Stability analysis model of *Bacillus antracis* using SEIQR population compartment with quarantine in Indonesia

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Abstract. In Indonesia there are many breeders of cattle that are actually used as a livelihood so that Indonesia is prone to the spread of anthrax disease. This disease can be transmitted through indirect contacts such as deep impurities, saliva and the like. Anthrax disease is a type of disease caused by bacteria and there is a link between livestock and humans as the host. Anthrax disease with quarantine special factors can be modelled with SEIQR where existed from susceptible, exposed, symptomatic infected, quarantine and recovered compartment with research method used that is quantitative method, so different with disease models caused by bacteria in general.

In this study we will determine the qualitative analysis of the anthrax disease distribution model with goal of research are to obtain model transmission Anthrax, to find equilibrium point of model and to find the basic reproduction number $R_0$, where $R_0$ aims to determine the spread of disease or the absence of disease spread through endemic equilibrium stability analysis. The goal from this research is compare stability analysis between model with quarantine and model without quarantine use Routh-Hurwitz criteria to prove that $E_1$ and $E_2$ are asymptotic stability equilibrium so from this research conclude that quarantine population can speed up recovered population to be free disease condition from Anthrax.

1. Introduction

Anthrax disease has become a widespread concern for the public because it has killed many victims both cattle and humans. Infection in human occurs when *Bacillus anthracis* penetrates through skin abrasions or mucous membranes when there is a contact with infected anthrax carcasses or animal products, inhalation of spores, or consumption of undercooked infected carcass [1]. Endemic hotspot areas for anthrax outbreaks exist in most parts of the world including Africa, Asia, United States and Australia [2]. China for instance, has experienced three large-scale anthrax outbreaks with 112.000 human cases from 1956-1997 [3].

Anthrax is epizootic throughout Africa, leading to considerable economic losses of livestock and wild animals, costs for laboratory testing and carcass disposal, and severe, sometimes fatal infection in humans. In Zimbabwe, during 1995-2005 a total 282 outbreaks and 2978 animal cases were reported [4]. The first case in Indonesia appeared in 1832 in Kaloka District, Southeast Sulawesi Province. In 2000 there were outbreaks in Purwakarta district of West Java with 32 cases, the increase continued since 2001 with the amount of 6.45% in 2001 to 27.6% in 2002 [5]. At that time, the cow was then slaughtered and consumed by the surrounding community and caused an infection in human kind so there was another outbreak in Central Java, namely in Sragen Regency [6]. The number of cases is
influenced by the livelihoods of Indonesians as farmers and the lack of knowledge of some
Indonesians on the impact of anthrax disease. In this research, we will analyze the stability of
mathematical model of anthrax to obtain basic reproduction number with SEIQR model compartment.
Before analyzing SEIQR model, we analyze SEIR model. The stability of discrete time SEIR epidemic
model was analyze using Micken discrete method [7]. Global dynamic analysis of an SEIR epidemic
model using Lyapunof function was done [8]. Previous research related to anthrax has been conducted
by Chaerul Basri and Nuning Maria Kiptiyah [9] from the Faculty of Veterinary Medicine of IPB and
Faculty of Health Sciences UI analyzing anthrax under the title "Holding Vulnerable Animals and
Handling Its Products at Great Risk of Anthrax Infection in Endemic Area" and previous research
about SEIQR has been conducted by T Li and Y Xue [10] in 2013 with title “Global Stability Analysis
of a delayed SEIQR Epidemic Model with Quarantine and Latent” but these studies have not yet
modeled anthrax and studied up to the quarantine compartment.

2. Formulation Model

2.1. Assumption
Anthrax infection occurs internally in the human body, changed in the population remain and covered
because \( \frac{dN}{dt} = 0 \), so the rate of birth is equal to the rate of death, the population of each district/city in
Indonesia is equal to the number of human population in Indonesia, the percentage of added the
number of human beings per compartment same, no other microorganisms attacked humans other
than Bacteria, the rate of recovery is constant, any infected quarantined will recover, viral deaths are
ignored, all infected humans have symptoms of Anthrax disease, free Bacteria multiply in population
Infected with rate of \( \alpha \) (Bacteria transmission rate), the rate of recovery from infected to recovered is
the same as quarantine to recovered, all parameters of positive value with the immune system (p) are
in the interval \( 0 < p < 1 \).

