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On Fractional Order Influenza A Epidemic Model

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Abstract: This paper examines the fractional order of influenza using an epidemic model. The stability of disease-free and positive fixed points is explored and studied. The Adams-Bashforth-Moulton algorithm is employed to determine the solution and also simulate the system of differential equations. It is observed that Adams-Bashforth-Moulton method gives similar results as obtained in Runge-Kutta technique and ODE 45.

Keywords: Fractional Order Calculus, Influenza A, Adams-Bashforth- Moulton

1. Introduction

The (2003–2004 outbreak of "flu") and the number of casualties associated with the outbreak, which was speculated to be the result of the interactions between domestic avian populations and humans in Asia and Africa (Cambodia, China, Indonesia, Japan, Laos, South Korea, Thailand, Vietnam and Morocco) has re-stimulated interest in finding a lasting solution to a disease which was taught have face extinction since the last massive outbreak of such a "flu" was the 1918 pandemic. The flue that occurred in Morocco took the world aback since the Asian flue had not happened in recent history. Generally, the intermittent outbreak of epidemic occurrence has been studied in the direction of communicable diseases such as rubeola and influenza [10]. In trying to understand the regular re-occurrences of such diseases, mathematical models have been applied to the study of mechanisms that are capable of generating recurrent, more importantly periodic, outbreaks [12;13]. Modern methods of examining the role played by qualitative dynamics of communicable on mechanisms such as quarantine of infectious individuals, age-structure and few others have been explored elsewhere.

Over the past century only three subtypes of influenza type A (H1N1, H2N2 and H3N2) have been indentified to be associated with influenza pandemics or epidemics which have occurred in many parts of the world. Point mutations in particular areas of the HA molecule "continuously" produces fresh strains within a certain subtype whilst major molecular variations have been associated with genetic shifts (new subtypes). The immune system of an individual has been tired to the high mortality rate of influenza type A. For influenza type A cross-immunity, that has capacity of an individual's immune system to connect with its history of preceding infections to either diminish the probability of new infections (by related strains) or to increase "virus control" (within each host) by strengthening the host's immune response, can influence the pathogen's transmission dynamics. To the best of our knowledge fractional order calculus has not been used in the study of the dynamics of influenza type A.

In this paper, we studied the fractional order influenza type A epidemic model. The stability of equilibrium points is determined and studied. Numerical solutions of the model are presented. We propose that fractional order equations are more appropriate than integer order ones in mathematical modeling of processes such biological, economic, and social systems. Adams-Bashforth-Moulton algorithm and other well known methods have been applied to solve and simulate the system of differential equations.

2. Mathematical Model

El hia et al., 2012 proposed Influenza A(H1N1) transmission model by taking into consideration that, an individual can be infected only through contacts with infectious individuals. The model also assumes that the host population size at time t, is partitioned into subclasses of individuals who are susceptible, $S(t)$, $I(t)$ and $R(t)$, respectively. In addition, the host population is recruited at a rate Λ. The per capita recovery rate of the hosts is given by r. Susceptible individuals begin carrying the pathogen after

getting into contact an infective host at a rate β. H1N1 induced mortality rate is denoted by d. This model is governed by the following system of non linear ordinary differential equations:

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - \mu S - \beta S \dfrac{I}{N} \\ \dfrac{dI}{dt} = \beta S \dfrac{I}{N} - (\mu + d + r) I \\ \dfrac{dR}{dt} = rI - \mu R \end{cases} \tag{2.1}$$

Now we incorporate fractional order in to the ODE model by El hia et al., 2012 in (2.1). The new system is described by the following set of fractional order differential equations:

$$\begin{aligned} D_t^\alpha S &= \Lambda - \mu S - \beta S \frac{I}{N} \\ D_t^\alpha I &= \beta S \frac{I}{N} - (\mu + d + r) I \\ D_t^\alpha R &= rI - \mu R \end{aligned} \tag{2.2}$$

where D_t^α represents the Caputo fractional derivative. Since model (2.2) monitors the dynamics of human populations, all the parameters are considered to be non-negative. In addition, it can be proved that all state variables of the model are non-negative for all time $t \geq 0$ (see, for instance, [6]).

