 | γ = 0.20

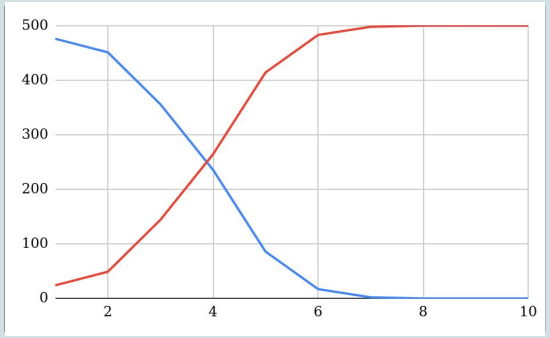
β = 0.001

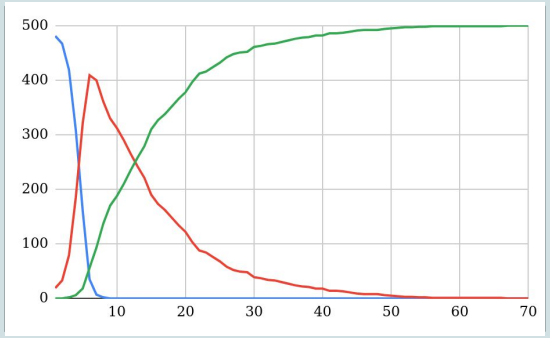


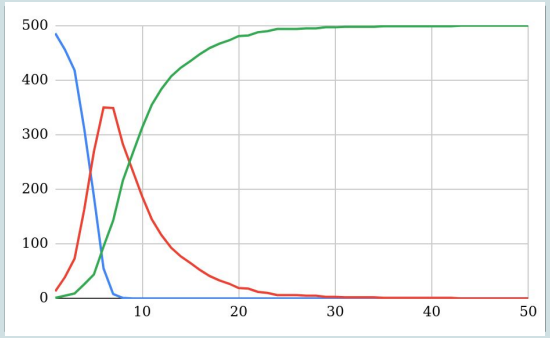




β = 0.002



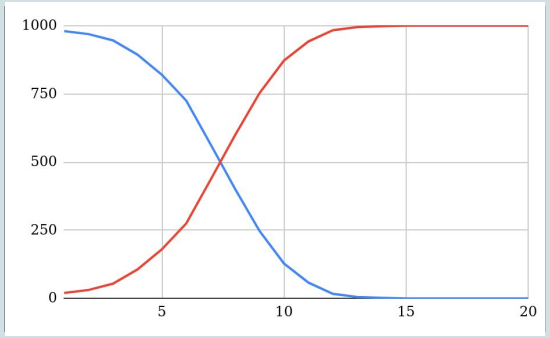


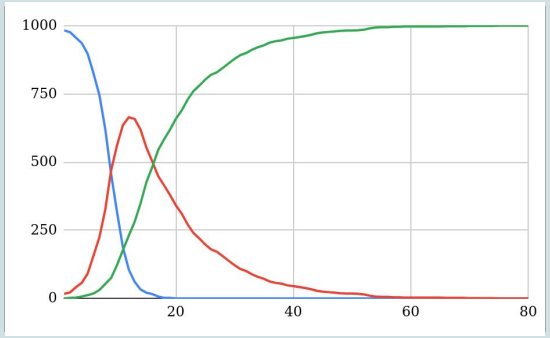


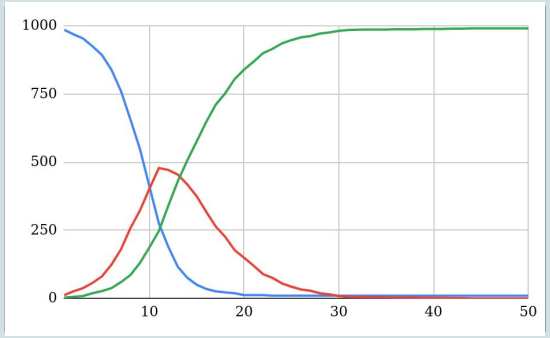
Fully-Mixed Model: n = 1000

γ = 0.00 | γ = 0.10 | γ = 0.20

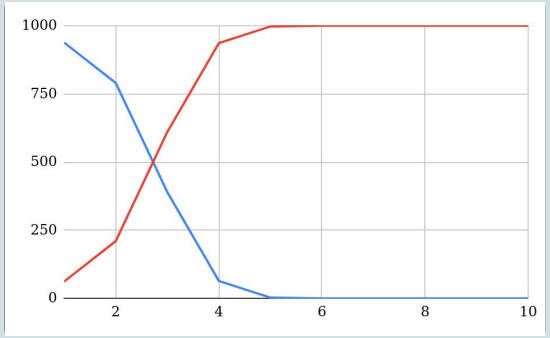
β = 0.001