2.2. Model Endemic Bacteria Bacillus antracis with Quarantine

From flow chart model in Figure 1, we get differential equation non linear as follow:

\[
\begin{align*}
\frac{ds}{dt} &= \delta - \alpha s(t) i_s(t) - \mu s(t) \quad s(0) > 0 \\
\frac{de}{dt} &= \alpha s(t) i_s(t) - \beta pe(t) - \mu e(t) \quad e(0) \geq 0 \\
\frac{di_s}{dt} &= \beta pe(t) - \theta i_s(t) - \mu i_s(t) \quad i_s(0) > 0 \\
\frac{dq}{dt} &= \theta i(t) - \rho q(t) - \mu q(t) \quad q(0) > 0 \\
\frac{dr}{dt} &= \rho q(t) - \mu r(t) \quad r(0) > 0 \\
N(t) &= s(t) + e(t) + i_s(t) + q(t) + r(t) \quad (6)
\end{align*}
\]
2.3. Model Endemic Bacteria Bacillus antracis without Quarantine

From flow chart model in Figure 2, we get the differential equation non-linear as follow:

\[
\begin{align*}
\frac{ds}{dt} &= \delta - \alpha s(t)i_s(t) - \mu s(t) \quad s'(0) > 0 \\
\frac{de}{dt} &= \alpha s(t)i_s(t) - \beta pe(t) - \mu e(t) \quad e'(0) \geq 0 \\
\frac{di_s}{dt} &= \beta pe(t) - \eta i_s(t) - \mu i_s(t) \quad i'(0) > 0 \\
\frac{dr}{dt} &= \eta i_s(t) - \rho r(t) \quad r'(0) > 0 \\
N(t') &= s(t) + e(t) + i_s(t) + r(t)
\end{align*}
\]

(7)

(8)

(9)

(10)

(11)

2.4. Description

The parameter that used in this research are presented in Table 1.

| Symbol | Description |
|--------|-------------|
| \(\delta\) | Constant birth rate |
| \(\mu\) | Constant dead rate |
| \(\alpha\) | Transmission rate of Bacteria Bacillus antracis |
| \(\beta\) | Probability of transmitting Bacteria Bacillus antracis to Human |
| \(\theta\) | The added rate of quarantined populations |
| \(p\) | Constants \((\frac{1}{IP})\) where IP is the period of Bacteria incubation in Humans |
| \(\rho\) | Constant of recovery rate |
| \(\delta\) | Constant birth rate |
| \(\mu\) | Constant dead rate |

3. Interpretation Model

The model discussed in this paper is the SEIQR model in which the population is divided into five distinct individual classes of susceptible, exposed, symptomatic infective (is), quarantine and recovered populations [9]. If the model is not quarantined then there is no compartment q, so that the model is obtained without quarantine with five equations. In the equation system, \(\mu\) denotes the rate of human mortality, \(\alpha\) is the rate of transmission of Anthrax disease, \(\beta_s\) is the probability of transmission of Anthrax disease to humans which makes the human become individual infected with symptoms,
\[ p = \frac{1}{IP} \]  where IP is Incubation Period i.e. incubation period Anthrax disease In the human body, \( \theta \) is the accreted population growth rate and \( \rho \) is the rate of human recovery.

### 4. Stability Analysis of Disease

#### 4.1. The Point of Illness-Free Equilibrium

By took \( \frac{ds}{dt} = 0, \frac{dt_i}{dt} = 0 \), we got the equilibrium point of the model [11]. If taken \( t^0 \neq 0 \), the disease-free equilibrium point will be obtained, where in this state all populations enter the susceptible population and no infected population can spread the disease. So the free equilibrium point of the human population is \( E_1 = (s^0, e^0, t_i^0, q^0) = \left( \frac{\delta}{\mu}, 0, 0, 0 \right) \).

#### 4.2. The Point of Free Disease Equilibrium

If taken \( t^0 \neq 0 \), it could be shown that the point of disease (bacteria) is free where there are infective humans that can spread the disease and cause endemic [9]. So that the epidemic equilibrium point in the human population is \( E_2 = (s^*, e^*, t_i^*, q^*) \) with:

\[
\begin{align*}
\frac{ds}{dt} &= \frac{\beta \mu p + \mu e^2 q + \theta \mu^2 + \mu^3}{\beta \mu + \mu + \mu^2 + \mu^3}, \\
\frac{de}{dt} &= -\frac{\alpha \mu p + \mu e^2 q + \theta \mu^2 + \mu^3}{\beta \mu + \mu + \mu^2 + \mu^3}, \\
\frac{dt_i}{dt} &= \frac{\delta}{\mu} - \theta - \mu, \\
\frac{dq}{dt} &= \beta \mu p - \mu - \mu.
\end{align*}
\]

Consequently the equilibrium point of the mathematical model of the **Bacillus antracis** transmission process in humans has two equilibrium points:The disease-free equilibrium point \( E_1 = (s^0, e^0, t_i^0, q^0) = \left( \frac{\delta}{\mu}, 0, 0, 0 \right) \) and Epidemic Equilibrium Points \( E_2 = (s^*, e^*, t_i^*, q^*) \).

