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Mathematical Analysis of Streptococcus Suis Infection in Pig-Human Population by Riemann-Liouville's Fractional Operator

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Abstract: We addressed a mathematical model for Streptococcus Suis, an uncommon infectious illness that is contaminated, in the current paper. The pig infection that eventually infects people is the source of the illness Streptococcus suis. This disease manifests in a highly severe form in human transmissions, with the potential for both significant sickness and death. Seven population groups (some from human populations and some from pig populations as well) have been examined in this article. We have analysed and studied the given mathematical model of the illness using the Riemann Liouville's fractional derivative and Laplace transformation. Using a graphical representation of the solutions, we have also confirmed their existence and oneness.

Keywords: Streptococcus Suis, mathematical model, existence and uniqueness, Riemann-Liouville's fractional derivative, stability analysis, Laplace transformation.

1 Introduction and Background

These days, one of the serious issues on the planet is zoonotic microorganism like SARS, pandemic flu H1N1, Avian flu, West Nile infection and Novel Coronavirus [1,2,3]. Streptococcus Suis is a disease which is generally tracked down in pigs all over the planet. This microorganism is primarily found in the swine's upper respiratory tract, genitalia, and intestinal areas [4,5]. The primary expert of septic and encephalitis in swine is the Gram-positive, shaped bacterium known as Suis [6,7]. Sickness can spread from one swine to another in a farm very quickly. Streptococcus suis has been reported to cause roughly 20 percent of pig deaths. Serotypes 1 to 31, 33, and 1 can all be grouped together under this category [8,9,10]. Pigs are typically found to have serotypes 1 through 9 and 14 all around the world. The primary human who contracted Streptococcus suis was located in Denmark in 1968. Suis can transfer from pigs to people, as the current situation indicates. Serotype 2 is taken into account because it is frequently found in human diseases, however occasionally the contaminations are caused by serotypes 4,5,9,14,16,21,24, and 31 [11,12,13,14]. Fever, migraines, meningitis, septicemia, joint pain, pneumonia, and hearing loss are typical adverse symptoms of this virus. The numerical display became a crucial tool for illustrating the components of the infection in order to stop the spread of the disease. They can make a number of assumptions about how the illness will behave in the future. The model's arrangements can be recreated while still adhering to the restrictions from the conjecture. As of late, numerous numerical models have been utilized to portray the way of behaving of the irresistible infection. The evenness and unevenness ideas can be connected to the plague model [15,16,17,18]. The proposed models consider the transmission on pigs as it were. Nonetheless, there has been an absence of exploration thinking about the sickness transmission among pigs and people.
In current article, we are going to analyze the problem with the help of mathematical modeling ([19,20,21,22,23]) and fractional calculus. Mathematical modeling is the essential tool in today's scenario for forecasting the impact and consequences of different factors. Modeling is widely being used in many fields including medical field, engineering

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sector, production sector etc. The best and recent example is prediction of covid 19. When modeling is used together with fractional calculus then it explains many typical phenomenon very well. Fractional calculus has vast background and explains its advantage and existence quite well. In recent time, extensive research is going on with the help of fractional calculus since it is attracting many researchers, scientists as well. fractional calculus is much in demand just because of the fact that we can analyze the behaviour of different factors affecting the problem, at very micro level and we can forecast as accurate as possible. In this article, we have put up a numerical model to represent how Streptococcus suis spreads across humans and swines. We have separated the number of inhabitants in pigs and people in 4 and 3 subclasses, separately. We have additionally taken a look at the presence and security of the arrangement of the model.

2 Preliminaries

In this segment, we are going to give brief information about the basic definitions of the operator and transformation used in the paper-

2.1 Riemann-Liouville's fractional operator

The Riemann-Liouville's fractional operator is explained below-

$$ {}^{RL}D_x^{\alpha}\{f(x)\} = \frac{1}{\Gamma(n-\alpha)}\frac{d^n}{dx^n}\int_0^x (x-y)^{n-\alpha-1} f(y)dy \tag{1}$$

where α is the order of the derivative and $0 < \alpha < 1$.

2.2 Laplace Transform

The Laplace transformation ([24]) is one of the important transform in mathematics. It usually converts the system to algebraic system which is easily solvable. The Laplace transform of $f(t)$ is represented by $L\{f(t)\}$ and is explained as:

$$L\{f(t)\} = \int_0^{\infty} e^{-st} f(t)dt, \ \ s > 0. \tag{2}$$

2.3 Laplace transform of Riemann-Liouville's fractional operator

The Laplace transform of the Riemann-Liouville's fractional operator of order α is defined below:

$$L\left[{}^{RL}D_t^{\alpha}\{f(t)\}\right] = s^{\alpha}F(s) - \sum_{k=0}^{n-1} s^{n-k-1}\left[D^k I^{n-\alpha} f(t)\right]_{t=0}, \ \ n-1 < \alpha < n \tag{3}$$

or sometimes we also used the following definition too-

$$L\left[{}^{RL}D_t^{\alpha}\{f(t)\}\right] = s^{\alpha}F(s) - s^{\alpha-1}f(0). \tag{4}$$

The paper is organized as follows; fragment 1 arrangements with the start of the issue, area 2 contains the pre-requirements, Section 3 is having the proposed mathematical model, portion 4 deals with the uniqueness and existence of the solution, segment 5 contains the numerical solution of the model by Laplace transform. Section 6 contains the stability analysis of the model while segment 7 is having mathematical and graphical conversation part. Last section manages the end and gauging of the issue.

3 Mathematical Model

In this section, we'll describe the hypothetical [25,26,27,28,29,30] scheme for how the Streptococcus Suis disease spreads to humans and pigs. We suggest the SIQR-SIR model as an alternative summary model of Streptococcus suis contamination in light of the outdated study of disease transmission model [31,32]. There are some ecological facts, such as temperature and relative humidity. As a result, we think about how the air's humidity affects the spread of disease in the pig ranch. There are two subpopulations within the studied population. These are the populations of pigs and people. Then, four and three subclasses are established for the two subpopulations of swines and humans, respectively. These are pig defenseless class (S_p), pig irresistible class (I_p), pig confined class (Q_p), pig recuperation class (R_p), human susceptible class (S_h), human irresistible class (I_h) and human recuperation class (R_h) . We anticipate that $N(t)$ is whole public at time t,

$$S_p(t)+I_p(t)+Q_p(t)+R_p(t)=N_p(t), \tag{5}$$

and

$$S_h(t)+I_h(t)+R_h(t)=N_h(t). \tag{6}$$

Furthermore,

$$S_p(t)+I_p(t)+Q_p(t)+R_p(t)+S_h(t)+I_h(t)+R_h(t)=N_h(t)+N_p(t)=N(t) \tag{7}$$

If the total population of humans is N_h and whole inhabitants of pigs is N_p at time t. Now, we may formulate dynamic connections for $N_p(t)$ and $N_h(t)$ as follows:

$$\frac{dN_p(t)}{dt}=\frac{dS_p(t)}{dt}+\frac{dI_p(t)}{dt}+\frac{dQ_p(t)}{dt}+\frac{dR_p(t)}{dt}, \tag{8}$$

$$\frac{dN_h(t)}{dt}=\frac{dS_h(t)}{dt}+\frac{dI_h(t)}{dt}+\frac{dR_h(t)}{dt}. \tag{9}$$

