

APPLICATION OF FRACTIONAL DIFFERENTIAL CALCULUS TO THE DYNAMICS OF EBOLA VIRUS DISEASE COMBINING VACCINE, CONDOM, QUARANTINE, ISOLATION AND TREATMENT DRUGS AS MEASURES

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Abstract: The main aim of this work is to formulate a transmission model of the dynamics of Ebola Virus Disease (EVD) by combining vaccine, condom use, quarantine, isolation and treatment drug together as control measures in a population consisting of human and animal populations using fractional order derivatives which has an added advantage over the integer order model because of its special property known as memory effect which seems to be useful for epidemic models such as ours. Our fractional order mathematical model initial value problem is based on the Caputo fractional order derivative. Using the next generation matrix approach the effective reproduction number for the model was obtained and used to analyze the stability of EVD - Free Equilibrium and EVD - Infection Equilibrium points of the model. The EVD - Free Equilibrium point was found to be locally asymptotically stable while the EVD - Infection Equilibrium point was unstable as the system exhibits a forward bifurcation. Finally, a brief comparison between the fractional order and integer order solution gets closer to the integer order solution as $alpha \rightarrow 1$ and the fractional solution experienced a chaotic motion at alpha = 0.01. This chaotic motion is not seen at any other value of alpha which means that the fractional order model of the transmission dynamics of Ebola Virus Disease shows more detail of what happens below alpha = 1 that the integer order solution does not show.

Keywords: Ebola virus disease; Fractional differential calculus; Bifurcation analysis.

1. Introduction

Ebola virus disease was first discovered in 1976 near the Ebola River in a country now known as the Democratic Republic of Congo^[19]. Ebola virus disease is a virus known for causing viral hemorrhagic fevers. It can cause disease in human and non-human primates ^[4]. Since the year 1976, there have been so many outbreaks of which the one of 2014 happened to be the largest one in the history of the disease because multiple countries were affected ^[30] which motivated this study. Research has shown that



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arthropods, rodents and bats could be the host for Ebola virus disease ^[14]. The virus can be transmitted to humans by direct transmission from reservoirs or secondary infected animals and then the virus spreads in the human population through human-to-human transmission ^[17]. Treatment drugs and vaccines such as ZMapp and rVSV-EBOV were showed to be 70% to 100% effective against the virus ^[31] and are now used during outbreaks. People now recover from the disease and there is no permanent immunity for those that recover from the disease ^[15]. Some cases where detected according to World Health Organization (WHO) as a result of persistent residual virus in the semen of Ebola virus disease recovered men which led to the assumption of sexual transmission of the virus ^{[6][32]}. Fractional calculus has been in existence for a long time now. It was first introduced by L'Hopital on the 30th of September 1695 in his letter to Leibniz^[26]. It has been widely applied in so many areas of Engineering and Sciences generally. In recent times, it has been used in the world of modelling to analyze epidemic models such as Ebola Virus Disease models^[3]. Even though the fractional derivative operator is more difficult to solve numerically than the classical one, it is still used in applied mathematics because of its property of index memory ^[24]. This property of index memory has made it a relevant tool in epidemiology because it can capture the history of the variable that the integer order derivative find difficult to capture. There are so many definitions of fractional derivative and the three most common ones among them are; the Riemann Liouville's definition, the Caputo's definition and the Grúnwald-Letnikov's definition^[26]. The Caputo's definition is what was applied in this work and is defined as follows; The Caputo fractional derivative of a function

(y) of order v > 0 is defined as;

$$D \ g^{(y)} = \frac{1}{\Gamma(\nu-\rho)} \int_{b}^{y} \frac{g^{(\rho)(\tau)}}{(y-\tau)^{\nu+1-\rho}} d \text{ ,or } \rho - 1 < \nu < \rho \text{ ,}$$

where $y \ge b \ge 0.$ (1)

With Caputo's derivative the initial conditions for the fractional order differential equations are in the same form as that of the classical or integer order differential equations. Many mathematical models had been developed in line with our study but none to the best of our knowledge had considered a fractional order model consisting of human and animal populations with the combined impact of vaccine, condom use, quarantine, isolation and treatment drug.

2. Model Formulation and Basic Properties

The model has two distinguished population types namely; human and animal populations, each subdivided into mutually-exclusive compartments at time t. The total population is denoted by N (t) = N (t) + N (t).The total human population is denoted by N (t) = S (t) + S (t) + S (t) + S (t) + E (t) + E (t) + I (t) + I (t) + I (t) + I (t) + R (t) + D (t) and the total animal population is denoted by N (t) = S (t) + E (t) + I (t).

