Spreading dynamic of infectious disease in two interacting areas

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Abstract. The spread of infectious disease in a heterogeneous area can be grouped as a homogeneous group. The graph theory approach to analyze the spread of infectious disease in the group using a mathematical model. Heterogeneity in a population can be caused by many factors. Within a group can be divided into several homogeneous groups based on clusterization, such as grouping the population based on age in the spread of infectious diseases. Population heterogeneity can be described as a network where each vertex represents a homogeneous group and an edge \((j, i)\) exists if and only if the disease can be transmitted from group \(i\) to group \(j\). The system of mathematical differential equations is formed based on the graph theory approach and the infectious disease distribution compartment diagram. Based on the numerical solution that we have obtained, the rate of change in the exposed population increases as the increasing of the disease transmission. And the rate of change in the infected population increases as the endemic appears.

1. Introduction

The infectious disease spread model that will be used as a mathematical model approach is in the form of a system of differential equations. With this mathematical model it will make it easier to analyze real problems. From the solution to this problem, we can simulate the problem. The model of disease spread that is modeled will be a paired non-linear differential equation system as a representation of the two groups.

The mathematical model of the rate of infectious disease spread is a system of differential equations which is a dynamic system, where one function affects another. A system of differential equations is an equation that contains the derivative of one or more unknown functions where the number of equations is more than one equation. In the spread of infectious diseases in heterogeneous populations, it is necessary to analyze the local stability and global stability of a multi-group epidemic model. In analyzing local stability the Routh - Hurwitz criterion is used, while the global stability is obtained through the construction of the Lyapunov function by applying graph theory\cite{1}.

Research on stability analysis of an infectious disease spread model has been widely conducted. The model for the spread of infectious diseases is analyzed from the interaction between susceptible \(S\), exposed \((E)\), infected \((I)\), recovered \((R)\), dead \((D)\) populations, and other well-defined populations\cite{6, 8, 7}. In this study, we will investigate cases of the spread of infectious diseases that occurred in two groups. The concept of the network for the spread of infectious diseases in the two groups is necessary because there are differences in the level of transmission...
between the two groups. With the graph theory approach, a network is formed by connecting each vertex of a homogeneous group and edges \((j, i)\) indicate disease transmission from group \(i\) to group \(j\)[9]. In this paper, the supporting theory for conducting this research is discussed in chapter 2, the research method is described in chapter 3, the completion analysis and simulation results are described in chapter 4, in chapter 5 the conclusions are written based on the results obtained.

2. Literature review

2.1. Graph theory

Directed graph \(G(V, E)\) contains two sets, namely the infinite set \(V(G) = \{1, 2, \ldots, n\}\) of objects called vertices and finite sets (possibly empty) \(E(G)\) whose elements are called edges \((i, j)\), such that each element \((i, j)\) in \(E(G)\) is an ordered pair of vertices \(V(G)\). A subgraph \(H\) of \(G\) is said to be stretched if \(H\) and \(G\) have the same set of vertices. At \(G\) graph is said to be weighted if each side \((j, i)\) is associated with a positive real number \((a_{ij})\), where the associated number is called a weight. The weight \(w(H)\) of a subgraph \(H\) is the sum of the weights of all arcs in \(H\).

Path is a finite (or infinite) sequence whose terms alternate vertices and sides where all vertices and edges can only occur once. Whereas a path with direction \(P\) on \(G\) is a subgraph with vertices \(\{(i_k, i_{(k+1)}), k = 1, 2, m - 1\}\). If \(i_m = i_1\), \(P\) is called a directed cycle. A connected subgraph \(T\) is called a tree if there are no cycles, directed or undirected. The \(i\) node is the root of a tree, if \(i\) is not the destination vertex of several arcs And each remaining vertex is the destination vertex of exactly one edge. A subgraph \(Q\) is called unicyclic if \(Q\) is a rooted tree where the root form is a directed cycle. And each vertex in \(Q\) is the destination vertex of exactly one edge. The rooted tree and unicyclic graph are shown in Figure 1.