The closed set $\Omega = \left\{ (S, I, R) \in \mathbb{R}_+^3 : S + I + R = \Lambda / \mu \right\}$ *is positively invariant with respect to model* (2.2).

Proof. The fractional derivative of the total population, obtained by summing all the equations of model (2.2) and is given by

$$D_t^\alpha N(t) = \Lambda - \mu N(t) - dI \tag{2.3}$$

The solution to (2.3) is expressed as $N(t) = N(0) E_{\alpha,1}(-\mu\, t^\alpha) + \Lambda t^\alpha E_{\alpha,1+1}(-\mu\, t^\alpha)$, where $E_{\alpha,\beta}$ is the Mittag-Leffler function. By considering the fact that the Mittag-Leffler function has an asymptotic behavour [6],

$$E_{\alpha,\beta}(z) \sim -\sum_{k=1}^{w} \frac{z^{-k}}{\Gamma(\beta - \alpha k)} + O\left(|z|^{-1-w}\right),$$

$$\left(|z| \to \infty, \frac{\alpha\pi}{2} < |ar(z)| \leq \pi \right).$$

One can examine that $N(t) \to \Lambda / \mu$ as $t \to \infty$. Therefore, all solutions of the model with initial conditions in Ω remain in Ω for all $t > 0$. Thus, region Ω is positively invariant with respect to model (2.2).

3. Equilibrium Points and Stability

In the following, we look at the stability of the corresponding fractional ordered dynamical system:

$$D_t^\alpha x_i = f_i(x_1, x_2, x_3), \qquad \alpha \in (0,1), \quad 1 \leq i \leq 3. \tag{3.1}$$

Let $E = (x_1^*, x_2^*, x_3^*)$ be an equilibrium point of system (3.1) and $x_i = x_i^* + \eta_i$, where η_i is a small disturbance from a fixed point. Then

$$D_t^\alpha \eta_i = D_t^\alpha x_i \tag{3.2}$$

System (3.2) can be written as:

$$D_t^\alpha \eta = J\eta, \tag{3.3}$$

where $\eta = (\eta_1, \eta_2, \eta_3)^\Gamma$ and J is the Jacobian matrix evaluated at the equilibrium points.

By applying Matignon's results [1], it follows that the linear autonomous system (3.3) is asymptotically stable if $|\arg(\lambda)| > \dfrac{\alpha\pi}{2}$ is satisfied for all eigenvalues of matrix J at the equilibrium point $E = (x_1^*, x_2^*, x_3^*)$. If $\phi(x) = x^3 + d_1 x^2 + d_2 x + d_3$, Let $D(\phi)$ denote the discriminant of a polynomial ϕ, then

$$D(\phi) = -\begin{vmatrix} 1 & d_1 & d_2 & d_3 & 0 \\ 0 & 1 & d_1 & d_2 & d_3 \\ 3 & 2d_1 & d_2 & 0 & 0 \\ 0 & 3 & d_1 & d_2 & 0 \\ 0 & 0 & 3 & 2d_1 & d_2 \end{vmatrix} = 18 d_1 d_2 d_3 + (d_1 d_2)^2 - 4 d_3 d_1^3 - 4 d_2^3 - 27 d_3^2.$$

Follow [2-4], we have the proposition.

Proposition. One takes into consideration that E_1 exists in $\mathbb{R}_+^3$.

To evaluate the equilibrium points let

$$D_t^\alpha S = 0, \quad D_t^\alpha I = 0, \quad D_t^\alpha R = 0.$$

Then $E_0 = (\Lambda / \mu, 0, 0)$. We denote the basic reproduction number as [5].

$$\Re_0 = \frac{\beta}{(\mu + d + r)}$$

It implies the average new infections generated by one infected individual during his lifespan when the population is at E_0. By (2.2), a positive equilibrium $E_1 = (S^*, I^*, R^*)$

satisfies

$$S^* = \frac{1}{\Re_0} N^*,$$

$$I^* = \frac{\mu(\Re_0 - 1)}{\Re_0(\mu + r)} N^*,$$

$$R^* = \frac{r(\Re_0 - 1)}{\Re_0(\mu + r)} N^*,$$

where

$$N^* = \frac{\Lambda \Re_0(\mu + r)}{\mu[(\Re_0 - 1)d + \Re_0(\mu + r)]}$$

The Jacobian matrix $J(E_0)$ for the system given in (2.2) evaluated at the disease-free equilibrium is as follows:

$$J(E_0) = \begin{pmatrix} -\mu & -\beta & 0 \\ 0 & \beta - (\mu + d + r) & 0 \\ 0 & r & -\mu \end{pmatrix}$$

Theorem 3.1. The disease-free equilibrium E_0 is locally asymptotically stable if $\Re_0 < 1$ and is unstable if $\Re_0 > 1$.

