Modeling, Analysis and Simulation of Tuberculosis

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Agenda

Introduction

Mathematical model of TB

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Simulation and results

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Introduction

- Tuberculosis is a contagious bacterial infection caused by Mycobacterium tuberculosis
  - affects the lungs, but can target other body parts such as kidney, spine and brain
  - transmitted by air when infected individual sneezes and coughs tiny contagious droplets

- Tuberculosis has been globally health concern for many years and its spread varies across different regions of the world

Introduction

- In North Macedonia records of TB are led from 1965 when the prevalence was 131.5/100000 individuals
- In the period 1965 to 1980 number of infected individuals significantly decreased, so that the prevalence in 1980 is 48.5/100000.
- Recently, the TB infection constantly declines with prevalence of 10.2/100000 in 2021.

Mathematical Modeling

- Mathematical modeling is an essential tool used in epidemiology to study the spread and dynamics of infectious diseases within populations.
    - allows to simulate different scenarios, understand disease transmission patterns, and evaluate the impact of interventions and control measures
- Mathematical modeling in epidemiology is an evolving field, and models can vary in complexity and assumptions depending on disease.
- Collaboration between epidemiologists, mathematicians, statisticians, and public health experts is crucial for developing accurate and useful models to inform public health decision-making.

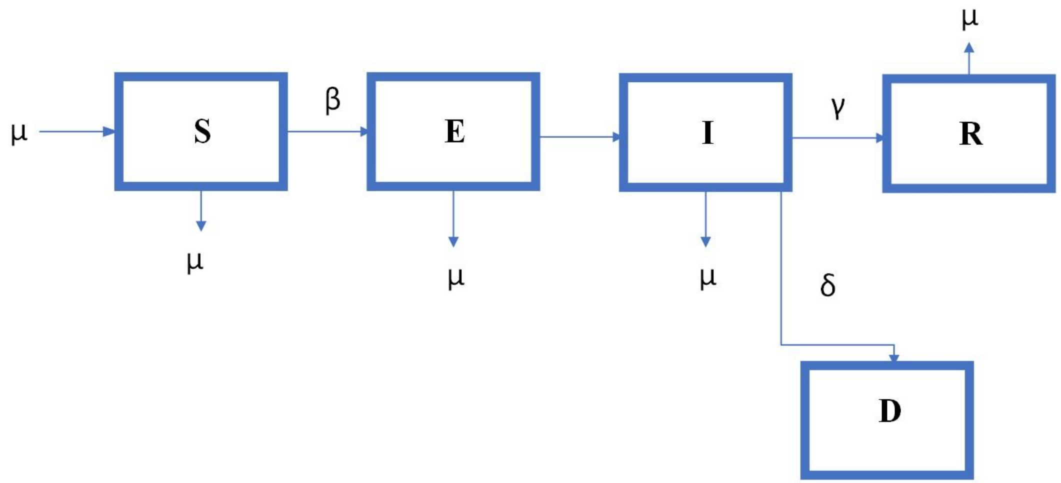
Mathematical Modeling

- Key components:
  - **Population**: specific geographical area or demographic group
  - **Compartments**: individuals are classified in different compartments based on their disease status
  - **Parameters** that quantify disease and population behavior, such as transmission rate, recovery rate, contact rate between individuals etc.
  - **Differential equations**: compartment model is represented using set of a differential equations that describe the rate of change of individuals moving between compartments
  - **Model calibration**: parameters need to be estimated using real data
  - **Scenarios**: Mathematical models allow evaluation of different strategies

SEIR+D Model

- Total population divided into 5 compartments:
  - Susceptible, exposed, infected, recovered and death

$$N(t) = S(t) + E(t) + I(t) + R(t) + D(t),$$



SEIR+D Model

- Modified SEIR+D model is given with the following system of stochastic differential equations:

$$\frac{dS(t)}{dt} = \mu N - \frac{\beta S(t) I(t)}{N} - \mu S(t)$$

$$\frac{dE(t)}{dt} = \frac{\beta S(t) I(t)}{N} - \varepsilon E(t) - \mu E(t)$$

$$\frac{dI(t)}{dt} = \varepsilon E(t) - \gamma I(t) - \delta I(t) - \mu I(t)$$

$$\frac{dR(t)}{dt} = \gamma I(t) - \mu R(t)$$

$$\frac{dD(t)}{dt} = \delta I(t)$$

$$S(0) = S_0 \geq 0$$
$$E(0) = E_0 \geq 0$$
$$I(0) = I_0 > 0$$
$$R(0) = R_0 \geq 0$$
$$D(0) = D_0 \geq 0$$