This disease in swine can be depicted by $\beta_{1(1)}MS_pI_p$ and new contamination in human can be portrayed by $\beta_{2(1)}S_hI_p+\beta_{3(1)}S_hI_h$ here each diseased pig in the susceptible class has a transmission coefficient per unit of time of $\beta_{1(1)}$, and each member of the susceptible class who comes into contact with infected pigs has a transmission coefficient per unit of time of $\beta_{2(1)}$. The amount of moisture in the air is M, and the transmission coefficient per person in susceptible class in contact with infected is $\beta_{3(1)}$. We also presume that a pig cannot contract the sickness from a human. All boundaries are supposed to be positive throughout the entire article. The following arrangement of differential equations can be used to address the model of sickness transmission by Streptococcus suis:

$$\frac{dS_p}{dt}=N_1-b_1S_p-\beta_{1(1)}MS_pI_p, \tag{10}$$

$$\frac{dI_p}{dt}=\beta_{1(1)}MS_pI_p-a_1I_p-b_1I_p-\delta_1I_p, \tag{11}$$

$$\frac{dQ_p}{dt}=\delta_1I_p-a_1Q_p-b_1Q_p-\varepsilon_1Q_p, \tag{12}$$

$$\frac{dR_p}{dt}=\varepsilon_1Q_p-b_1R_p, \tag{13}$$

$$\frac{dS_h}{dt}=N_2-\beta_{2(1)}S_hI_p-\beta_{3(1)}S_hI_h-\mu_1S_h, \tag{14}$$

$$\frac{dI_h}{dt}=\beta_{2(1)}S_hI_p+\beta_{3(1)}S_hI_h-\alpha_1I_h-\gamma_1I_h-\mu_1I_h, \tag{15}$$

$$\frac{dR_h}{dt}=\gamma_1I_h-\mu_1R_h. \tag{16}$$

where b_1 is the ejection rate for pigs, a_1 is the ejection rate brought on by illness, the rate in pigs from the enticing class to the disconnected class is δ_1, ε_1 is the rate of infection from detached class to recovered class, μ_1 is average mortality rate for humans, the mortality rate attributable to sickness is α_1, and the rate at which an infectious class

transmits information to a recovery class is γ_1. The model is legitimate provided that $a_1 \leq b_1$ and $\alpha_1 \leq \mu_1$. $S_p(0)$, $I_p(0)$, $Q_p(0)$, $R_p(0)$, $S_h(0)$, $I_h(0)$ and $R_h(0)$ denote the underlying population, for instance at time t=0. The upsides of populace classes $S_p(t), I_p(t), Q_p(t), R_p(t), S_h(t), I_h(t), R_h(t)$ at time t are non-negative values. Now, we define a new model based on Riemann- Liouville's fractional differential operator, also we see that the RHS of the system has the unit (dimension) $time^{-1}$ but we have changed the derivative order to α, so the dimension at the LHS of system becomes $time^{-\alpha}$. To overcome this mismatching, we have modified our system in following way:

$$\left.\begin{array}{l} {}^{RL}D_t^{\alpha}\left\{S_p\right\} = N_1 - b_1^{\alpha} S_p - \beta_{1(1)}^{\alpha} M S_p I_p \\ {}^{RL}D_t^{\alpha}\left\{I_p\right\} = \beta_{1(1)}^{\alpha} M S_p I_p - a_1^{\alpha} I_p - b_1^{\alpha} I_p - \delta_1^{\alpha} I_p \\ {}^{RL}D_t^{\alpha}\left\{Q_p\right\} = \delta_1^{\alpha} I_p - a_1^{\alpha} Q_p - b_1^{\alpha} Q_p - \varepsilon_1^{\alpha} Q_p \\ {}^{RL}D_t^{\alpha}\left\{R_p\right\} = \varepsilon_1^{\alpha} Q_p - b_1^{\alpha} R_p \\ {}^{RL}D_t^{\alpha}\left\{S_h\right\} = N_2 - \beta_{2(1)}^{\alpha} S_h I_p - \beta_{3(1)}^{\alpha} S_h I_h - \mu_1^{\alpha} S_h \\ {}^{RL}D_t^{\alpha}\left\{I_h\right\} = \beta_{2(1)}^{\alpha} S_h I_p + \beta_{3(1)}^{\alpha} S_h I_h - \alpha_1^{\alpha} I_h - \gamma_1^{\alpha} I_h - \mu_1^{\alpha} I_h \\ {}^{RL}D_t^{\alpha}\left\{R_h\right\} = \gamma_1^{\alpha} I_h - \mu_1^{\alpha} R_h \end{array}\right\} \tag{17}$$

Further, for the sake of convenience, we have replaced the power terms by some other constant where $b_1^{\alpha} = b$, $\beta_{1(1)}^{\alpha} = \beta_1$, $a_1^{\alpha} = a$, $\delta_1^{\alpha} = \delta$, $\varepsilon_1^{\alpha} = \varepsilon$, $\beta_{2(1)}^{\alpha} = \beta_2$, $\beta_{3(1)}^{\alpha} = \beta_3$, $\mu_1^{\alpha} = \mu$, $\alpha_1^{\alpha} = \alpha$ and $\gamma_1^{\alpha} = \gamma$. Then the system reduces to:

$$\left.\begin{array}{l} {}^{RL}D_t^{\alpha}\left\{S_p\right\} = N_1 - bS_p - \beta_1 M S_p I_p \\ {}^{RL}D_t^{\alpha}\left\{I_p\right\} = \beta_1 M S_p I_p - aI_p - bI_p - \delta I_p \\ {}^{RL}D_t^{\alpha}\left\{Q_p\right\} = \delta I_p - aQ_p - bQ_p - \varepsilon Q_p \\ {}^{RL}D_t^{\alpha}\left\{R_p\right\} = \varepsilon Q_p - bR_p \\ {}^{RL}D_t^{\alpha}\left\{S_h\right\} = N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h \\ {}^{RL}D_t^{\alpha}\left\{I_h\right\} = \beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h \\ {}^{RL}D_t^{\alpha}\left\{R_h\right\} = \gamma I_h - \mu R_h \end{array}\right\} \tag{18}$$

where $0 < \alpha < 1$.

4 Existence and Uniqueness of the Solution

Theorem 1 Define k_1, k_2, k_3, k_4, k_5, k_6 and k_7 for the given system of equations and also find their relationships.
Proof Since we have the system defining the Streptococcus Suis as given below:

$$\left.\begin{array}{l} {}^{RL}D_t^{\alpha}\left\{S_p\right\} = N_1 - bS_p - \beta_1 M S_p I_p \\ {}^{RL}D_t^{\alpha}\left\{I_p\right\} = \beta_1 M S_p I_p - aI_p - bI_p - \delta I_p \\ {}^{RL}D_t^{\alpha}\left\{Q_p\right\} = \delta I_p - aQ_p - bQ_p - \varepsilon Q_p \\ {}^{RL}D_t^{\alpha}\left\{R_p\right\} = \varepsilon Q_p - bR_p \\ {}^{RL}D_t^{\alpha}\left\{S_h\right\} = N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h \\ {}^{RL}D_t^{\alpha}\left\{I_h\right\} = \beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h \\ {}^{RL}D_t^{\alpha}\left\{R_h\right\} = \gamma I_h - \mu R_h \end{array}\right\} \tag{19}$$

Now, applying the fundamental theorem of calculus, we have:

$$\left.\begin{array}{l} S_p(t) - S_p(0) = {}^{RL}I_t^{\alpha}\left[N_1 - bS_p - \beta_1 M S_p I_p\right], \\ I_p(t) - I_p(0) = {}^{RL}I_t^{\alpha}\left[\beta_1 M S_p I_p - aI_p - bI_p - \delta I_p\right], \\ Q_p(t) - Q_p(0) = {}^{RL}I_t^{\alpha}\left[\delta I_p - aQ_p - bQ_p - \varepsilon Q_p\right], \\ R_p(t) - R_p(0) = {}^{RL}I_t^{\alpha}\left[\varepsilon Q_p - bR_p\right], \\ S_h(t) - S_h(0) = {}^{RL}I_t^{\alpha}\left[N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h\right], \\ I_h(t) - I_h(0) = {}^{RL}I_t^{\alpha}\left[\beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h\right], \\ R_h(t) - R_h(0) = {}^{RL}I_t^{\alpha}\left[\gamma I_h - \mu R_h\right]. \end{array}\right\} \tag{20}$$