Proof. The disease-free equilibrium is locally asymptotically stable if all the eigenvalues, $\lambda_i, i = 1,2,3$ of the Jacobian matrix $J(E_0)$ satisfy the following condition [1, 3]:

$$\left| \arg(\lambda_i) > \frac{\alpha\pi}{2} \right| \tag{3.4}$$

The eigenvalues of the Jacobian matrix (E_0) are $\lambda_1 = -\mu$, $\lambda_2 = -\mu$ and $\lambda_3 = -(d + r + \mu - \beta)$

Since all the eigenvalues of the Jacobian matrix $J(E_0)$ are negative hence E_0 is locally asymptotically stable if $\Re_0 < 1$ and is unstable if $\Re_0 > 1$.

We now discuss the asymptotic stability of the endemic (positive) equilibrium of the system given by (2.2).

The Jacobian matrix $J(E_1)$ evaluated at the endemic equilibrium is given as

$$J(E_1) = \begin{pmatrix} -\mu & \frac{-\beta I^*}{\mu N} & 0 \\ \frac{-\beta I^*}{\mu N} & \left(\frac{\beta S^*}{\mu N} - (\mu + d + r)\right) & 0 \\ 0 & r & -\mu \end{pmatrix}$$

Theorem 3.2. If $\Re_0 > 1$, the endemic equilibrium point E_1 of system (2.2), is locally asymptotically stable.

Proof. The disease-free equilibrium is locally asymptotically stable if all the eigenvalues, $\lambda_i, i = 1,2,3$ of the Jacobian matrix $J(E_1)$ satisfy the following condition [2]:

$$\left| \arg(\lambda_i) > \frac{\alpha\pi}{2} \right| \tag{3.5}$$

The eigenvalues of the Jacobian matrix (E_1) are $\lambda_1 = -\mu$,

$$\lambda_2 = \frac{-(d\mu^2 + r\mu^2 + \mu^3) + NS\beta\mu + \sqrt{-4N^2\beta^2\mu^2 + (-NS\beta\mu + d\mu^2 + r\mu^2 + \mu^3)^2}}{2\mu^2},$$

$$\lambda_3 = \frac{-(d\mu^2 + r\mu^2 + \mu^3) + NS\beta\mu - \sqrt{-4N^2\beta^2\mu^2 + (-NS\beta\mu + d\mu^2 + r\mu^2 + \mu^3)^2}}{2\mu^2}$$

Since all the eigenvalues of the Jacobian matrix $J(E_1)$ are negative hence E_1 is locally asymptotically stable if $\Re_0 > 1$.The endemic equilibrium is locally asymptotically stable if all the eigenvalues, $\lambda_i, i = 1,2,3$ of the Jacobian matrix $J(E_1)$ satisfy the following condition [2-4].

4. Numerical Methods and Simulations

In view of the fact that most of the fractional order differential equations do not have exact analytic solutions, so approximation and numerical techniques must be employed. Numerous analytical and numerical methods have been put up to solve the fractional order differential equations. For numerical solutions of the system (2.2) one can apply the generalized Adams-Bashforth- Moulton method. To provide the exact solution by means of this algorithm, we take into account the following nonlinear fractional differential equation [7]:

$$D_t^\alpha y(t) = f(t, y(t)), \quad 0 \le t \le T,$$

$$y^{(k)}(0) = y_0^k, \quad k = 0,1,2,\ldots,m-1, \text{ where } m = [\alpha].$$

This equation is equivalent to Volterra integral equation:

$$y(t) = \sum_{k=0}^{m-1} y_0^k \frac{t^k}{k!} + \frac{1}{\Gamma(\alpha)} \int_0^t (t-s)^{\alpha-1} f(s, y(s)) ds \tag{4.1}$$