SEIR+D Model

- Disease- free equilibrium state:
  - the right side of system of differential equation is set to zero;
  - The number of infected individual is i=0;

- Disease- free equilibrium point is:

$$(s, e, i, r, d) = (1, 0, 0, 0, 0)$$

SEIR+D Model

- Basic reproduction number:
  - represents the expected number of secondary cases that will arise from a single infections individual;
  - Indicates the rate at which infectious disease spreads
  - calculated as the largest eigenvalue of the next generation matrix;

$$F = \begin{bmatrix} 0 & \beta s \\ 0 & 0 \end{bmatrix} \qquad V = \begin{bmatrix} \mu + \varepsilon & 0 \\ \varepsilon & -(\mu + \gamma) \end{bmatrix}$$

- The next generation matrix

$$G = FV^{-1} = \begin{pmatrix} \dfrac{\beta\varepsilon}{(\mu+\varepsilon)(\mu+\gamma)} & -\dfrac{\beta\varepsilon}{\mu+\gamma} \\ 0 & 0 \end{pmatrix}$$

SEIR+D Model

- The reproduction number is:

$$\mathcal{R}_o = \frac{\beta\varepsilon}{(\mu+\varepsilon)(\mu+\gamma)}$$

- When $R_0 > 1$ indicates that each infected individual, on average, is transmitting the infection to more than one susceptible individual. In such cases, the infection is likely to spread within the population.
- If $R_0 < 1$, each infected individual on average is transmitting the infection to fewer than one susceptible individual, and the infection is likely to decline and eventually die out.

SEIR+D Model

- Parameter Calibration:

  - Transmission rate $\beta = 0.2$
  - Exposed rate: the incubation period for TB is approximately 6 weeks, thus $\varepsilon = \frac{1}{6} = 0{,}166/weeks$
  - Recovery rate: expected duration of infection is 2.5 weeks, thus $\gamma = \frac{1}{2{,}5} = 0.4$
  - Mortality rate in N. Macedonia in 2018 $\mu = \frac{28516}{2065000} = 0.0138$
  - Mortality rate TB $\delta = 0.1$

SEIR+D Model

- Initial conditions:
  - In 2018 in N. Macedonia 217 new cases of TB have been detected
  - The total population in N. Macedonia in 2018 is 2065000