Now, considering the one equation at a time, we have:

$$S_p(t) - S_p(0) = {}^{RL}I_t^{\alpha}\left[N_1 - bS_p - \beta_1 M S_p I_p\right],$$

or

$$S_p(t)-S_p(0)=\frac{1}{\Gamma\alpha}\int_0^x\left\{N_1-bS_p-\beta_1MS_pI_p\right\}(x-\upsilon)^{\alpha-1}d\upsilon,$$

or

$$S_p(t)=S_p(0)+\frac{1}{\Gamma\alpha}\int_0^x\left\{N_1-bS_p-\beta_1MS_pI_p\right\}(x-\upsilon)^{\alpha-1}d\upsilon.$$

Let us consider the following kernel;

$$k_1=N_1-bS_p-\beta_1MS_pI_p, \tag{21}$$

Similarly, we can find the other kernels as well, given below:

$$k_2=\beta_1MS_pI_p-aI_p-bI_p-\delta I_p, \tag{22}$$

$$k_3=\delta I_p-aQ_p-bQ_p-\varepsilon Q_p, \tag{23}$$

$$k_4=\varepsilon Q_p-bR_p, \tag{24}$$

$$k_5=N_2-\beta_2S_hI_p-\beta_3S_hI_h-\mu S_h, \tag{25}$$

$$k_6=\beta_2S_hI_p+\beta_3S_hI_h-\alpha I_h-\gamma I_h-\mu I_h, \tag{26}$$

and

$$k_7=\gamma I_h-\mu R_h. \tag{27}$$

Theorem 2 Establish that all kernels i.e. k_1, k_2, k_3, k_4, k_5, k_6 and k_7 satisfy the Lipschitz condition [33,34].
Proof Initially, we will prove the Lipschitz condition for k_1. Now suppose that S_p and S_{p_1} are two functions, then

$$\left\|k_1(t,S_p)-k_1(t,S_{p_1})\right\|=\left\|(N_1-bS_p-\beta_1MS_pI_p)-(N_1-bS_{p_1}-\beta_1MS_{p_1}I_p)\right\|,$$

$$\left\|k_1(t,S_p)-k_1(t,S_{p_1})\right\|=\left\|-bS_p-\beta_1MS_pI_p+bS_{p_1}+\beta_1MS_{p_1}I_p\right\|,$$

$$\left\|k_1(t,S_p)-k_1(t,S_{p_1})\right\|=\left\|b(S_{p_1}-S_p)+\beta_1MI_p(S_{p_1}-S_p)\right\|,$$

$$\left\|k_1(t,S_p)-k_1(t,S_{p_1})\right\|=\left\|(S_{p_1}-S_p)(b+\beta_1MI_p)\right\|,$$

$$\left\|k_1(t,S_p)-k_1(t,S_{p_1})\right\|\leq\left\|(S_{p_1}-S_p)\right\|\left\|(b+\beta_1MI_p)\right\|,$$

$$\left\|k_1(t,S_p)-k_1(t,S_{p_1})\right\|\leq H\left\|(S_{p_1}-S_p)\right\|,$$

where $\left\|(b+\beta_1MI_p)\right\|\leq H$. In the same way, we get

$$\left\|k_2(t,I_p)-k_2(t,I_{p_1})\right\|=\left\|(\beta_1MS_pI_p-aI_p-bI_p-\delta I_p)-(\beta_1MS_pI_{p_1}-aI_{p_1}-bI_{p_1}-\delta I_{p_1})\right\|,$$

or

$$\left\|k_2(t,I_p)-k_2(t,I_{p_1})\right\|=\left\|-\beta_1MS_p(I_{p_1}-I_p)+a(I_{p_1}-I_p)+b(I_{p_1}-I_p)+\delta(I_{p_1}-I_p)\right\|,$$

$$\left\|k_2(t,I_p)-k_2(t,I_{p_1})\right\|=\left\|(I_{p_1}-I_p)(a+b+\delta-\beta_1MS_p)\right\|,$$

$$\left\|k_2(t,I_p)-k_2(t,I_{p_1})\right\|\leq\left\|(I_{p_1}-I_p)\right\|\left\|(a+b+\delta-\beta_1MS_p)\right\|,$$

$$\left\|k_2(t,I_p)-k_2(t,I_{p_1})\right\| \leq H_1 \left\|(I_{p_1}-I_p)\right\|,$$

where $\left\|(a+b+\delta-\beta_1 MS_p)\right\| \leq H_1$.
In the same manner, we get other expressions as well

$$\left\|k_3(t,Q_p)-k_3(t,Q_{p_1})\right\| \leq H_2 \left\|(Q_{p_1}-Q_p)\right\|,$$

where $\|(a+b+\varepsilon)\| \leq H_2$.

$$\left\|k_4(t,R_p)-k_4(t,R_{p_1})\right\| \leq H_3 \left\|(R_{p_1}-R_p)\right\|,$$

where $\|b\| \leq H_3$.

$$\left\|k_5(t,S_h)-k_5(t,S_{h_1})\right\| \leq H_4 \left\|\left(S_{h_1}-S_h\right)\right\|,$$

where $\left\|(\beta_2 I_p+\beta_3 I_h+\mu)\right\| \leq H_4$.

$$\left\|k_6(t,I_h)-k_6(t,I_{h_1})\right\| \leq H_5 \left\|\left(I_{h_1}-I_h\right)\right\|,$$

where $\|(\alpha+\gamma+\mu-\beta_3 S_h)\| \leq H_5$,
and

$$\left\|k_7(t,R_h)-k_7(t,R_{h_1})\right\| \leq H_6 \left\|\left(R_{h_1}-R_h\right)\right\|.$$

where $\|\mu\| \leq H_6$.

Now, consider the recursive relation, given as follows:

$$S_{p(n)}(t) = S_p(0) + \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_{p(n-1)}\right)(x-\upsilon)^{\alpha-1}d\upsilon, \tag{28}$$

Suppose that $U_n(t) = S_{p(n)}(t) - S_{p(n-1)}(t)$ So,

$$U_n(t) = \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_{p(n-1)}\right)(x-\upsilon)^{\alpha-1}d\upsilon - \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_{p(n-2)}\right)(x-\upsilon)^{\alpha-1}d\upsilon,$$

$$U_n(t) = \frac{1}{\Gamma\alpha}\int_0^x \left\{k_1\left(\upsilon, S_{p(n-1)}\right) - k_1\left(\upsilon, S_{p(n-2)}\right)\right\}(x-\upsilon)^{\alpha-1}d\upsilon.$$

Taking norms both sides, we have

$$\|U_n(t)\| = \frac{1}{\Gamma\alpha}\left\|\int_0^x \left\{k_1\left(\upsilon, S_{p(n-1)}\right) - k_1\left(\upsilon, S_{p(n-2)}\right)\right\}(x-\upsilon)^{\alpha-1}d\upsilon\right\|,$$

or

$$\|U_n(t)\| = \frac{1}{\Gamma\alpha}\int_0^x \left[\left\|\left\{k_1\left(\upsilon, S_{p(n-1)}\right) - k_1\left(\upsilon, S_{p(n-2)}\right)\right\}\right\|\left\|(x-\upsilon)^{\alpha-1}\right\|\right]d\upsilon.$$

Since k_1 satisfies Lipschitz condition,

$$\|U_n(t)\| = \frac{1}{\Gamma\alpha}H\int_0^x \left\|S_{p(n-1)} - S_{p(n-2)}\right\|\left\|(x-\upsilon)^{\alpha-1}\right\|d\upsilon. \tag{29}$$