Diethelm et al. employed the predictor-correctors scheme [8; 9] based on the Adams-Bashforth-Moulton algorithm to integrate [8]. By using this scheme to the fractional order influenza A epidemic model and setting $h = T/N, t_n = nh$,

and $n = 0,1,2,...,N \in Z^+$, [9] can be discretized as follows [7]:

$$S_{n+1} = S_0 + \frac{h^\alpha}{\Gamma(\alpha+2)}\left(\Lambda - \mu S^p_{n+1} - \beta S^p_{n+1}\frac{I^p_{n+1}}{N}\right) + \frac{h^\alpha}{\Gamma(\alpha+2)}\sum_{j=0}^{n} a_j, n+1\left(\Lambda - \mu S_j - \beta S_j \frac{I_j}{N}\right),$$

$$I_{n+1} = I_0 + \frac{h^\alpha}{\Gamma(\alpha+2)}\left(\beta S^p_{n+1}\frac{I^p_{n+1}}{N} - (\mu+d+r)I^p_{n+1}\right) + \frac{h^\alpha}{\Gamma(\alpha+2)}\sum_{j=0}^{n} a_j, n+1\left(\beta S_j \frac{I_j}{N} - (\mu+d+r)I_j\right),$$

$$R_{n+1} = R_0 + \frac{h^\alpha}{\Gamma(\alpha+2)}\left(rI^p_{n+1} - \mu R^p_{n+1}\right) + \frac{h^\alpha}{\Gamma(\alpha+2)}\sum_{j=0}^{n} a_j, n+1\left(rI_j - \mu R_j\right),$$

where

$$S^p_{n+1} = S_0 + \frac{1}{\Gamma(\alpha)}\sum_{j=0}^{n} b_j, n+1\left(\Lambda - \mu S_j - \beta S_j \frac{I_j}{N}\right),$$

$$I^p_{n+1} = I_0 + \frac{1}{\Gamma(\alpha)}\sum_{j=0}^{n} b_j, n+1\left(\beta S_j \frac{I_j}{N} - (\mu+d+r)I_j\right),$$

$$R^p_{n+1} = R_0 + \frac{1}{\Gamma(\alpha)}\sum_{j=0}^{n} b_j, n+1\left(rI_j - \mu R_j\right),$$

$$a_j, n+1 = \begin{cases} n^{\alpha+1} - (n-\alpha)(n+1), & j = 0, \\ (n-j+2)^{\alpha+1} + (n-j)^{\alpha+1} & 1 \le j \le n, \\ -2(n-j+1)^{\alpha+1}, & \\ 1, & j = n+1, \end{cases}$$

$$b_{j,n+1} = \frac{h^\alpha}{\alpha}\left((n-j+1)^\alpha - (n-j)^\alpha\right), \quad 0 \le j \le n.$$

Table 1. *Parameter values for the numerical simulation.*

Notation	Parameter Values	Sources
Λ	20	Assumed
β	0.75	Hattaf and Yousfi,2009
μ	3.9139×10^{-5}	Hattaf and Yousfi,2009
r	0.2	El hia et al., 2012
d	0.63	El hia et al., 2012

Table 2. *Initial conditions.*

$S(0)$	30×10^6
$I(0)$	30
$R(0)$	28

We solve numerically the equation (2.2) with initial conditions by employing the Adams-Bashforth-Moulton. Again the forth-order Runge-Kutta and ODE 45 numerical method are also applied for numerical solution for the same equation (2.2). For these simulation results we employ a set of parameters provided in Table 1. In order to show the usefulness of intended algorithm as an approximate instrument for computing the nonlinear fractional differential equation (2.2) for given large time t, we employ Adams-Bashforth-Moulton algorithm on the interval [0-100].