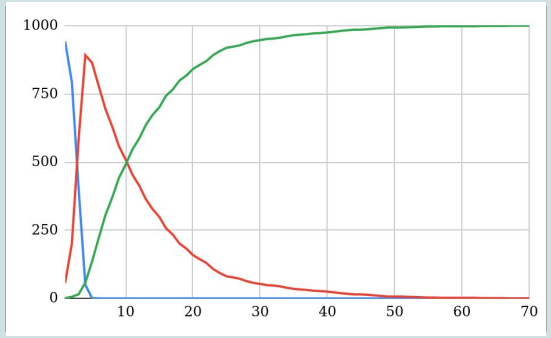


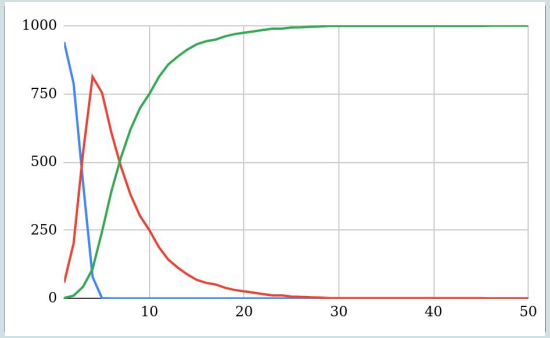




β = 0.002



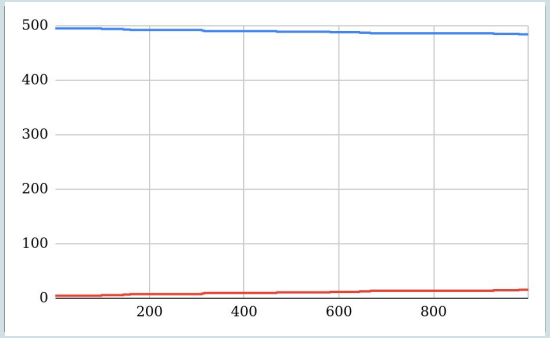


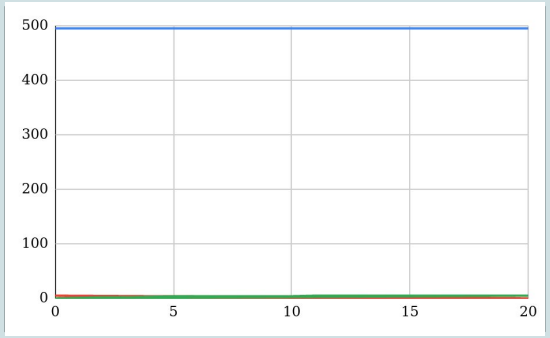


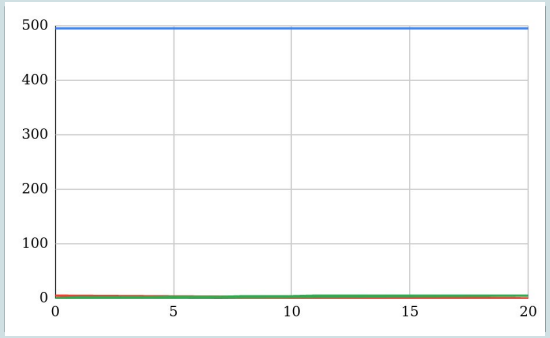
Small-World Model: B = 0.05

γ = 0.00 | γ = 0.10 | γ = 0.20

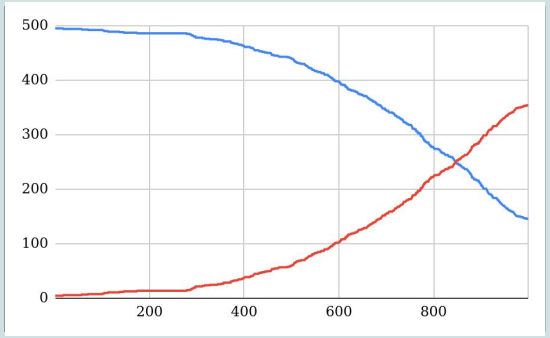
β = 0.001

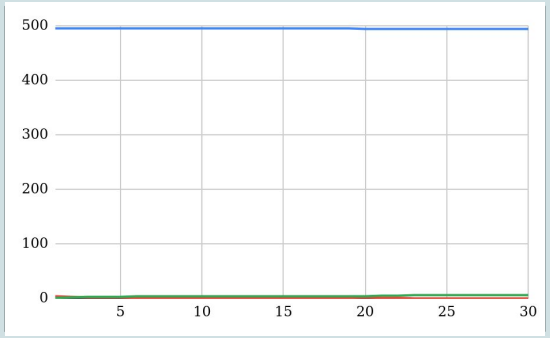


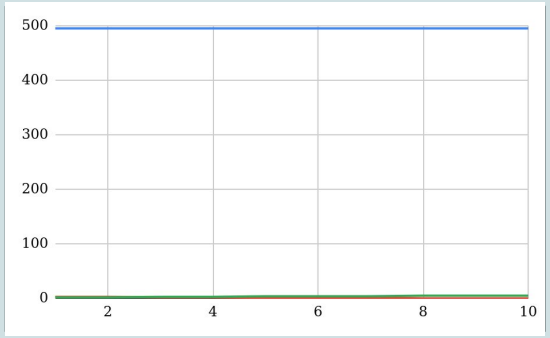