In the same manner, we can find other expressions too,

$$\|V_n(t)\| = \frac{1}{\Gamma\alpha}H_1\int_0^x \left\|I_{p(n-1)} - I_{p(n-2)}\right\|\left\|(x-\upsilon)^{\alpha-1}\right\|d\upsilon, \tag{30}$$

$$\|W_n(t)\| = \frac{1}{\Gamma\alpha} H_2 \int_0^x \left\|Q_{p(n-1)} - Q_{p(n-2)}\right\| \left\|(x-\upsilon)^{\alpha-1}\right\| d\upsilon, \tag{31}$$

$$\|T_n(t)\| = \frac{1}{\Gamma\alpha} H_3 \int_0^x \left\|R_{p(n-1)} - R_{p(n-2)}\right\| \left\|(x-\upsilon)^{\alpha-1}\right\| d\upsilon, \tag{32}$$

$$\|X_n(t)\| = \frac{1}{\Gamma\alpha} H_4 \int_0^x \left\|S_{h(n-1)} - S_{h(n-2)}\right\| \left\|(x-\upsilon)^{\alpha-1}\right\| d\upsilon, \tag{33}$$

$$\|Y_n(t)\| = \frac{1}{\Gamma\alpha} H_5 \int_0^x \left\|I_{h(n-1)} - I_{h(n-2)}\right\| \left\|(x-\upsilon)^{\alpha-1}\right\| d\upsilon, \tag{34}$$

and

$$\|Z_n(t)\| = \frac{1}{\Gamma\alpha} H_6 \int_0^x \left\|R_{h(n-1)} - R_{h(n-2)}\right\| \left\|(x-\upsilon)^{\alpha-1}\right\| d\upsilon. \tag{35}$$

Theorem 3 Prove that the disease model with fractional order is a minimum system of Streptococcus Suis model.
Proof Since, we can see that equations (29)-(35) are bounded and we have also shown that kernels satisfy Lipschitz condition, so the following results are obtained from the equations (29)-(35) using the iterative technique:

$$\|U_n(t)\| \leq \left\|S_p(0)\right\| + \left\{\frac{1}{\alpha\Gamma\alpha} H t^{\alpha}\right\}^n,$$

$$\|V_n(t)\| \leq \left\|I_p(0)\right\| + \left\{\frac{1}{\alpha\Gamma\alpha} H_1 t^{\alpha}\right\}^n,$$

$$\|W_n(t)\| \leq \left\|Q_p(0)\right\| + \left\{\frac{1}{\alpha\Gamma\alpha} H_2 t^{\alpha}\right\}^n,$$

$$\|T_n(t)\| \leq \left\|R_p(0)\right\| + \left\{\frac{1}{\alpha\Gamma\alpha} H_3 t^{\alpha}\right\}^n,$$

$$\|X_n(t)\| \leq \|S_h(0)\| + \left\{\frac{1}{\alpha\Gamma\alpha} H_4 t^{\alpha}\right\}^n,$$

$$\|Y_n(t)\| \leq \|I_h(0)\| + \left\{\frac{1}{\alpha\Gamma\alpha} H_5 t^{\alpha}\right\}^n,$$

and

$$\|Z_n(t)\| \leq \|R_h(0)\| + \left\{\frac{1}{\alpha\Gamma\alpha} H_6 t^{\alpha}\right\}^n.$$

Hence, the existence of solution is checked and which is found to be continuous. So, we have

$$S_p(t) = S_{p(n)}(t) + P_n(t),$$

$$I_p(t) = I_{p(n)}(t) + B_n(t),$$

$$Q_p(t) = Q_{p(n)}(t) + C_n(t),$$

$$R_p(t) = R_{p(n)}(t) + D_n(t),$$

$$S_h(t) = S_{h(n)}(t) + E_n(t),$$

$$I_h(t) = I_{h(n)}(t) + F_n(t),$$

and

$$R_h(t) = R_{h(n)}(t) + J_n(t),$$

where $P_n(t), B_n(t), C_n(t), D_n(t), E_n(t), F_n(t)\, and\, J_n(t)$ are the reminder terms of the series solutions. So,

$$S_p(t) - S_{p(n)}(t) = \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_{p(n)}\right)(x-\upsilon)^{\alpha-1}d\upsilon,$$

or

$$S_p(t) - S_{p(n)}(t) = \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_p - P_n(\upsilon)\right)(x-\upsilon)^{\alpha-1}d\upsilon,$$

or

$$S_p(t) - S_p(0) - \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_p\right)(x-\upsilon)^{\alpha-1}d\upsilon = P_n(t) + \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_p - P_n(\upsilon)\right)(x-\upsilon)^{\alpha-1}d\upsilon.$$

Now

$$\left\| S_p(t) - S_p(0) - \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_p\right)(x-\upsilon)^{\alpha-1}d\upsilon \right\| \leq \|P_n(t)\| + \left\{\frac{1}{\alpha\Gamma\alpha}Ht^{\alpha}\right\}\|P_n(t)\|.$$

Now taking $n \to \infty$, we get

$$S_p(t) = S_p(0) + \frac{1}{\Gamma\alpha}\int_0^x k_1\left(\upsilon, S_p\right)(x-\upsilon)^{\alpha-1}d\upsilon. \tag{36}$$

We can conclude that the provided system's solution exists since we can also discover the other expressions in a similar manner.

Theorem 4 Show that the given system of equation representing the disease has a unique solution.
Proof Let's assume that the given system has another set of solutions in order to demonstrate the solution's uniqueness. As we are only demonstrating the system's initial equation at this time, suppose that $S_{p(1)}(t)$ be another solution, hence

$$S_p(t) - S_{p(1)}(t) = \frac{1}{\Gamma\alpha}\int_0^x \left\{k_1\left(\upsilon, S_p\right) - k_1\left(\upsilon, S_{p(1)}\right)\right\}(x-\upsilon)^{\alpha-1}d\upsilon.$$

Now, taking norms both sides, we have

$$\left\|S_p(t) - S_{p(1)}(t)\right\| = \frac{1}{\Gamma\alpha}\int_0^x \left\|k_1\left(\upsilon, S_p\right) - k_1\left(\upsilon, S_{p(1)}\right)\right\| \left\|(x-\upsilon)^{\alpha-1}\right\| d\upsilon,$$

Now using Lipschitz condition, we have

$$\left\|S_p(t) - S_{p(1)}(t)\right\| < \left\{\frac{1}{\alpha\Gamma\alpha}Ht^{\alpha}\right\}^n,$$

which is true for all n, so $S_p(t) = S_{p(1)}(t)$, $I_p(t) = I_{p(1)}(t)$, $Q_p(t) = Q_{p(1)}(t)$, $R_p(t) = R_{p(1)}(t)$, $S_h(t) = S_{h(1)}(t)$, $I_h(t) = I_{h(1)}(t)$ and $R_h(t) = R_{h(1)}(t)$.
Hence, it shows that system has a unique solution.

5 Solution of the Model by Using Laplace Transformation

We are having the mathematical model denoting the disease Streptococcus Suis as follows. In this section, we are going to apply the Laplace transform [33,34,35,36] in our modified disease system for the mathematical analysis ([30,37,38, 39]) of the system.
Now changing the derivatives to Riemann Lioville's fractional derivatives, we have

$$\begin{aligned}
&{}^{RL}D_t^{\alpha}\{S_p\} = N_1 - bS_p - \beta_1 M S_p I_p,\\
&{}^{RL}D_t^{\alpha}\{I_p\} = \beta_1 M S_p I_p - aI_p - bI_p - \delta I_p,\\
&{}^{RL}D_t^{\alpha}\{Q_p\} = \delta I_p - aQ_p - bQ_p - \varepsilon Q_p,\\
&{}^{RL}D_t^{\alpha}\{R_p\} = \varepsilon Q_p - bR_p,\\
&{}^{RL}D_t^{\alpha}\{S_h\} = N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h,\\
&{}^{RL}D_t^{\alpha}\{I_h\} = \beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h,\\
&{}^{RL}D_t^{\alpha}\{R_h\} = \gamma I_h - \mu R_h.
\end{aligned} \tag{37}$$

Since we know that

$$L\left\{{}^{RL}D^{\alpha}f(t)\right\} = s^{\alpha}F(s) - s^{\alpha-1}f(0)$$

where $0 < \alpha < 1$.