From the graphical results produced in Figs 1-3, it shows the approximate solutions obtained using the Adams-Bashforth-Moulton (ABM) and the classical Runge-Kutta method of $S(t), I(t)$ *and* $\mathrm{R}(t)$ and for $\alpha = 1$. From the graphical result of these figures, it can be seen that the results obtained using the ABM go with the results of the classical Runge-Kutta method very well

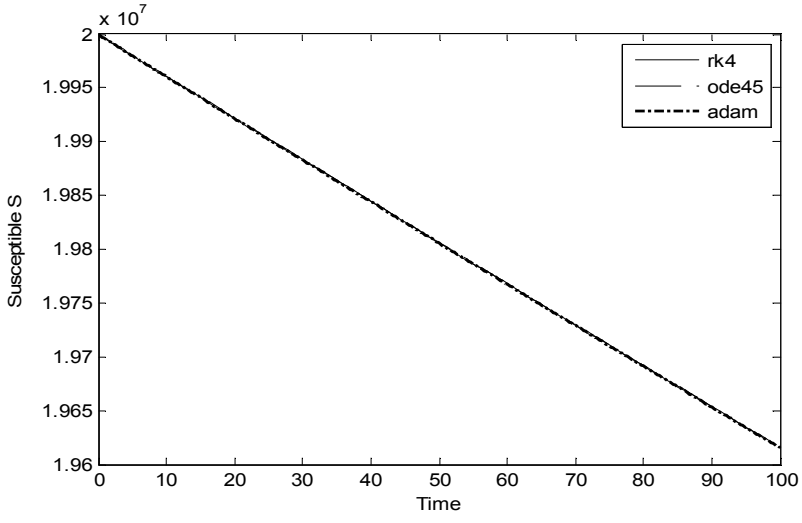

Figure 1. *The plot shows the susceptible individuals.*

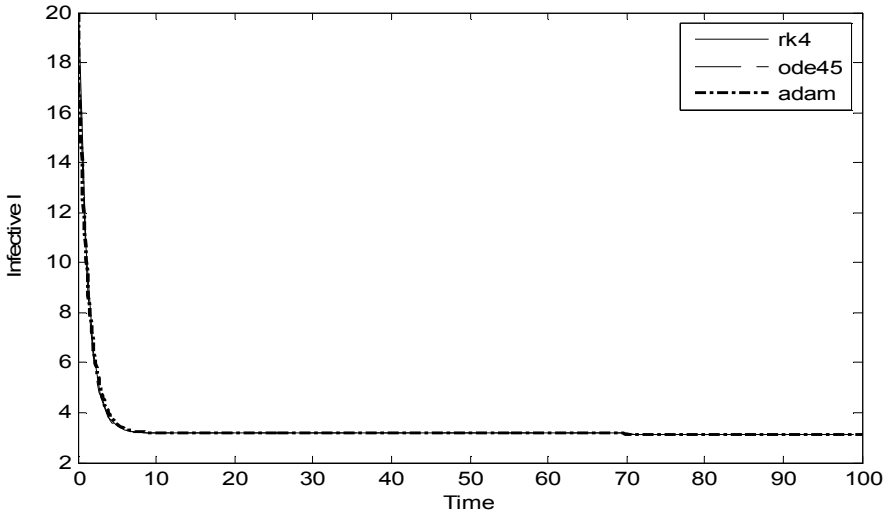

Figure 2. *The plot shows the infected individuals.*

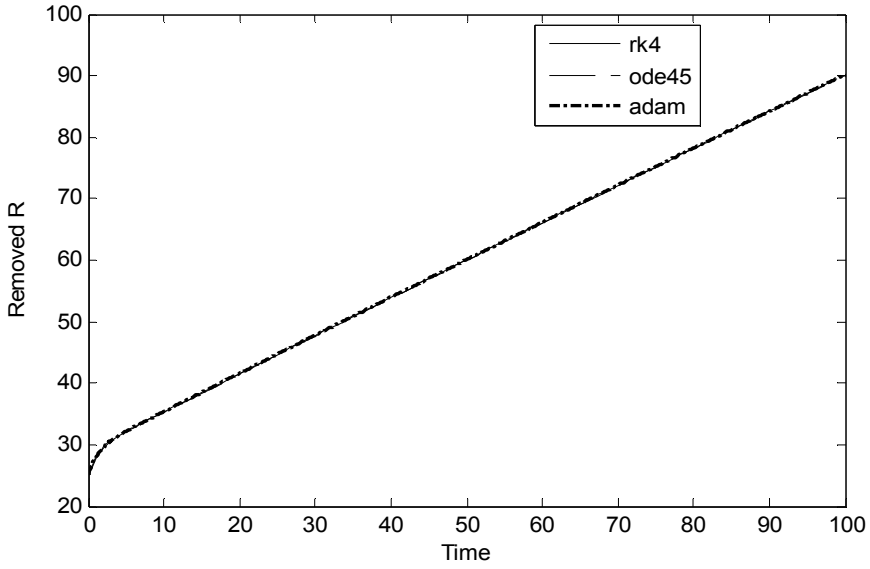

Figure 3. *The plot shows the recovered individuals.*

5. Conclusion

In this paper, we examined a fractional order system for SIR (Susceptible-Infected-Recovered) Influenza A epidemic model. Adams-Bashforth-Moulton method is applied to compute an approximate solution of the model in fractional order. This method is very accurate since the solution obtained is close to other standard method. The results obtained are compared with those forth order Runge-Kutta technique and ODE45 method in the integer perspectives. Some numerical results are shown.

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References

[1] Matignon D. Stability results for fractional differential equations with applications to control processing, *Computational Engineering in Systems and Applications, Multi-conference, vol. 2, IMACS, IEEE-SMC Proceedings, Lille, France*, 2,(1996) 963-968.

[2] E. Ahmed E, El-Sayed A. M. A., El-Mesiry E. M., El-Saka. H. A. A.(2005).Numerical solution for the fractional replicator equation, *IJMPC*,(2005) 16, 1–9.

[3] Ahmed E., El-Sayed A. M. A., El-Saka H. A. A. On some Routh-Hurwitz conditions for fractional order differential equations and their applications in Lorenz, Rossler, Chua and Chen systems, *Physics Letters A*, 358 (2006), 1–4.

[4] Ahmed E., El-Sayed A. M. A., El-Saka. H. A. A. Equilibrium points, stability and numerical solutions of fractional-order predator-prey and rabies models, *J. Math. Anal. Appl*, 325 (2007), 542–553.