β = 0.002



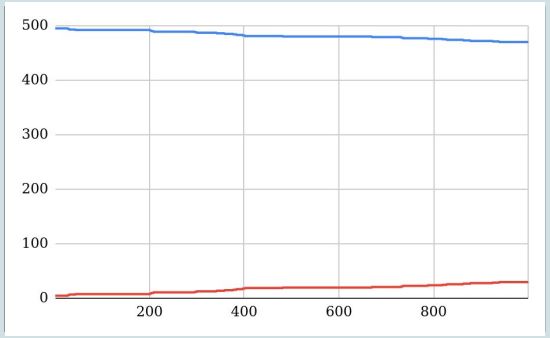


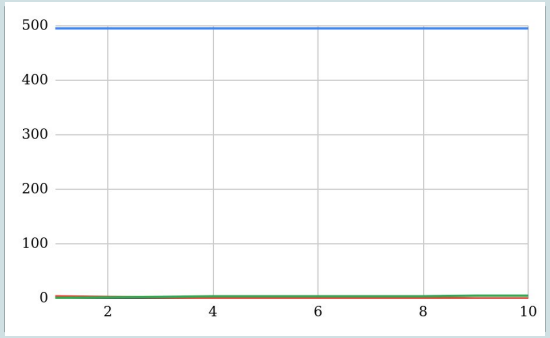


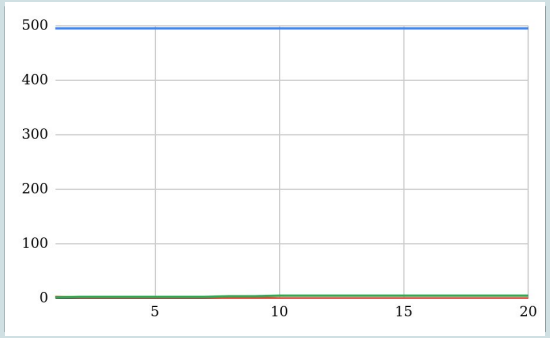
Small-World Model: B = 0.10

γ = 0.00 | γ = 0.10 | γ = 0.20

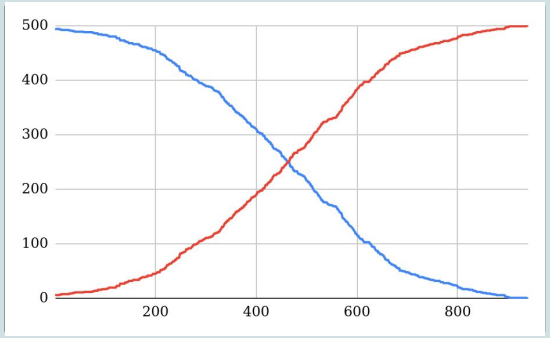
β = 0.001

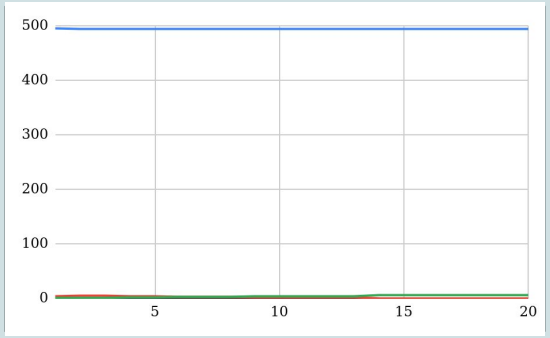


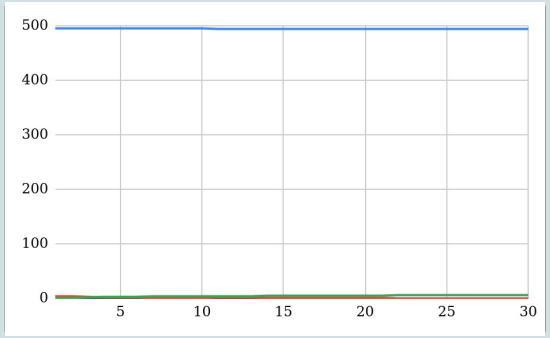




β = 0.002



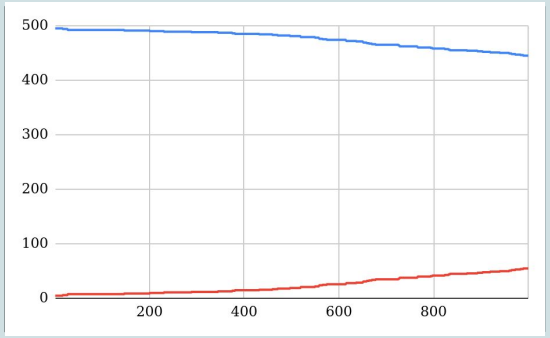