Now applying Laplace transform both sides,

$$\left.\begin{aligned}
&L\left[{}^{RL}D_t^{\alpha}\{S_p\}\right] = L\{N_1 - bS_p - \beta_1 M S_p I_p\},\\
&L\left[{}^{RL}D_t^{\alpha}\{I_p\}\right] = L\{\beta_1 M S_p I_p - aI_p - bI_p - \delta I_p\},\\
&L\left[{}^{RL}D_t^{\alpha}\{Q_p\}\right] = L\{\delta I_p - aQ_p - bQ_p - \varepsilon Q_p\},\\
&L\left[{}^{RL}D_t^{\alpha}\{R_p\}\right] = L\{\varepsilon Q_p - bR_p\},\\
&L\left[{}^{RL}D_t^{\alpha}\{S_h\}\right] = L\{N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h\},\\
&L\left[{}^{RL}D_t^{\alpha}\{I_h\}\right] = L\{\beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h\},\\
&\textit{and}\\
&L\left[{}^{RL}D_t^{\alpha}\{R_h\}\right] = L\{\gamma I_h - \mu R_h\}.
\end{aligned}\right\} \tag{38}$$

Hence, from the first equation of the system, we have

$$L\left[{}^{RL}D_t^{\alpha}\{S_p\}\right] = L\{N_1 - bS_p - \beta_1 M S_p I_p\},$$

doing some simplifications, we get

$$F(s) = \frac{S_p(0)}{s} + \frac{1}{s^{\alpha}}L\{N_1 - bS_p - \beta_1 M S_p I_p\}.$$

Now, again applying inverse Laplace transform both sides,

$$S_p = S_p(0) + L^{-1}\left[\frac{1}{s^{\alpha}}L\{N_1 - bS_p - \beta_1 M S_p I_p\}\right].$$

Similarly, from the second equation of the system, we have

$$L\left[{}^{RL}D_t^{\alpha}\{I_p\}\right] = L\{\beta_1 M S_p I_p - aI_p - bI_p - \delta I_p\},$$

or

$$F(s) = \frac{I_p(0)}{s} + \frac{1}{s^{\alpha}}L\{\beta_1 M S_p I_p - aI_p - bI_p - \delta I_p\}.$$

Now taking the inverse Laplace transform both sides, we get

$$I_p = I_p(0) + L^{-1}\left[\frac{1}{s^{\alpha}}L\{\beta_1 M S_p I_p - aI_p - bI_p - \delta I_p\}\right].$$

In the same way, we get the remaining expressions,

$$Q_p = Q_p(0) + L^{-1}\left[\frac{1}{s^\alpha}L\left\{\delta I_p - aQ_p - bQ_p - \varepsilon Q_p\right\}\right],$$

$$R_p = R_p(0) + L^{-1}\left[\frac{1}{s^\alpha}L\left\{\varepsilon Q_p - bR_p\right\}\right],$$

$$S_h = S_h(0) + L^{-1}\left[\frac{1}{s^\alpha}L\left\{N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h\right\}\right],$$

$$I_h = I_h(0) + L^{-1}\left[\frac{1}{s^\alpha}L\left\{\beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h\right\}\right],$$

and

$$R_h = R_h(0) + L^{-1}\left[\frac{1}{s^\alpha}L\left\{\gamma I_h - \mu R_h\right\}\right].$$

6 Stability Analysis of Model

Theorem 1 Deduce the equilibrium points [40,41,42,43,44] of the model.
Proof We know that the equilibrium points of the system can be found be equating the equations to zero, so

$$\left.\begin{array}{l} N_1 - bS_p - \beta_1 M S_p I_p = 0 \\ \beta_1 M S_p I_p - aI_p - bI_p - \delta I_p = 0 \\ \delta I_p - aQ_p - bQ_p - \varepsilon Q_p = 0 \\ \varepsilon Q_p - bR_p = 0 \\ N_2 - \beta_2 S_h I_p - \beta_3 S_h I_h - \mu S_h = 0 \\ \beta_2 S_h I_p + \beta_3 S_h I_h - \alpha I_h - \gamma I_h - \mu I_h = 0 \\ \gamma I_h - \mu R_h = 0 \end{array}\right\} \tag{39}$$

By above system, we obtain equilibrium points given below, they are-
(1) Disease free equilibrium point

$$E_1 = \left(\frac{N_1}{b}, 0, 0, 0, \frac{N_2}{\mu}, 0, 0\right) \tag{40}$$

(2) Swine disease free equilibrium point

$$E_2 = \left(\frac{N_1}{b}, 0, 0, 0, \frac{A}{\beta_3}, \frac{\beta_3 N_2 - \mu A}{\beta_3 A}, \frac{\gamma}{\mu}\frac{\beta_3 N_2 - \mu A}{\beta_3 A}\right) \tag{41}$$

here $A = \alpha + \gamma + \mu$ and remember that E_2 exists provided that $\beta_3 N_2 - \mu A \geq 0$.
(3) Endemic equilibrium point

$$E_3 = \left(S_p^*, I_p^*, Q_p^*, R_p^*, S_h^*, I_h^*, R_h^*\right) \tag{42}$$

where $S_p^* = \frac{B}{\beta_1 M}$, $I_p^* = \frac{\beta_1 M N_1 - bB}{\beta_1 BM}$, $Q_p^* = \frac{\delta I_p^*}{(a+b+\varepsilon)}$, $R_p^* = \frac{\varepsilon \delta I_p^*}{b(a+b+\varepsilon)}$,
$I_h^* = \frac{1}{2\beta_3 A}\left(X + \sqrt{X^2 + 4A\beta_2\beta_3 N_2 I_p^*}\right)$, $S_h^* = \frac{N_2}{\beta_2 I_p^* + \beta_3 I_h^* + \mu}$ and
$R_h^* = \frac{\gamma I_h^*}{\mu}$ where $X = \beta_3 N_2 - A\left(\beta_2 I_p^* + \mu\right)$, $B = a + b + \delta$.
Note that E_3 exists only when $\beta_1 M N_1 - bB \geq 0$.

Theorem 2 The disease free point E_1 is locally asymptotically stable if $\beta_3 N_2 < \mu A$ and $\beta_1 M N_1 < bB$.
Proof The Jacobian matrix of the given system at E_1 is-

$$J_1 = \begin{bmatrix} -b & -\frac{\beta_1 M N_1}{b} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_1 M N_1}{b} - B & 0 & 0 & 0 & 0 & 0 \\ 0 & \delta & -(a+b+\varepsilon) & 0 & 0 & 0 & 0 \\ 0 & 0 & \varepsilon & -b & 0 & 0 & 0 \\ 0 & -\frac{\beta_2 N_2}{\mu} & 0 & 0 & -\mu & -\frac{\beta_3 N_2}{\mu} & 0 \\ 0 & \frac{\beta_2 N_2}{\mu} & 0 & 0 & 0 & \frac{\beta_3 N_2}{\mu} - A & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma & -\mu \end{bmatrix} \tag{43}$$

The eigenvalues of J_1 are

$$\lambda_1 = \lambda_2 = -b, \lambda_3 = \lambda_4 = -\mu, \lambda_5 = -(a+b+\varepsilon), \lambda_6 = \frac{\beta_1 M N_1}{b} - B$$

and $\lambda_7 = \frac{\beta_3 N_2}{\mu} - A$.
Note that λ_6 and λ_7 are only negative when $\beta_1 M N_1 < bB$ and $\beta_3 N_2 < \mu A$. Hence the disease free equilibrium of the model is locally asymptotically stable when $\beta_1 M N_1 < bB$ and $\beta_3 N_2 < \mu A$.