2.1 Assumptions about the model

□ Isolated individuals are under close surveillance and do not contribute to the transmission of the infection.

□ Vaccine, condoms, treatment drug, place of quarantine for the exposed and place for isolation for the infectious are all available and accessible to the population.

□ The exposed individuals are infected but not yet infectious.

The recovered individuals become susceptible to the virus again after some time.

□ The Ebola virus disease recovered individuals are still infectious through semen.

□ Ebola infected and infectious animals in the population have interactions with the susceptible human population.

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2.2 THE SCHEMATIC DIAGRAM OF THE MODEL



2.3 MODEL VARIABLES' DESCRIPTION Table A: Model Variables Descriptions

Variables	Descriptions	Variables	Descriptions
S	Susceptible Human Population	Ι	Infectious Human Population
S	Susceptible Vaccinated Population	Ι	Infectious Treated Human Population
S	Susceptible Unvaccinated Population	Ι	Infectious Isolated Human Population
S	Susceptible Vaccinated condom users	Ι	Infectious Not Treated Human Population
S	Susceptible Vaccinated non condom	R	Recovered Human Population
	users		
S	Susceptible Unvaccinated condom	D	Dead and Unburied Human Population
	users		
S	Susceptible Unvaccinated non condom	S	Susceptible Animal Population
	users		
Ε	Exposed Human Population	Ε	Exposed Animal Population
Ε	Exposed Quarantined Human	Ι	Infectious Animal Population
	Population		
Ε	Exposed Treated Human Population		

2.4 MODEL PARAMETERS' DESCRIPTION



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Table B: Model Parameters Description

Parameters	Descriptions	Parameters	Descriptions
Р	Human recruitment rate	α	Exposed rate of quarantine
Λ	Animal recruitment rate	α	Exposed rate of taking treatment drug
μ	Human natural death rate	heta	Exposed quarantined rate of being
			infectious
μ	Animal natural death rate	θ	Exposed treated rate of being
			infectious
r	Vaccination rate	J	Recovery rate for the infectious treated
K	Vaccination modification parameter	J	Recovery rate for the infectious
			isolated
K	Vaccinated condom users	S	Infectious rate of taking treatment drug
	modification parameter		
K	Unvaccinated condom users	S	Infectious rate of isolation
	modification parameter		
λ	Vaccinated condom use rate	S	Infectious rate of not receiving
			treatment
σ	Unvaccinated condom use rate	ξ	Infectious treated diseased induced
			death rate
τ	Recovered rate of susceptibility	ξ	Infectious isolated diseased induced
		_	death rate
ρ	Exposed treated recovery rate	ξ	Infectious not treated diseased induced
			death rate
ω	Susceptible animal exposure rate	ξ	Infectious animal diseased induced
Ţ			death rate
${\cal P}$	Exposed animal rate of infectious	q	Dead and unburied rate of burial
m, m, m, m, m,	Infectivity rate for vaccinated condom	n, n, n, n, n,	Infectivity rate for unvaccinated
m	users	n	condom users
<i>e</i> , <i>e</i> , <i>e</i> , <i>e</i> , <i>e</i>	Infectivity rate for vaccinated non	<i>t</i> , <i>t</i> , <i>t</i> , <i>t</i> , <i>t</i>	Infectivity rate for unvaccinated non
	condom users		condom users

2.5 The Model Equations

With our assumptions about the model and Figure 1 the following classical or integer order model system of equation was formulated;





2.5 Fractional Order Model

We hereby rewrite the system (2) in terms of fractional differential equations in the Caputo sense with the same initial conditions to obtain;



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 $D S(t) = P - (\mu + r + K (1 - r))S + \tau R$ (1) $D S (t) = rS - (\mu + \lambda + K (1 - \lambda))S$ (2) $D S (t) = K (1-r)S - (\mu + \sigma + K (1-\sigma))S$ (3) $(t) = \lambda S - (\mu + \beta)S$ DS (4)DS(t) = $K(1-\lambda)S - (\mu + \beta)S$ (5) DS $(t) = \sigma S - (\mu + \beta) S$ (6) $(t) = K(1-\sigma)S - (\mu+\beta)S$ DS (7) $D E(t) = \beta S + \beta S + \beta S + \beta S$ (8) $(\mu + \alpha)$ $+\alpha E$ $D E (t) = \alpha E - (\mu + \theta) E$ (9) $D E (t) = \alpha E - (\mu + \theta + \rho)E$ (10)(11)D I(t) =θΕ $+\theta$ (4) $-(\mu + s + s + s)I$ Ε $D I (t) = s I - (\mu + \xi + J)I$ (12) $s I - (\mu + \xi + J)I$ DI(t) =(13) $s I - (\mu + \xi)I$ (14) DI(t) = $D R(t) = J I + J I + \rho E - (\mu + \mu)$ (15) τR $D D (t) = \xi I + \xi I + \xi I$ (16) -qD $\Lambda - (\mu$ $+\omega)S$ DS(t) =(17) D E(t) = $\omega S - (\mu$ $(+ \Phi)E$ (18) DI(t) = $\Phi E - (\mu$ $+\xi$)I (19)