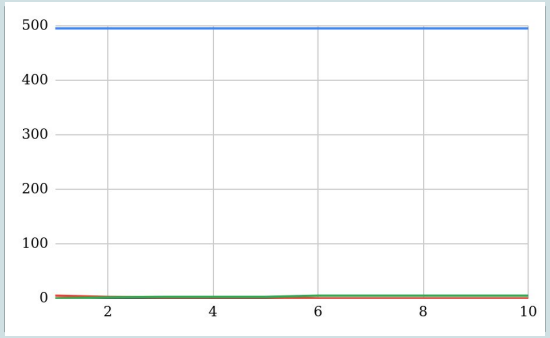


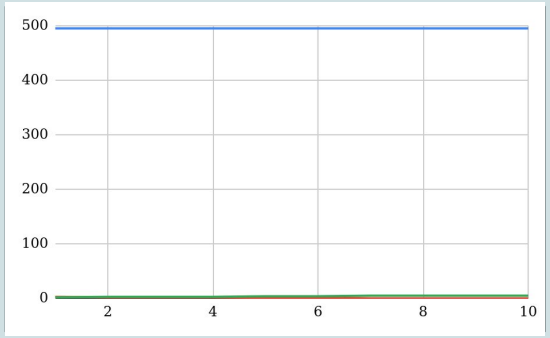
Small-World Model: B = 0.20

γ = 0.00 | γ = 0.10 | γ = 0.20

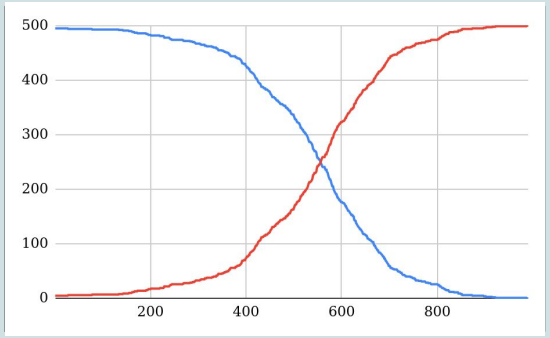
β = 0.001

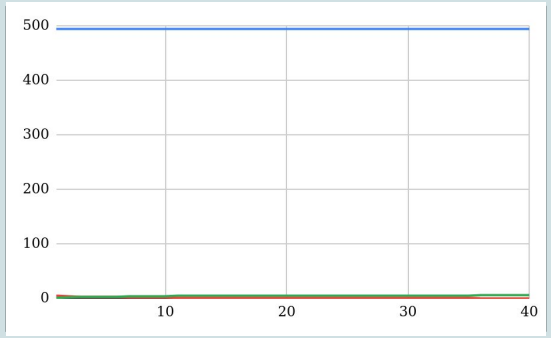


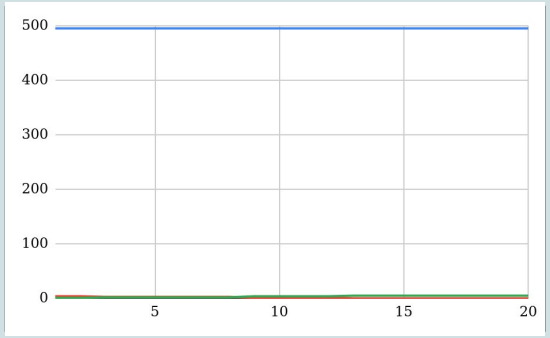




β = 0.002



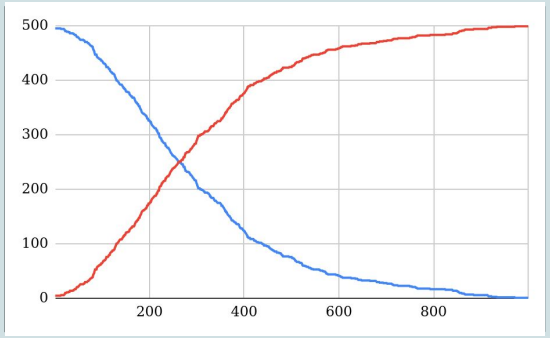


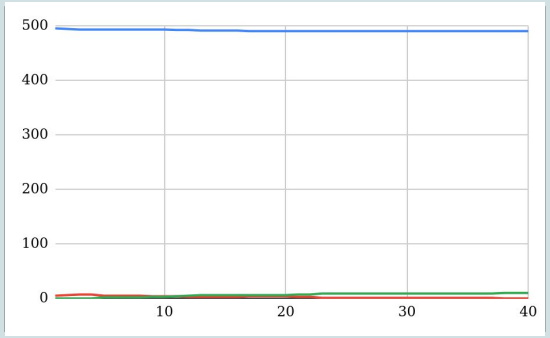


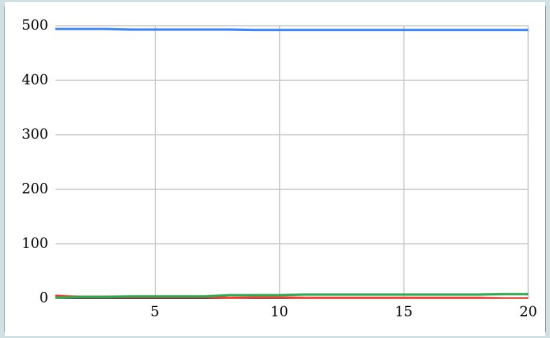