N_0=2065000

$S_0 = 2063389$

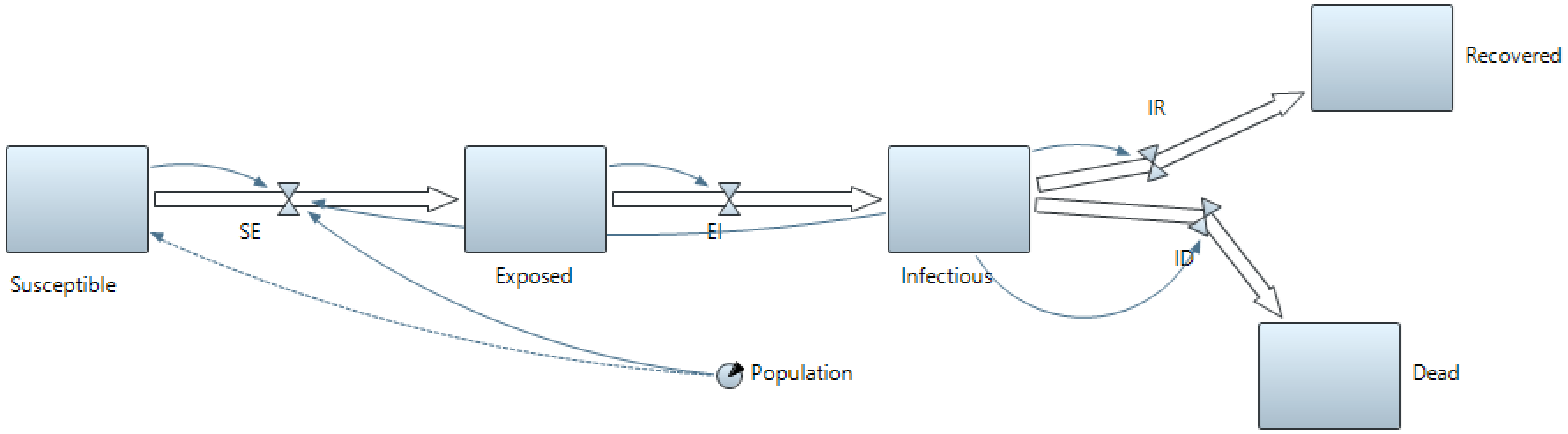
$E_0 = 1307$

$I_0 = 217$

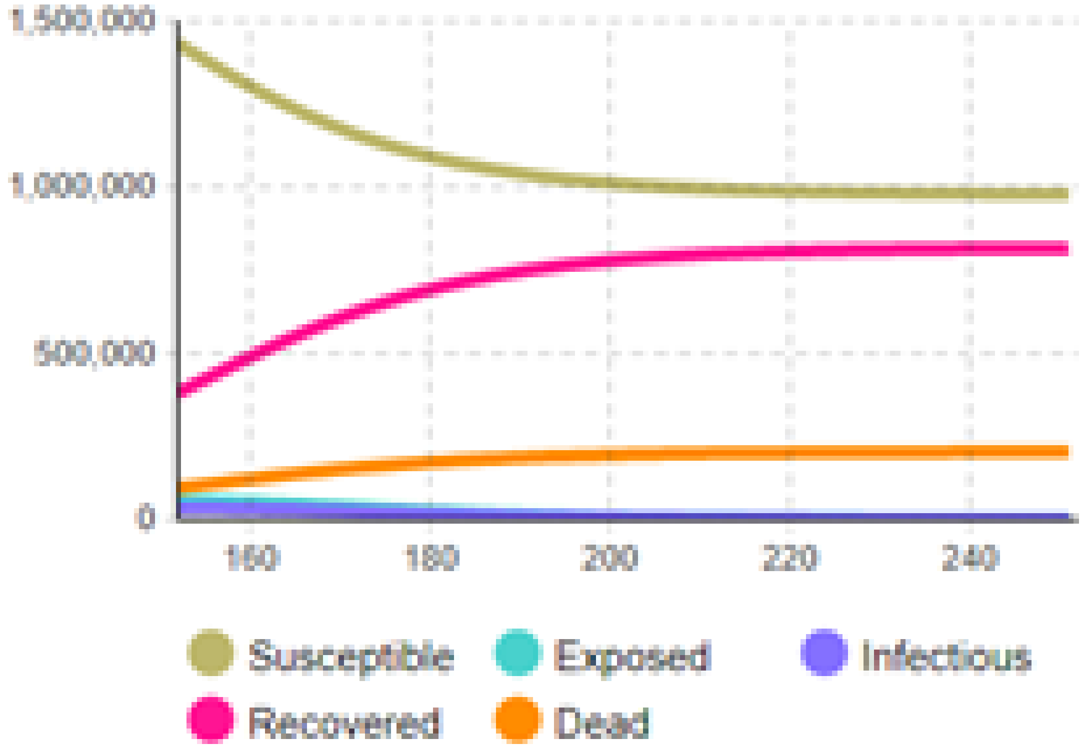
$R_0 = 87$

SEIR+D Model

- The model is deployed in AnyLogic



SEIR+D Model



1,500,000
1,000,000
500,000
0
160
180
200
220
240
Susceptible
Exposed
Infectious
Recovered
Dead

Conclusion

- In this paper a TB model is deployed without quarantine and vaccination.
- Based on this, the number of death individual is high.
- The further research will be performed with vaccination that we led to significantly decreasing number of death individuals.

Thank you