Theorem 3 The pig disease free point E_2 is locally asymptotically stable if $\beta_3 N_2 > \mu A$ and $\beta_1 M N_1 < bB$.
Proof The Jacobian matrix of the given system at E_2 is-

$$J_2 = \begin{bmatrix} -b & -\frac{\beta_1 M N_1}{b} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_1 M N_1}{b} - B & 0 & 0 & 0 & 0 & 0 \\ 0 & \delta & -(a+b+\varepsilon) & 0 & 0 & 0 & 0 \\ 0 & 0 & \varepsilon & -b & 0 & 0 & 0 \\ 0 & -\frac{\beta_2 A}{\beta_3} & 0 & 0 & -\frac{\beta_3 N_2}{A} & -A & 0 \\ 0 & \frac{\beta_2 A}{\beta_3} & 0 & 0 & \frac{\beta_3 N_2}{A} - \mu & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma & -\mu \end{bmatrix} \tag{44}$$

The corresponding Eigen values are

$$\lambda_1 = \lambda_2 = -b, \lambda_3 = -\mu, \lambda_4 = -(a+b+\varepsilon), \lambda_5 = \frac{\beta_1 M N_1}{b} - B,$$
$$\lambda_6 = \frac{\frac{-\beta_3 N_2}{A} + \sqrt{\frac{\beta_3^2 N_2^2}{A^2} - 4\mu A\left(\frac{\beta_3 N_2}{\mu A} - 1\right)}}{2}$$

and $\lambda_7 = \frac{\frac{-\beta_3 N_2}{A} - \sqrt{\frac{\beta_3^2 N_2^2}{A^2} - 4\mu A\left(\frac{\beta_3 N_2}{\mu A} - 1\right)}}{2}$.
From here, we see that λ_5 is negative if $\beta_1 M N_1 < bB$ and λ_6, λ_7 have negative real part when $\beta_3 N_2 > \mu A$. Hence the pig disease free equilibrium of the model is local asymptotically stable if $\beta_1 M N_1 < bB$ and $\beta_3 N_2 > \mu A$.

Theorem 4 Endemic equilibrium E_3 is locally asymptotically balanced if $\beta_3 N_2 < \mu A$ and $\beta_1 M N_1 > bB$.
Proof The Jacobian matrix of the given system at E_3 is-

$$J_3 = \begin{bmatrix} -b-\Psi_1 & -\Psi_2 & 0 & 0 & 0 & 0 & 0 \\ \Psi_1 & \Psi_2 - B & 0 & 0 & 0 & 0 & 0 \\ 0 & \delta & -(a+b+\varepsilon) & 0 & 0 & 0 & 0 \\ 0 & 0 & \varepsilon & -b & 0 & 0 & 0 \\ 0 & -\beta_2 S_h^* & 0 & 0 & -\Psi_3 - \mu & -\beta_3 S_h^* & 0 \\ 0 & \beta_2 S_h^* & 0 & 0 & \Psi_3 & \beta_3 S_h^* - A & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma & -\mu \end{bmatrix} \tag{45}$$

where $\Psi_1 = \frac{\beta_1 M N_1}{B} - b$, $\Psi_2 = B$ and $\Psi_3 = \frac{-\beta_2(\beta_1 M N_1 - Bb)}{\beta_1 M B} + \beta_3 I_h^*$.
The corresponding Eigen values are

$$\lambda_1 = -b, \lambda_2 = -\mu, \lambda_3 = -(a+b+\varepsilon), \lambda_4 = \frac{-\left[\beta_1 M\left(I_p^* - S_p^*\right) + B + b\right] + Y_1}{2}$$

$$\lambda_5 = \frac{-\left[\beta_1 M\left(I_p^* - S_p^*\right) + B + b\right] - Y_1}{2}, \lambda_6 = \frac{-\left[\beta_2 I_p^* + \beta_3\left(I_h^* - S_h^*\right) + A + \mu\right] + Y_2}{2}$$

and

$$\lambda_7 = \frac{-\left[\beta_2 I_p^* + \beta_3\left(I_h^* - S_h^*\right) + A + \mu\right] - Y_2}{2}$$

where $Y_1 = \sqrt{\left[\beta_1 M\left(I_p^* - S_p^*\right) + B + b\right]^2 - 4\left[\beta_1 M\left(BI_p^* - bS_p^*\right) + Bb\right]}$
and $Y_2 = \sqrt{\left[\beta_2 I_p^* + \beta_3\left(I_h^* - S_h^*\right) + A + \mu\right]^2 - 4\left[\beta_2 A I_p^* + \beta_3 A I_h^* + \mu\left(A - \beta_3 S_h^*\right)\right]}$

From above, it is clear that λ_4 and λ_5 have negative real part if $\beta_1 M N_1 > bB$ and λ_6 and λ_7 have negative real part if $\beta_3 N_2 < \mu A$. Therefore, the system is local asymptotically stable under the given conditions.

7 Numerical Analysis of Model

During the numerical analysis of the proposed model, we have used some numeric values of the populations and the parameters used. The values are given in the following table [45,46]:

S.N.	Symbol	Detail	Numeric Value
1	$S_p(0)$	Initial Pig susceptible	4057
2	$S_h(0)$	Initial Human susceptible	50000
3	$I_p(0)$	Initial Infected Pigs	1000
4	$I_h(0)$	Initial Infected Humans	1000
5	$Q_p(0)$	Initial Isolated Pigs	0
6	$R_p(0)$	Initial Recovered Pigs	0
7	$R_h(0)$	Initial Recovered Humans	0
8	α	Death rate by disease	0.9
9	β_1	Trans.Coeff./unit time/pig contact with infected	0.000365
10	β_2	Trans.Coeff./unit time/soul contact with infected pig	0.1
11	β_3	Trans.Coeff./unit time/soul prone contact with infected	0.000465
12	N_1	The recruitment rate of lone into swine farm	3275
13	N_2	The recruitment rate of lone in humans	500
14	a	Pig Death Rate by Disease	0.9
15	b	Pig Removal Rate	0.75
16	μ	Human natural death rate	0.9
17	γ	Trans. rate from infectious class to recovery class	0.9
18	M	Moisture in air	0.9
19	δ	Rate from Infection class to Isolated class in pigs	0.9
20	ε	Trans. rate from isolated class to recovery class	0.9

Table 1: Table with initial value and parameters

Now, using the above data into our proposed model, we got numerical results and by using these results, we plot different graphs representing the mathematical situations of the different factors at different order of system. The figures are given as below:
From these obtained results, we can see that human recovery rate is much faster than the pig recovery rate while human infection is going down rapidly while pig infection is going higher side. At the point when we see the mathematical and graphical solutions, we observe that our outcomes are more sensible in current situation. Thus, we can state that this illness is more irresistible in pigs when contrasted with people.

8 Conclusion

We have define and studied the Streptococcus Suis fractional model with Riemann-Liouville fractional operator and also proved the existence and uniqueness of their solution. We also calculated their numerical and graphical solutions as well. When we studied the numerical solutions, we found that our results are more realistic and closer results in current scenario. So, we can conclude that this disease is more infectious in pigs as compared to humans. We have constructed a mathematical model using the SIQR model, which only takes into account the pig population, to forecast the disease transmission of Streptococcus suis between pigs and humans. The SIQR-SIR model, which describes the epidemiology of Streptococcus suis transmission between pigs and humans, is studied.