![Figure 1. (A) Rooted tree; (B) Acyclic graph](image)

Given a digraph with weight \(G\) with \(n\) vertices, for example the weight of the matrix \(A = (a(i,j))_{(n \times n)}\) where \(a(i,j)\) is the weight of the side \((j, i)\) if any. And for a directed graph \(G\) is said to be strongly connected if for any pair of vertices, there exist a directed path that connects from one to another. A connected weighted graph \((G, A)\) is strongly connected if and only if the weight of the matrix \(A\) is not reduced. The Laplacian Matrix of \((G, A)\) is defined as follows[4]:

\[
\begin{pmatrix}
\sum_{k \neq 1} a_{1k} & -a_{12} & \cdots & -a_{1n} \\
-a_{21} & \sum_{k \neq 2} a_{2k} & \cdots & -a_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
-a_{n1} & -a_{n2} & \cdots & \sum_{k \neq n} a_{nk}
\end{pmatrix}
\]

where \(c_i\) is the cofactor of the \(i\)th diagonal element of \(L\).

Here are some definitions and theorems related to this research[4].

**Definition 2.1.** Assumed, \(n \geq 2\) and,

\[
c_i = \sum_{\tau \in T_i} w(\tau), \quad i = 1, 2, 3, \ldots n
\]
where $T_i$ is the set of all stretching trees $T$ from $(G, A)$ rooted at vertex $i$, and $w(T)$ is the weight of $T$. If $(G, A)$ is strongly connected, then $c_i \geq 0$.

**Definition 2.2.** Assumed, $E = (e_{i,j})_{n \times n}, F = (f_{i,j})_{n \times n}$ are non-negative matrix. $E \geq F$ if $e_{i,j} \geq f_{i,j}$ for all of $i$ and $j$. And $E > F$ if $E \geq F$ and $E \neq F$. Assumed :

(i) If $E$ is not negative, then the spectral distance $\rho(E)$ from $E$ is an eigenvalue, and $E$ has a non-negative eigenvector corresponding to $\rho(E)$.

(ii) If $E$ is neither negative nor reduced, then $\rho(E)$ is a simple eigenvalue, and $E$ has a positive eigenvector $x$ corresponding to $\rho(E)$.

(iii) If $0 \leq E \leq F$, then $\rho(E) \leq \rho(F)$. In addition, if $0 \leq E \leq F$ and $E + F$ is not reduced, then $\rho(E) < \rho(F)$.

(iv) If $E$ is neither negative nor reduced, and $F$ is a diagonal and positive matrix, then $EF$ is not reduced.

where $\rho(E)$ is an eigenvalue. If $\lambda$ is the eigenvalue of $E$ then $|\lambda| = \rho(E)$.

**Theorem 2.1.** Assumed $n \geq 2$, and $c_i$ is given to Definition I, then it applies :

$$\sum_{i,j=1}^{n} c_i a_{ij} F_{ij}(x_i, x_j) = \sum_{Q \in Q} w(Q) \sum_{(s,r) \in E(C_Q)} F_{rs}(x_r, x_s)$$  \hspace{1cm} (2)

$F_{ij}(x_i, x_j), 1 \leq i, j \leq n$ is arbitrary function, $Q$ is the set of all unicyclic graphs extending from $(G, A)$, $w(Q)$ is the weight of $Q$, $C_Q$ indicates that the directed cycle is di $Q$, $E(C_Q)$ is the set of arcs of the directed cycle in $Q$.

**Theorem 2.2.** Assumed $n \geq 2$, and $c_i$ is given to Definition I, then it applies :

$$\sum_{i,j=1}^{n} c_i a_{ij} G_i(x_i) = \sum_{i,j=1}^{n} c_i a_{ij} G_j(x_j)$$  \hspace{1cm} (3)

where, $G_i(x_i), 1 \leq i \leq n$ is arbitrary function.

**Theorem 2.3.** Assumed to be fulfilled,

(i) There exist functions $V_i(t, u_i), F_{ij}(t, u_i, u_j)$, and constants $a_{ij} > 0$ such that

$$\dot{V}(t, u) \leq \sum_{j=1}^{n} a_{ij} F_{ij}(t, u_i, u_j), t > 0, u_i \in D_i, \quad i = 1, 2, 3$$

(ii) Approximately each directed cycle $C$ of directed graph $(G, A)A = (a_{ij})$,

$$\sum_{(s,r) \in E(C)} F_{rs}(t, u_i, u_j) \leq 0, t > 0, u_r \in D_r, u_s \in D_s$$

(iii) The constant $c$ is given in equation 2.1 then $\dot{V}(t, u) \leq 0$ for $t > 0$ dan $u \in D$, $V$ is the Lyapunov function.
2.2. Epidemic of multigroups model
The model describes the spread of infectious diseases in a heterogeneous population, which is divided into \( n \) homogeneous groups\([5]\). Each \( i^{th} \) group is further divided into \( S_i, E_i \) dan \( I_i \), by:

- \( S_i \): Population in group \( i \) that is susceptible to disease (Susceptible)
- \( E_i \): Population in group \( i \) that is infected with the disease and can transmit the disease but has not shown any initial symptoms (exposed)
- \( I_i \): Population in group \( i \) experiencing symptoms (infected, infectious and diagnosed)
- \( d_S^i \): Natural death rate of \( S_i \)
- \( d_E^i \): Natural death rate of \( E_i \)
- \( d_I^i \): Natural death rate of \( I_i \)
- \( \Lambda^i \): Recruitment rate of population in group \( i \)
- \( \beta_{ij} \): Chances of cross-transmission between the separate groups \( S_i \) and \( I_j \)
- \( \gamma_i \): The cure rate of infected individuals in group \( i \)
- \( \epsilon_i \): Incubation rate in group \( i \)
- \( f_{ij}(S_i, I_j) \): Functions of the rate of cross transmission between groups \( S_i \) and \( I_j \)

Given the basic assumptions for the \( f_{ij}(S_i, I_j) \) function are:

(i) \( 0 < \lim_{I_j \to 0^+} \frac{f_{ij}(S_i, I_j)}{I_j} = C_{ij}S_i \leq +\infty, 0 < S_i \leq S_0^i \)

(ii) \( f_{ij}(S_i, I_j) \leq C_{ij}S_iI_j \) for \( I_j \) quite small

(iii) \( f_{ij}(S_i, I_j) \leq C_{ij}S_iI_j \) for \( I_j > 0 \)

(iv) \( C_{ij}S_i < C_{ij}S_0^i, 0 < S_i < S_0^i \)

The form of \( f_{ij}(S_i, I_j) \) which satisfies \( i - iv \) includes the general transmission rate such as:

\[
f_{ij}(S_i, I_j) = I_jS_i, f_{ij}(S_i, I_j) = I_j^{p_i}I_i^{p_j}
\]

and

\[
f_{ij}(S_i, I_j) = \frac{\gamma_i^{p_j} \gamma_j^{p_i}}{I_j + A_jI_j + A_j}
\]

3. Research methods
3.1. Literature review section
At this section references are collected in which there are basic theories that support the discussion of the problem of infectious disease spread, such as; Routh-Huwirtz stability and equilibrium point, local stability and stability criteria. Furthermore, it will also be studied further about the spread of disease from the two groups of society.

3.2. Developing mathematical modelling and designing the solution
In this section, we develope a mathematical modelling of the infectious disease using compartment diagram. We create this model using logical thinking to approach the real condition as close as possible. Once the mathematical modelling is developed, we further to create numerical solution technique.

3.3. Numerical solution section
At this section, a numerical solution will be carried out, namely from the differential equation system as a model for the infectious spread between the two groups which is solved numerically using the Runge Kutta 4\(^{th}\) Order Method.
3.4. Numerical simulation section
At this section, a numerical simulation using MATLAB is carried out to obtain the numerical solution, e.g. The rate of spread of the infectious disease. And also we further show the figure of the numerical solutions.

3.5. Summary section
At this section, we take the conclusion of the numerical results.

4. Analysis and discussion
In this section, we further conduct analyze the problem using compartment diagram following big formulating the mathematical of the problem.

4.1. Model in compartment diagram
The spread of infectious disease is show as follows:

![Compartment Diagram](image)

Figure 2. Compartment diagram for two groups with non-linear transmission rate

4.2. Multi group differential equations
Epidemic model of two groups of SEI with nonlinear transmission rate of infectious disease consists of $S_i, E_i$ and $I_i$. With $i = 1, 2$. Index $i = 1$ refers to the model for the first group and $i = 2$ for other group.

- **Susceptible**
  Susceptible is at high risk of being infected from infectious disease. Thus the differential equation for the Susceptible population in group $i$ is
  \[
  \dot{S}_i = \lambda_i - d_i^S S_i - \sum_{j=1}^{n} \beta_{ij} f_{ij}(S_i, I_j)
  \]

- **Exposed**
  Individuals are infected with infectious disease and they can transmit it to other people, but they have not shown any early symptoms of disease. Thus the differential equation for the group $i$ exposed population is:
  \[
  \dot{E}_i = \sum_{j=1}^{n} \beta_{ij} f_{ij}(S_i, I_j) - (d_i^E + \epsilon_i)E_i
  \]
The Basic Reproduction Number can be derived from the following equation:

\[
R_0 = \frac{\beta_{ij} \epsilon_i C_{ij} S_i^0}{(\epsilon_i + \epsilon_j)(d_i^j + \gamma_j)}
\]