3 Ebola Virus Disease Equilibrium Points

The Ebola virus disease free equilibrium state is the state of total absence of the disease in the entire population ($\beta = \beta = \beta$ = $\beta = \omega = 0$). The disease free equilibrium points of the model are as follows;

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Therefore, in the absence of the infection, the Ebola Virus Disease (EVD) - free equilibrium of the model exists and is given as;





In this study, the effective reproduction number (R) is defined as the average number of new infections generated in a population where vaccine, condom, quarantine, isolation and treatment drug are combined as control measures when a typically Ebola Virus Disease – infectious individual is introduced in the population being considered. Using the next generation method described by Dickmann and Heesterbeek ^[16] we obtain the effective reproduction number for our Ebola Virus Disease model system which is the spectra radius (χ) of the next generation matrix *GQ* that is $R = \chi(GQ)$. The spectra radius is the maximum eigenvalue of *GQ* where G is a nonzero matrix that represents all new infection terms and Q is an M-matrix representing all disease worsening terms. Considering the compartments *E*, *, E*, *I*, *I*, *I*, *I*, *R*, *D*, *E* and *I* we have the following;



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$-\alpha$		0		0	0
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θ		0	c		0
		0	$-\theta$ (μ	$\iota + s + s +$	s) 0 0
$Q = \mathbf{I} = 0$		0	0	-s	$(\mu + \xi + J) = 0$
			0	-s	$0 \qquad (\mu + \xi$

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		<u>n</u>	$n_5 S_{vc} + n_5$	Svn+e5 N	$S_{uc}+t_5S_{un}$,	$F = \frac{m_2 S_{vc} + m_1}{m_2 S_{vc} + m_2}$	$\frac{a_2 S_{vn} + e_2 S_{uc} + t_2 S_{un}}{N}, Y =$	$\frac{m_1S_{vc}+n_1S_{vn}+e_1S_{uc}+t_1S_{un}}{N}$
I	m_4S_1	** vc+n ₄ S	$\frac{b_{vn}^{**} + e_4 S_u^*}{N}$	$_{c}^{*}+t_{4}S_{u_{1}}^{**}$	$\frac{1}{2}, Z = \frac{m_3 S_1}{2}$	$\frac{v_{vc}^{**}+n_{3}S_{vn}^{**}+e_{3}S_{v}^{*}}{N}$	$\sum_{ic}^{i**} + t_3 S_{un}^{i**}$	
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	(μ	$+\xi$)	000	$(\mu 0$				
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Using MATLab computation software we computed the eigenvalues of GQ and obtained our effective reproduction number of the fractional order EVD model (the largest eigenvalue) as;

0 () $-\xi$ 0 0 0 0 0 0 0 0 00 0 $(\mu + \Phi) = 0$ $-\Phi \quad (\mu + \xi)$ $E = \left[\frac{P(\alpha_{1}\theta_{1} \ \mu + \theta_{2} + \rho \ + \alpha_{2}\theta_{2} \ \mu + \theta_{1})}{\mu N(\mu + r + K_{1}(1 - r))(\mu + \alpha_{1} + \alpha_{2})(\mu + \theta_{2} + \rho)(\mu + \theta_{1})(\mu + s_{1} + s_{2} + s_{3})}\right] \left[\left[\frac{r}{(\mu + \lambda + K_{2}(1 - \lambda))}\right] \left(\frac{s}{s-s-2} \ Rm \ \lambda + n \ K \ (1 - \lambda) + \frac{r}{(\mu + \lambda + K_{2}(1 - \lambda))}\right) \left(\frac{s}{(\mu + \xi_{1} + J_{2})}\left(\frac{r}{(\mu + \lambda + K_{2}(1 - \lambda))}\left(m_{2}\lambda + n_{2}K_{2}(1 - \lambda)\right) + \frac{K_{1}(1 - r)}{(\mu + \sigma + K_{3}(1 - \sigma))}\right) e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu + \xi_{3})(\mu + \xi_{2} + J_{1}) + s_{2}\xi_{2}(\mu + \xi_{3})(\mu + \xi_{1} + J_{2}) + s_{3}\xi_{3}(\mu + \xi_{1} + J_{2})(\mu + \xi_{2} + J_{1})}\right) \left(\frac{r}{(\mu - \kappa)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\right) e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e \ \sigma + t \ K \ (1 - \sigma) + \frac{1}{(\mu - \sigma)}\right) + \frac{1}{(\mu - \sigma)}\left(e$) $m \lambda + n K (1 - \lambda) + \underbrace{\qquad}_{()} e \sigma + t K (1 - \sigma)$)() ()(