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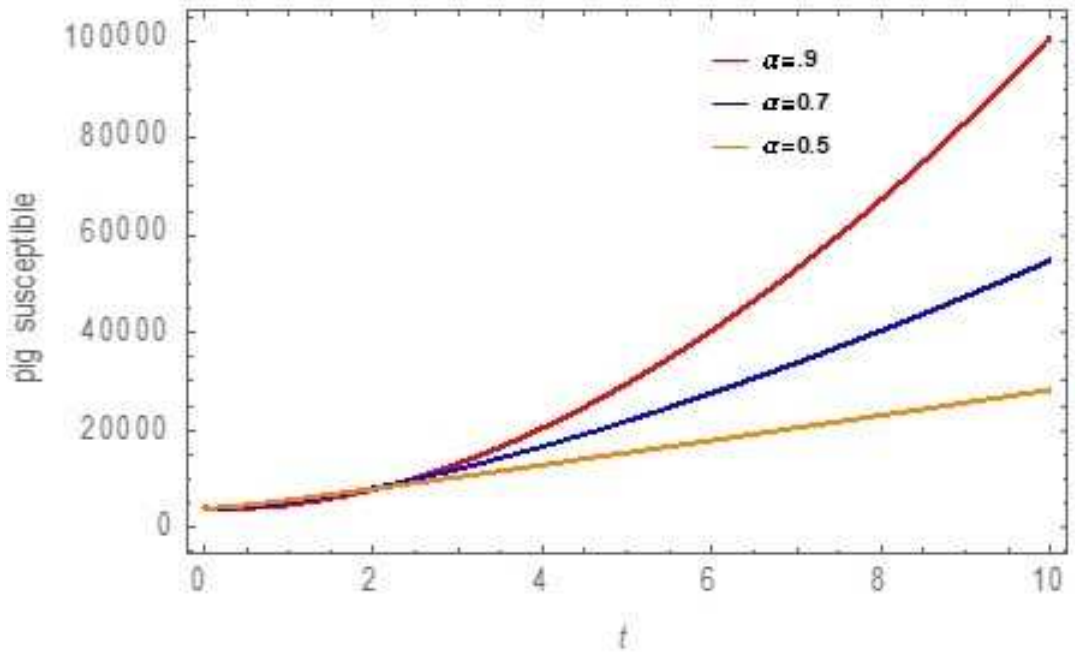

Fig. 1: Graph of pig susceptible w. r.t. time t, for α= 0.5, 0.7 and 0.9

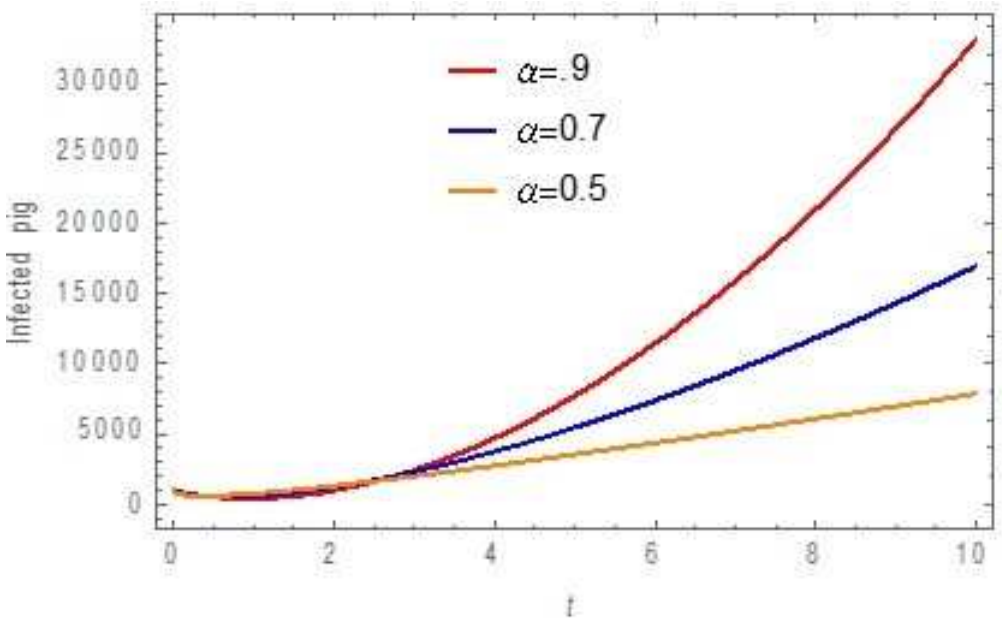

Fig. 2: Graph representing pig infection with respect to time t, for α= 0.5, 0.7 and 0.9

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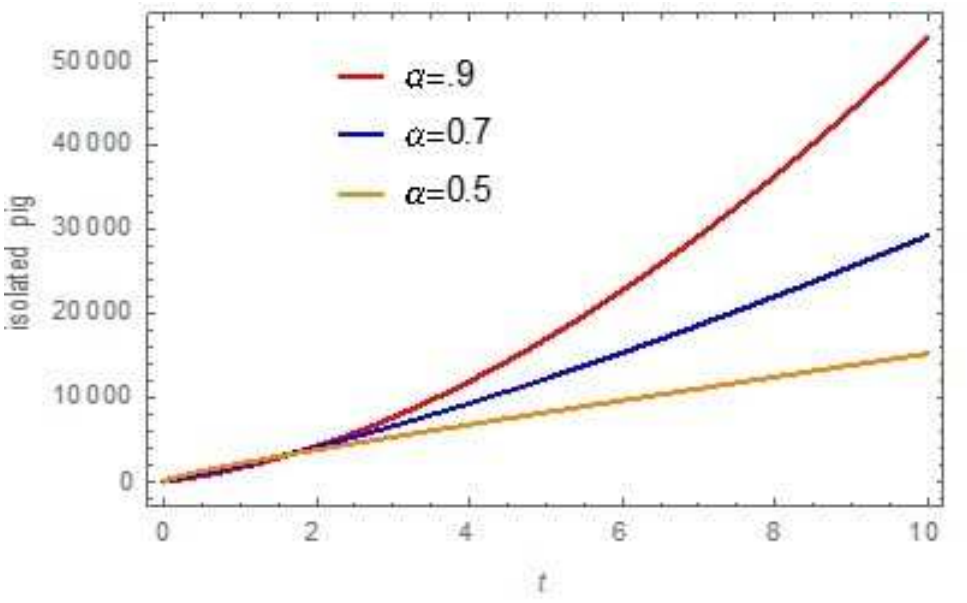

Fig. 3: Graph of pig isolated with respect to time t, for α= 0.5, 0.7 and 0.9

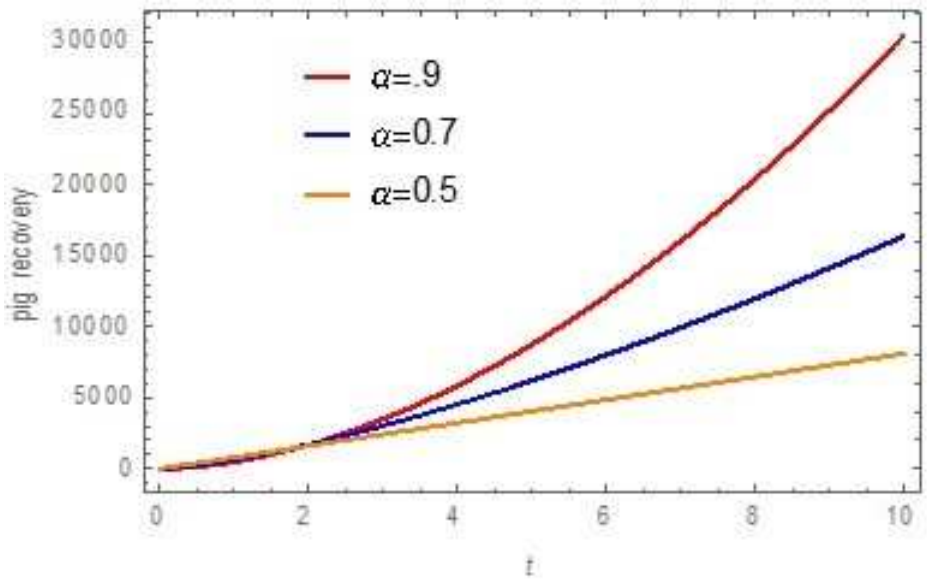

Fig. 4: Graph showing pig recovery with respect to time t, for α= 0.5, 0.7 and 0.9