#### 4.3. Basic Reproduction Number \((R_0)\)

To determine the basic reproduction rate is to assume \( t_i^* > 0 \). Based on equilibrium point epidemic \( E_2 \) obtained \( \frac{(\beta \mu p + \mu^2)(\theta + \mu)}{a \beta \mu} \). Defined \( R_0 = \frac{(\beta \mu p + \mu^2)(\theta + \mu)}{a \beta \mu} \), based on the value of \( R_0 \), through free disease equilibrium analysis will be proven that:If \( R_0 \leq 1 \) then the quarantine model system has one equilibrium point i.e the equilibrium-free equilibrium point \( E_1 = (s^0, e^0, t_i^0, q^0) \) and if \( R_0 > 1 \) then the quarantine model equation system has two equilibrium points, the equilibrium point of disease \( E_1 \) and the equilibrium point of free disease \( E_2 = (s^*, e^*, t_i^*, q^*) \).

### 5. Free Disease Equilibrium Analysis

Given a Jacobian matrix on human populations:

\[
J(E_1) = \begin{bmatrix}
-\mu & 0 & -\frac{\delta}{\mu} & 0 \\
0 & -\beta p - \mu & \frac{\delta}{\mu} & 0 \\
0 & -\beta p - \theta - \mu & 0 & 0 \\
0 & 0 & \mu & -\rho - \mu
\end{bmatrix}
\]

The eigen value is obtained from \( \det (J(E_1) - \lambda I) = 0 \), the characteristic equation is obtained:

\[-(\rho + \mu + \lambda)(\beta \mu^2 p + a \beta \mu^2 + \beta \mu^2 + \mu^2 + \mu^2 + \mu^2 + \mu^2)\]

so obtained eigen value as follows:

\[
\lambda_1 = -\rho = \mu, \quad \lambda_2 = -\mu, \quad \lambda_3 = \frac{1}{2} (\mu p - \mu^2 + \mu^2 + \mu^2 + \mu^2), \quad \lambda_4 = -\frac{1}{2} (\mu p + \mu^2 + \mu^2 + \mu^2 + \mu^2)
\]

with \( F = \beta^2 \mu^2 p^2 - 2 \mu^2 \mu^2 p^2 + \mu^4 \theta^2 - 4 \alpha \beta \mu \mu^2 + 2 \beta \mu^2 p^2 - 2 \mu^4 + \mu^4 + \mu^4 \). The equilibrium point of a system is said to be stable if the roots of the characteristic equation of a matrix have eigen values with a real negative part.

**Lemma 1.**

1. If \( \lambda < 0 \) then the equilibrium point \( E_1 \) of the model equations system is stable asymptotically
2. If $\lambda > 0$ then the equilibrium point $E_1$ of the model equation system is unstable

**Proof:** From the equation above, the eigenvalue $\lambda_1 = -\mu$, where it is known that $\mu$ is positive, so the real part of the first eigen value is negative. From the above equation, the eigenvalue $\lambda_2 = -\rho - \mu$, whereas it is known that $\rho$ is positive, so the real part of the second eigen value is negative. Because the values of all compartments are positive, whereas the values of the first and second eigen are negative, so the eigen values of $\lambda_3$ and $\lambda_4$ are either negative or are complex numbers with real numbers negative. Thus the model equation has the root of the part whose real part is negative. So it can be concluded that $E_1$ is a local asymptotic stable point. We get proof Lemma 1 with numerical that explain in sub bab Numerical Simulation.

Next we will look for the Jacobian matrix in the human population at the equilibrium point $E_2 = (s^*, e^*, t^*, q^*)$:

$$
J(E_2) = 
\begin{bmatrix}
A & 0 & B & 0 \\
B & -\beta p - \mu & a(\beta \theta p + \beta \mu p + \theta \mu p + \mu^2) & 0 \\
0 & -\beta p & -\theta - \mu & 0 \\
0 & 0 & \theta & -\rho - \mu
\end{bmatrix}
$$

With: $A = -\alpha(\frac{-\alpha \beta p + \beta \mu p + \beta \mu^2 + \mu^3}{(\beta \theta p + \beta \mu p + \theta \mu p + \mu^2)} - \mu, B = -\alpha(\frac{\beta \theta p + \beta \mu p + \theta \mu p + \mu^2}{a \beta p} - \mu^2), C = \alpha(\frac{-\alpha \beta p + \beta \mu p + \beta \mu^2 + \mu^3}{(\beta \theta p + \beta \mu p + \theta \mu p + \mu^2)} - \mu^2)$.