Applying the parameter values of the fractional order model in Table C to (5) by substitution and evaluation we estimate our effective reproduction number as follows;

0.127799389

$$R = ____[(0.001912591004 + 0.007533267211) + 0.795041204(0.00001912591004 + 0.00007533267211)]$$



< 1^[16]

0.124788753

 $+\ 0.605751386 (0.01912591004 + 0.07533267211) + 0.707675087 (0.0001912591004 + 0.0007533267211)]$

- R = 1.02412586[0.009445858215 + 0.00007509846488 + 0.057218416 + 0.0006684598534]
- $R = 1.02412586 \times 0.067407832$

R = 0.069034104

Thus, our R < 1, This means that a small number of infected individuals introduced into the considered population will not generate a heavy and strong outbreak. Comparing our estimated R with those estimated by others; Legrand et al., (2007) estimated R =0.4 with the implementation of barrier nursing measure , Rivers et al., (2014) estimated R = 2.23 with the implementation of pharmaceutical measure and Madubueze et al., (2018) that estimated their R =0.3722121449 with the implementation of non pharmaceutical measures such as contact tracing and quarantine. It becomes clearer that with the combined implementation of pharmaceutical and non pharmaceutical control measures such as vaccine, condom, quarantine, isolation and treatment drug during an EVD outbreak will speedily reduce the EVD spread and certainly eliminate the disease from the population within a short period. With our effective reproduction number less than one we have the following theorems; Theorem 1

The EVD – free equilibrium point ζ^{**} is locally asymptotically stable if R < 1 and unstable if $R > 1^{[16]}$. Theorem 2

The EVD – Infection equilibrium point ζ^* is locally asymptotically stable if

R

> 1 and unstable if *R*5 Bifurcation Analysis of the Ebola Virus Disease(EVD) Model

We study the stability of our system equilibria using bifurcation analysis. To do this we apply the center manifold theory ^[23] described by Castillo – Chavez and Song (2004)^[11] to investigate the stability of our EVDequilibria near R = 1. This approach is used in examining the existence of forward and backward bifurcation at R = 1. When the bifurcation result is a forward bifurcation it shows that the EVD - free equilibrium is locally asymptotically stable for R < 1 and the EVD – Infection equilibrium is unstable for $R < 1^{[23]}$. A backward bifurcation means that R < 1 is not enough condition for the disease to be extinguished from a population where it is endemic but adequate enough to avoid an epidemic which is caused by the introduction of few initially infected individuals in the population. When the bifurcation is forward it is possible to have global asymptotical stability of both equilibria, which may also be impossible when the bifurcation is backward ^[23]. By applying this approach we let $S = x_1$, $S_v = x_2$, $S_u = x_3$, $S_{vc} = x_4$, $S_{vn} = x_5$, $S_{uc} = x_6$, $S_{un} = x_7$, $E = x_7$ x_8 , $E_Q = x_9$, $E_T = x_{10}$, $I = x_{11}$, $I_T = x_{12}$, $I_i = x_{13}$, $I_N =$ x_{14} , $R = x_{15}$, $D_u = x_{16}$, $S_r = x_{17}$, $E_r = x_{18}$, $I_r = x_{19}$ and then express the model equation as $_ = F(x)$. Thus,



J

We linearize the system (6) to obtain the jacobian matrix given as;