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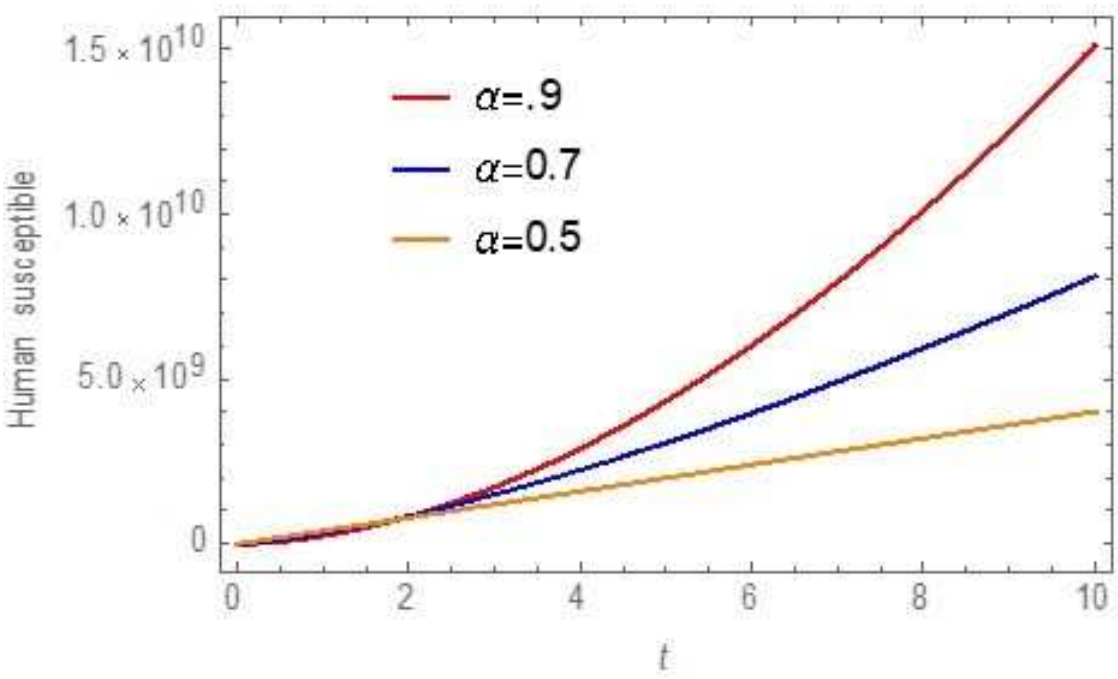

Fig. 5: Graph showing human susceptible with respect to time t, for α= 0.5, 0.7 and 0.9

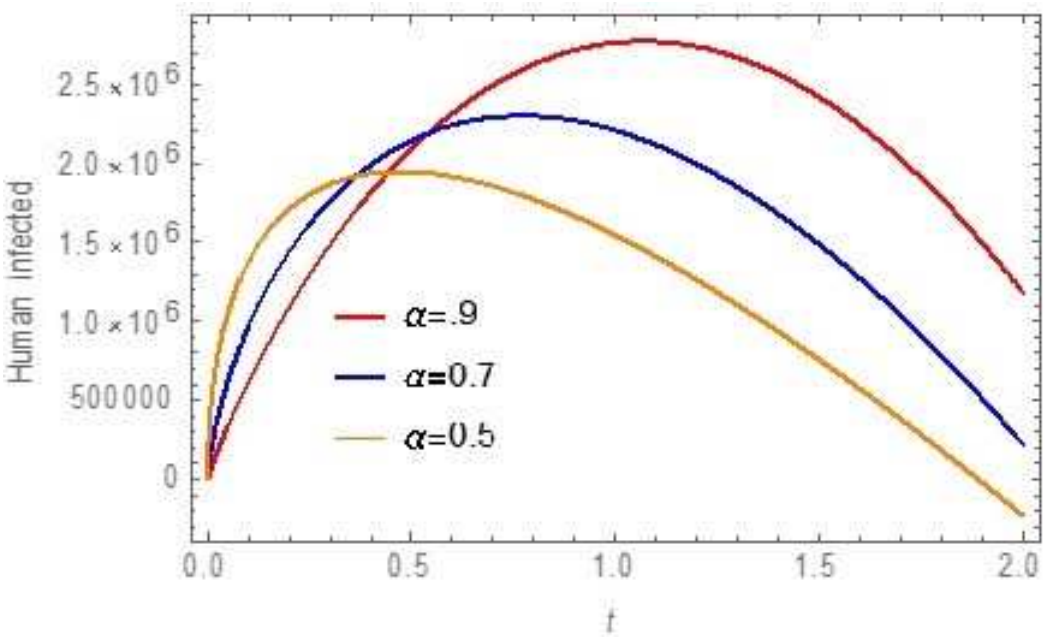

Fig. 6: Graph representing human infection with respect to time t, for α= 0.5, 0.7 and 0.9

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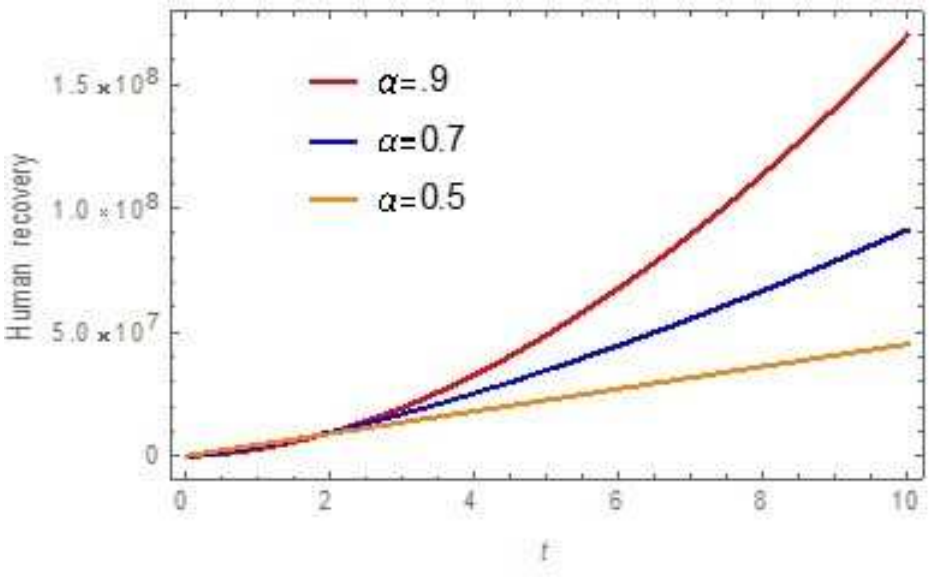

Fig. 7: Graph showing human recovery with respect to time t, for α= 0.5, 0.7 and 0.9

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