Barabasi-Albert Model: m = 5

γ = 0.00 | γ = 0.10 | γ = 0.20

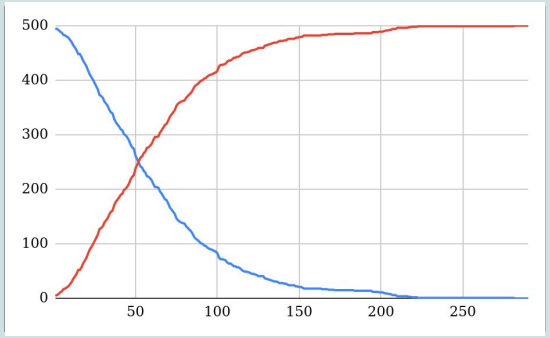
β = 0.001

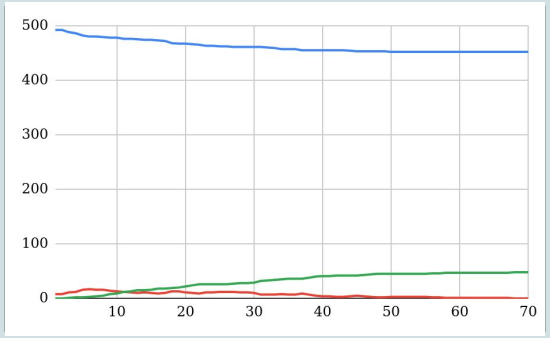


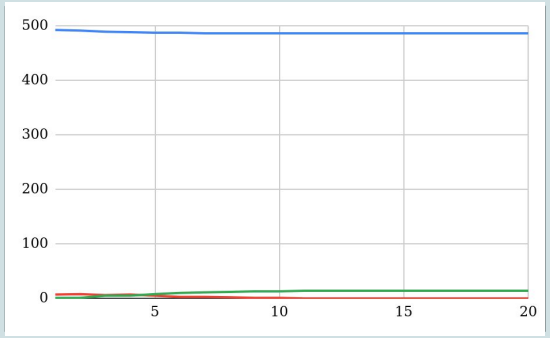




β = 0.002



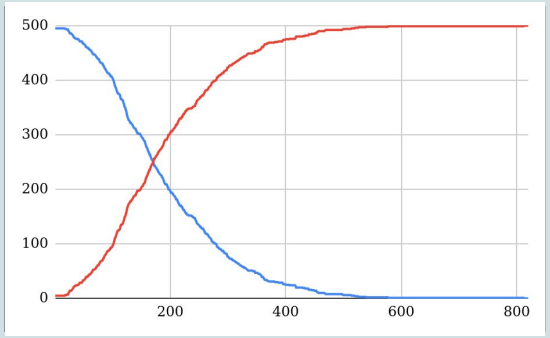


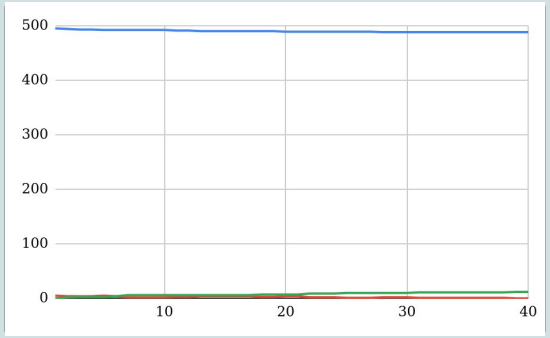


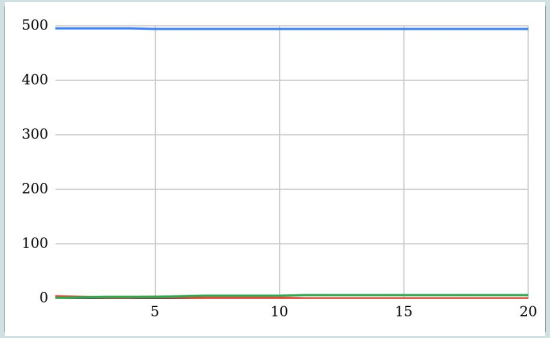
Barabasi-Albert Model: m = 10

γ = 0.00 | γ = 0.10 | γ = 0.20

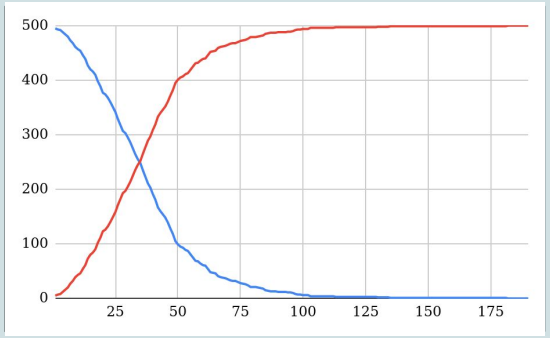