[5] Liu X., Takeuchib Y., Iwami S. SVIR epidemic models with vaccination strategies, *Journal of Theoretical Biology*, 253 (2008), 1–11.

[6] Elbasha E. H., Gumel. A. B. Analyzing the dynamics of an SIRS vaccination model with waning natural and vaccine-induced immunity, *Trends in Parasitology*, 12 (2011) ,2692–2705.

[7] Li and C., Tao C. On the fractional Adams method," *Computers and Mathematics with Applications*, vol. 58, no. 8,(2009) pp. 1573–1588.

[8] Diethelm K. An algorithm for the numerical solution of differential equations of fractional order," *Electronic Transactions on Numerical Analysis*, vol. 5,(1997) pp. 1–6.

[9] Diethelm K., Ford N. J. Analysis of fractional differential equations," *Journal of Mathematical Analysis and Applications*, vol. 265, no. 2,(2002) pp. 229–248.

[10] R. Anderson and R. May, *Infectious Diseases of Humans: Dynamics and Control*, Oxford University Press, Oxford, 1991

[11] S. B. Thacker, *The persistence of influenza in human populations*, Epidemiol. Rev., 8, (1986),129–142.

[12] H. W. Hethcote, *Qualitative analyses of communicable disease models*, Math. Biosci., 28, (1976),335–356.

[13] H. W. Hethcote, *The mathematics of infectious diseases*, SIAM Rev., 42(4),(2000), 599–653.

[14] M. Nu˜no, Z. Feng, M. Martcheva, C. C. Chavez, *Dynamics of two-strain influenza with isolation and cross-protection*, SIAM J. Appl. Math., 65, 3,(2005), 964–982.

[15] Kilbas A.A., Srivastava H. M., Trujillo J. J. (2006) *Theory and Application Fractional Differential Equations*, Elseviesr, Amsterdam, The Netherlands,(2006).

[16] M. El hia , O. Balatif , J. Bouyaghroumni, E. Labriji, M. Rachik. Optimal control applied to the spread of Inuenza A(H1N1). Applied Mathematical Sciences, Vol. 6, 2012, no. 82,(2007), 4057 – 4065.

[17] K. Hattaf. K and N. Yousfi. Mathematical Model of the Influenza A(HIN1) Infection. Advanced Studies in Biology, Vol.1,no.8,(2009),383-390.