Assumed, \( R_0 = \rho(M_0) \),

\[
M_0 = M \left( S_1^0, S_2^0 \right) = \left( \frac{\beta_{ij} \epsilon_i C_{ij} S_i^0}{(\epsilon_i + \epsilon_j)(d_i^j + \gamma_j)} \right)_{1 \leq i, j \leq 2}
\]

if \( f_{ij}(S_i, I_j) = I_j^{p_{ij}} S_i^{q_{ij}} \), then \( C_{ij}(S_i^0) = p_j I_j^{p_{ij}-1} S_i^{q_{ij}} \),

\[
\lambda^2 - \left( \frac{\beta_{ij} \epsilon_i C_{ij} S_i^0}{(\epsilon_i + \epsilon_j)(d_i^j + \gamma_j)} \right) \lambda - \left( \frac{\beta_{ij} \epsilon_i C_{ij} S_i^0}{(\epsilon_i + \epsilon_j)(d_i^j + \gamma_j)} \right) = 0
\]

And we can rewrite,

\[
\lambda^2 - (p + q) \lambda + (pq - rs) = 0
\]
with,

\[ p = \frac{\beta_1 \epsilon_2 p_2 I_2^{p_2-1} S_1^{\delta_{p_1}}}{(d_1^E + \epsilon_1)(d_1^I + \gamma_1)} \]

\[ q = \frac{\beta_2 \epsilon_2 p_1 I_1^{p_1-1} S_2^{\delta_{p_2}}}{(d_2^E + \epsilon_2)(d_2^I + \gamma_2)} \]

\[ r = \frac{\beta_1 \epsilon_2 p_2 I_2^{p_2-1} S_1^{\delta_{p_1}}}{(d_1^E + \epsilon_1)(d_1^I + \gamma_1)} \]

\[ s = \frac{\beta_2 \epsilon_2 p_1 I_1^{p_1-1} S_2^{\delta_{p_2}}}{(d_2^E + \epsilon_2)(d_2^I + \gamma_2)} \]

Applied \( R_0 = \rho(M_0) = \max_i |\lambda_i| \), with \( \rho \) is spectral radius,

\[ \lambda = -\frac{(p + q) + \sqrt{(p + q)^2 - (pq - rs)}}{2a} \]

\[ \lambda = \frac{1}{2} \left[ (p + q) + \sqrt{(p - q)^2 + 4rs} \right] \] (6)

and applied for \( p, q, r, t \),

\[ R_0 = \frac{1}{2} \left[ \frac{\beta_1 \epsilon_2 p_2 I_2^{p_2-1} S_1^{\delta_{p_1}}}{(d_1^E + \epsilon_1)(d_1^I + \gamma_1)} + \frac{\beta_2 \epsilon_2 p_1 I_1^{p_1-1} S_2^{\delta_{p_2}}}{(d_2^E + \epsilon_2)(d_2^I + \gamma_2)} + \right. \\
\left. \sqrt{\left( \frac{\beta_1 \epsilon_2 p_2 I_2^{p_2-1} S_1^{\delta_{p_1}}}{(d_1^E + \epsilon_1)(d_1^I + \gamma_1)} - \frac{\beta_2 \epsilon_2 p_1 I_1^{p_1-1} S_2^{\delta_{p_2}}}{(d_2^E + \epsilon_2)(d_2^I + \gamma_2)} \right)^2 + 4 \frac{\beta_1 \epsilon_2 p_2 I_2^{p_2-1} S_1^{\delta_{p_1}}}{(d_1^E + \epsilon_1)(d_1^I + \gamma_1)} \frac{\beta_2 \epsilon_2 p_1 I_1^{p_1-1} S_2^{\delta_{p_2}}}{(d_2^E + \epsilon_2)(d_2^I + \gamma_2)}} \right] 

The \( R_0 \) denotes the basic reproduction number of a two-group epidemic model with a non-linear transmission rate.