The eigen value is obtained from $det(J(E_2) - \lambda I) = 0$, the characteristic equation is obtained according to Routh-Hurwitz criteria, it is said to be asymptotically local if the eigen value of the real part is negative [13]. By looking for characteristic and qualifying equations $b_1, b_2, b_3 > 0$ and $b_1b_2 - b_3 > 0$

From according above, we use Maple 18 software to proof that $E_2$ is stability asymptotically with qualifying Routh-Hurwitz criteria, and we get characteristic equation with $b_1, b_2, b_3$ and $b_0 > 0$ and $b_1b_2 - b_3 > 0$ so we can conclude that $E_2$ is asymptotic stability equilibrium [12]. We get proof if $E_2$ is asymptotic stability equilibrium with numerical that explain in sub bab Numerical Simulation.

6. Numerical Simulation

The numerical simulation in this paper aims to see the spread of Anthrax disease. The initial population number is set as follows: $S(0) = 80.738, E(0) = 41.61, I_s(0) = 41.756, Q(0) = 23.798, R(0) = 415.437, N(t) = 1.695.306$. $S(t_1) = 549.936, E(t_1) = 283.421, I(t_1) = 284.415, Q(t_1) = 162.097, R(t) = 415.437.$ With parameter: Incubation Period 12 until 14 day, $\delta = 43.2/day = 0.72, \mu = 43.2/day = 0.72, \alpha = 0.1134/day = 0.002, \beta = 1.03, \theta = 18/day = 0.3, p = \frac{1}{10} = \frac{1}{3} = 0.08, \rho = 46.8/day = 0.78$.

So from initial population number above we can proof Lemma 1 that $\lambda_1 = -0.72, \lambda_2 = -1.50, \lambda_3 = -0.21628$ and $\lambda_4 = -0.80212$ and we can proof that $b_1 = 4.89, b_2 = 5.17, b_3 = 1.77 > 0$ and $b_1b_2 - b_3 = 23.535 > 0.$ With the help of Maple 18 software using parameter above. Simulation model with quarantine is done for case $R_0 > 0$, taken $= 0.002$ From parameter above we get $R_0 = 4966.31 > 0$ with $E_1 = \left(\frac{\delta}{\mu}, 0, 0, 0\right)$ and $E_2 = (s^*, e^*, t^*, q^*) = (33.72, 4455.413, 359.928, 71.986)$. So we can get graph in Figure 3, Figure 4, Figure 5, and Figure 6.
Figure 3. Susceptible Graph
It appears that the growth rate of susceptible cell population decreases. This happens because the susceptible cell population is infected with the Bacteria and enters the infectious group. At the rate of susceptible cell growth it is seen that this population will not change at a particular time \( t \). In such circumstances, the system is in equilibrium.

Figure 4. Exposed Graph
This is a figure shows Exposed chart, Exposed cell proportion is up and down. This increase is due to susceptible cells infected and eventually become infectious cell groups. But then the infectious cell goes down to the point where the movement of the infected cell is unchanged or in equilibrium. This decrease is due to the absence of the addition of susceptible cells into infected cells.

Figure 5. Infected Graph
This is a figure shows the infected graph decreased at a certain time \( t \). This decrease occurs because the infected cells also decreased. The population of this Bacteria will continue to decrease to the extent that the growth rate of the Bacteria does not change or in a state of equilibrium. Based on numerical results, Bacteria population in equilibrium is 0 at a certain time \( t \), meaning Infected has switched to recovered.

Figure 6. Recovered in 10 year future
This is a figure shows Recovered in 10 year future

7. Conclusion
Mathematical model of Anthrax disease with quarantine is different with Mathematical model of Anthrax without quarantine, it is seen that the graphs have not significant differences, but the model charts with quarantine and without quarantine are not identical. So it can be concluded that the quarantine compartment in Anthrax give positive effect on the spread of Anthrax disease in humans. The conclusion that can be drawn from the above results is the mathematical model of human population Anthrax disease with quarantine better than human population Anthrax disease without quarantine.

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