β = 0.001

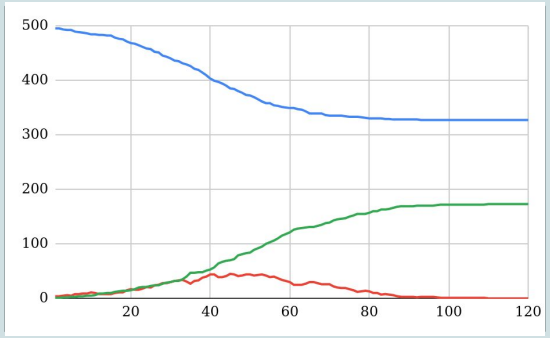


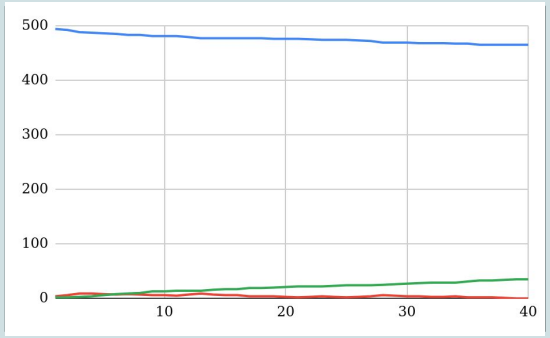




β = 0.002



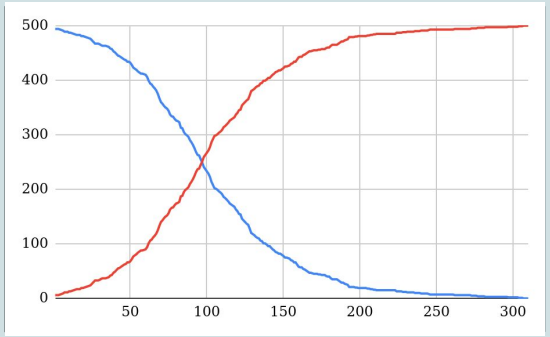


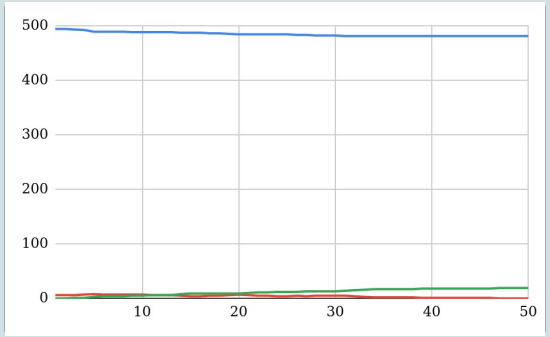


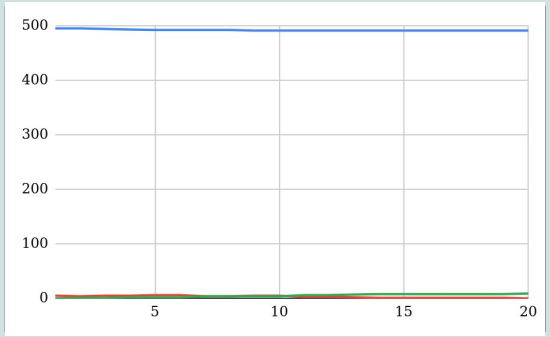
Barabasi-Albert Model: m = 20

γ = 0.00 | γ = 0.10 | γ = 0.20

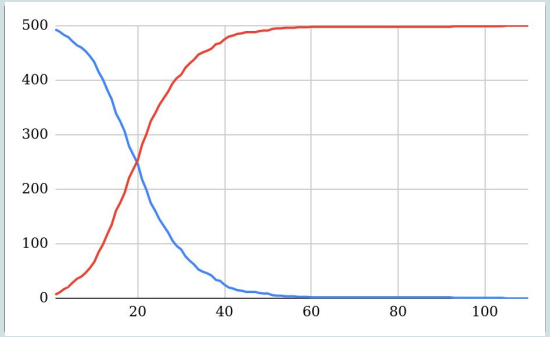
β = 0.001

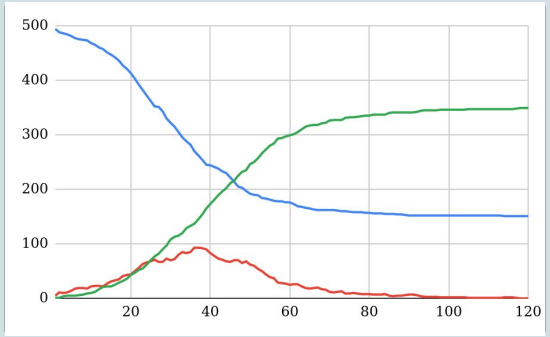