4.4. Numerical solution and analysis

The first numerical simulation based on this parameters,

**Table 1.** The parameters that we use to conduct for first numerical simulations

| 1st Group | 2nd Group | Initial | Transmission Rate |
|-----------|-----------|---------|-------------------|
| \( \Lambda_1 = 0.2 \) | \( \Lambda_1 = 0.1 \) | \( S_1(0) = 15 \) | \( \beta_{11} = 0 \) |
| \( d_1^S = 0.009 \) | \( d_1^S = 0.002 \) | \( E_1(0) = 1 \) | \( \beta_{12} = 0 \) |
| \( d_1^E = 0.02 \) | \( d_1^E = 0.002 \) | \( I_1(0) = 4 \) | \( \beta_{21} = 0 \) |
| \( d_1^I = 0.025 \) | \( d_2^I = 0.002 \) | \( S_2(0) = 20 \) | \( \beta_{22} = 0.007 \) |
| \( \epsilon_1 = 0.003 \) | \( \epsilon_2 = 0.02 \) | \( E_2(0) = 2 \) |
| \( \gamma_1 = 0.003 \) | \( \gamma_2 = 0.012 \) | \( I_2(0) = 6 \) |

with \( p_1 = 1; q_1 = 1; p_2 = 1; q_2 = 1 \). By using these parameters, the value of \( R_1 = 9.09 > 1 \) is obtained, and the rate of population change is shown in Figure 3.
Figure 3. The rate of change for infectious disease in the first group is free conditions when the other group is endemic

- Rate of Change in Susceptible Populations
  The rate of change in the susceptible population in the first group increases for the early time and then following constant. This is due to no disease for the first group. In the second group the rate of change in the susceptible population decreases due to an increase in population infected, so that some susceptible populations in the second group enter the exposed population.

- Rate of Change in the Exposed Population
  The rate of change in the population of exposed to the first group decreases becomes zero, this is due to no infectious disease spread. Whereas in the second group, the rate of change in the exposed population experience fluctuation as the spread of infectious disease.

- Rate of Change in the Infection Population
  The rate of change in the infected population in the first group decrease to become zero. This indicates that the disease disappeared. Meanwhile, the rate of change in the infected population in the second group increased because some exposed populations entered the infected population. Then the rate of change curve decreases and is constant because there is no addition of exposed individuals who have developed disease symptoms.

The second simulation based on parameters that shown in Table 2 and we use $p_1 = 1; q_1 = 1; p_2 = 1; q_2 = 1$. By using these parameters, the value of $R_1 = 7.81 > 1$ is obtained, and the rate of population change is shown in Figure 4.

- Rate of Change in Susceptible Populations
  In the first group, the rate of change in the susceptible population decreased, while in the second group, it increased because there was no spread of disease.

- Rate of Change in the Exposed Population
  The rate of change in the population exposed in first group increases for the early time and then following constant. Meanwhile, the rate of change in the population exposed to the second group decreased become zero. The rate of change in the exposed population
Table 2. The parameters that we use to conduct for 2nd numerical simulations.

| $1^{st}$ Group | $2^{nd}$ Group | Initial | Transmission Rate |
|----------------|----------------|---------|-------------------|
| $\Lambda_1 = 0.2$ | $\Lambda_1 = 0.1$ | $S_1(0) = 30$ | $\beta_{11} = 0.005$ |
| $dS_1 = 0.003$ | $dS_2 = 0.007$ | $E_1(0) = 2$ | $\beta_{12} = 0$ |
| $dE_1 = 0.004$ | $dE_2 = 0.017$ | $I_1(0) = 8$ | $\beta_{21} = 0$ |
| $dI_1 = 0.005$ | $dI_2 = 0.002$ | $S_2(0) = 10$ | $\beta_{22} = 0$ |
| $\epsilon_1 = 0.02$ | $\epsilon_2 = 0.001$ | $E_2(0) = 1$ |
| $\gamma_1 = 0.011$ | $\gamma_2 = 0.003$ | $I_2(0) = 3$ |

Figure 4. The rate of change for endemic conditions in the first group when free condition in other group was also inversely proportional to the cases where the first group was disease free and the second group was endemic.

- Infected Population Change Rate
  The rate of change in the infected population in the first group increased due to the spread of disease. Then it decreased following constant, indicating that the first group was endemic. Meanwhile, the rate of change in the infected population in the second group is decrease and constant to zero.

5. Conclusion
From the analysis that has been carried out on the spread of infectious disease between two groups, we take the conclusion as follow:

(i) The rate of change in the exposed population increased equally in both of groups. This is due to the presence of a large enough disease transmission rate, so that many individuals in the exposed population must be take attention.
(ii) The rate of change in the infected population increases because the population is endemic. The increase in the rate of change in the infected population depends on the number of individuals in the exposed population.

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