MATHEMATICAL EPIDEMIOLOGY:
SPATIAL PATCH MODELS OF MEASLES
STRUCTURE OF PRESENTATION

- Project Overview
- Background Information
- Methodology: The Model
- Analytical and Numerical Results
- Conclusion
- Q&A
PROJECT OVERVIEW

• Measles outbreaks in U.S. due to decreased vaccination rates
• Create a model for disease spread
• Mathematically and numerically analyze our model’s behavior
• Disease model results can give insight into public health policy
• Measles is a respiratory disease caused by the virus Rubeola that is extremely contagious and kills over 100,000 people every year worldwide.

• Measles vaccines have been developed that confer lifelong immunity to the disease at a high efficacy rate.

• However, during January–September 2019, 1,249 U.S. measles cases were reported, the highest annual number since 1992.

You have the power to protect your child.

Provide your children with safe and long-lasting protection against measles by making sure they get the measles-mumps-rubella (MMR) vaccine according to CDC’s recommended immunization schedule.

WWW.CDC.GOV/MEASLES
**Figure 1:** $S(t)$, $E(t)$, $I(t)$, and $R(t)$ represent the number of susceptible, exposed, infected, and recovered individuals at time $t$, respectively.
THE PATCH MODEL

\[ \lambda_i = \sum_{j=0}^{1} \beta_{i,j} I_j \]

\[
\frac{dS_i(t)}{dt} = b(1 - p_i)N_i - (\mu + \lambda_i)S_i \\
\frac{dE_i(t)}{dt} = \lambda_i S_i - (\mu + \epsilon)E_i \\
\frac{dI_i(t)}{dt} = \epsilon E_i - (\mu + \delta + \gamma)I_i \\
\frac{dR_i(t)}{dt} = b p_i N_i + \gamma I_i - \mu R_i
\]

- This is a schematic of the patch model based on Tessa’s one-population model that was used in our study.
- There is no movement of individuals across populations, \( N_0 \) and \( N_1 \).
- Infected individuals in \( N_0 \) are marked red, and infected individuals in \( N_1 \) are marked green.
THE BASIC REPRODUCTION RATIO ($R_0$)

- **Fundamental Descriptor:**
  - **The Basic Reproduction Ratio ($R_0$)**
  - Expected # cases resulting from a single infectious individual in an entirely susceptible population

- **We used the “Next-Generation-Matrix Method” to calculate $R_0$ (Diekmann)**

- Define: $R_p = \text{The Basic Reproduction Ratio } R_0$ in the presence of vaccination, $(p_0, p_1) \neq (0, 0)$. 
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UNPACKING TESSA’S ANALYSIS ON OPTIMAL VACCINATION STRATEGY

\[ R_0(1 - p_c) < 1 \] is a necessary condition!!

**SINGLE VACCINATION STRATEGY:**
- **Coverage = .99** needed for disease control
- Difficult to reach such large proportion of population

**TWO VACCINATION STRATEGY:**
(W.H.O. RECOMMENDED)

Let \( v \) be the successful proportion vaccinated.

\[ v + v(1 - v) = p_c, \ v = 0.76 \]

\( \frac{\text{Critical Vaccine Coverage} \times \text{Vaccine efficacy}}{v} \)

- **Coverage = .79** needed for disease control
- Easier to reach population proportion
CORRECTING THE TESSA MODEL

• Models of ODE’s can be analyzed around steady-states by linearization

• Simple disease models have two steady states:
  1) A disease-free steady state (I=0)
  2) An endemic steady state (I≠0)

The Model presented by Tessa et al. DOES NOT HAVE (1) (unless S=R=0), and they falsely assumed it’s existence leading to incorrect analysis

\[
\begin{align*}
\frac{dS}{dt} &= b(1-p)N - \beta S \frac{I}{N} - \mu S \\
\frac{dE}{dt} &= \beta S \frac{I}{N} - (\sigma + p)E \\
\frac{dI}{dt} &= \sigma E - (\gamma + \mu + \delta)I \\
\frac{dR}{dt} &= \gamma I + \mu R
\end{align*}
\]

3 Stability of the disease-free state

The Jacobian of (1) at the equilibrium point \((S^*, E^*, I^*, R^*)\) is
PROVING THE STABILITY CONDITIONS OF THE DISEASE-FREE STEADY STATE

• **Theorem:** The disease-free equilibrium is locally stable if $R_p < 1$
• **Method of Proof:** (using symbolic manipulation in Mathematica)
  1. Get explicit formula for $R_p$ using Next-Generation Matrix approach
  2. Formulate the Jacobian matrix around the disease-free steady state
  3. Calculate the matrix’s eigenvalues ($\lambda_i$)
  4. Observe that $R_p < 1$ implies $\lambda_i < 0$
NUMERICAL IMPLEMENTATION: MATLAB

• Applied model to data obtained from 2018-2019 Brooklyn Measles outbreak from www.nyc.gov
• ode45
• Utilized parameters already estimated in published measles literature
• Needed to estimate contact parameters, $\beta_{i,j}$
• fminsearch (over square error function)
OBSERVATION: MISMATCH
MODEL CONSIDERATIONS

- False assumption about populations dichotomy. There are more than 2 populations that we need to consider in this outbreak.
- Individuals can migrate between populations in real life.
- NYC school vaccination rates range from 55%-100%
- Very limited data set
- Possible Population overestimation
- Model is deterministic, but stochastic elements are more realistic
REFERENCES


• V. Capasso and G. Serio, A generalization of the kermack-mckendrick deterministic epidemic model, Mathematical Biosciences, 42 (1978), pp. 43–61.


• M. Manisha Patel, National update on measles cases and outbreaks, united states, january 1 to october 1, 2019, MMWR Morb Mortal Wkly, (2019).


QUESTIONS?

Low-Vaccinated Community, $N_0$

- $\mu S_0$
- $\mu E_0$
- $\gamma I_0$
- $\mu R_0$
- $bN_0$
- $(\beta_{0,0} I_0 + \beta_{0,1} I_1) S_0$
- $\epsilon E_0$
- $(\mu+\delta) I_0$

High-Vaccinated Community, $N_1$

- $\mu S_1$
- $\mu E_1$
- $\gamma I_1$
- $\mu R_1$
- $bN_1$
- $S_1(\beta_{1,0} I_0 + \beta_{1,1} I_1)$
- $\epsilon E_1$
- $(\mu+\delta) I_1$