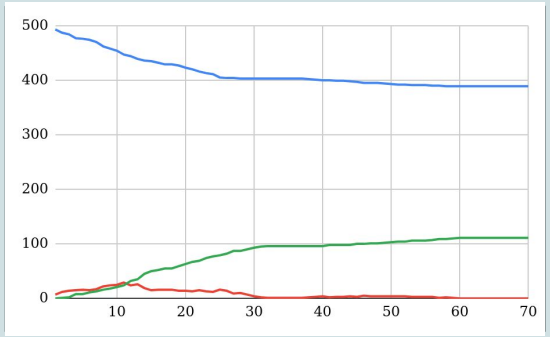




β = 0.002







Findings

- Fully-Mixed models
  - Larger populations spread disease faster due to complete network topography
    - Reaches peak number of infections faster
  - Increasing recovery rate initially extends simulation, then shortens
    - Lower rate balances infection
    - Higher rate quickly eliminates infection
- Small-World
  - SI models slow down significantly
  - SIR models show no meaningful disease spread
    - Perhaps a much higher *d* needed
- Barabasi-Albert
  - Both models slow down as in Small-World
  - Possibly more capable of showing meaningful disease spread

Tasks

- Aumkaareshwar: Methodology and Presentation
- Jeremy Anunwah: Repast Simphony implementation
- Yurii Lebid: Repast Simphony setup
- Bill Kim: Simulation graphs and Presentation

Thank You