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B)v	I			$\frac{dt}{dt}$ $\frac{dx_{10}}{dt}$ $\frac{dx_{11}}{dt}$	(4)	= <i>f</i>	=	λx	- (µ +
φ) x (5)	= f	$= K_{ }(1-\lambda)$)x $-(\mu+\beta)x$	$\frac{dt}{dx_{12}}$ $\frac{dt}{dt}$					
(6)	= f	$= \sigma x - (\mu + \mu)$	β)x	$\frac{dt}{dt}$ $\frac{dx_{14}}{dt}$ $\frac{dt}{dt_{15}}$					
(7)	= <i>f</i>	$= K(1-\sigma)\mathbf{x}$	$-(\mu + \beta)x$	$\frac{dt}{dt_{16}}$					
(8)	= f	$= \beta x + \beta x + \beta x$	+ $\beta \mathbf{x} - (\mu + \alpha + \alpha) \mathbf{x}$	dt $\frac{dx_{18}}{dt}$ dx_{19}					
(9)	= <i>f</i>	$= \alpha \mathbf{x} - (\mu + \theta)$)x						
(10)	= <i>f</i>	$= \alpha \mathbf{x} - (\mu + \theta)$	(6) + ρ)x (6)						
(11)	= <i>f</i>	$= \theta x + \theta x$	$-(\mu+s+s+s)\mathbf{x}$	I					
(12)	= <i>f</i>	= <i>s</i> x	$-(\mu+\xi+J)\mathbf{x}$						
(13)	= <i>f</i>	= <i>s</i> x	$-(\mu + \xi + J)\mathbf{x}$						
(14)	= <i>f</i>	= <i>s</i> x	$-(\mu+\xi)\mathbf{x}$ $ $						
(15)	= f	$= J \mathbf{x} + J \mathbf{x}$	$+\rho x - (\mu + \tau) x$						
(16)	= f	$= \xi x + \xi x$	$+\xi \mathbf{x} - q\mathbf{x}$						
(17)	= f	= Λ	$-(\mu + \omega)\mathbf{x}$						
(18)	= f	= 0	$\omega x = (\mu + \Phi)x$	I					
(19)	= f	= 4	$\Phi_{\mathbf{X}} = (\mu + \xi) \mathbf{x}$						
1	• (I = I = I = I = I = I = I = I = I = I =	(. 1 . T (1 1)) A	(. 17 (1	>> •	(0)	•	<u> </u>

where; $A_1 = -(\mu + r + K (1 - r)), A_2 = -(\mu + \lambda + K (1 - \lambda)), A_3 = -(\mu + \sigma + K (1 - \sigma)), A_4 = -(\mu + \beta), A_5 = -(\mu + \beta), A_6 = -(\mu + \beta), A_7 = -(\mu + \beta), A_8 = -(\mu + \alpha + \alpha), A_9 = (\mu + \theta_1), A_{10} = -(\mu + \theta + \rho), A_{11} = -(\mu + s + s + s), A_{12} = -(\mu + \beta), A_{13} = -(\mu + \beta), A_{14} = -(\mu + \beta), A_{15} = -(\mu + \beta), A_{15} = -(\mu + \beta), A_{16} = -(\mu + \beta), A_{17} = -(\mu + \beta), A_{18} = -(\mu + \beta$



$$\begin{aligned} &+ \xi + J \), \ A_{13} = -(\mu + \xi + J \), \ A_{14} = -(\mu + \xi \), \ A_{15} = -(\mu + \tau), & A_{16} = -q, \ A_{17} = -(\mu + \omega), \ A_{18} = -(\mu + \Phi), \ A_{19} = -(\mu + \xi), \ M_{19} = -(\mu + \Phi), \ A_{19} = -(\mu + \Phi), \ A_{19}$$

 $q(\mu + \xi + J)(\mu + \xi + J)(\mu + \xi)$

Supposing that the Jacobian matrix H has V and W as its left and right eigenvectors respectively associated with its zero eigenvalues and are chosen in such a way that W. H = 0 and V. H = 0 with V. W = 1, where W = (w₁, w₂, w₃, ..., w₁₈, w₁₉)^T and V = (v₁, v₂, v₃, ..., v₁₈, v₁₉)^T. Then, it follows that; $w_2 = \frac{-rw_1}{2}, w_{15} = \frac{-A_1w_1}{2}, w_2 = \frac{K_1(1-r)w_1}{2}, w_4 = \frac{\lambda rw_1}{2}, w_5 = \frac{K_2(1-\lambda)rw_1}{2}, w_6 = \frac{\sigma K_1(1-r)w_1}{2}$

$$w_{2} = \frac{1}{A_{2}}, w_{15} = \frac{1}{\tau}, w_{3} = \frac{1}{A_{3}}, w_{4} = \frac{1}{A_{2}A_{4}}, w_{5} = \frac{1}{A_{2}A_{5}}, w_{6} = \frac{1}{A_{3}A_{6}}$$

$$w_{7} = \frac{K_{3}(1-\sigma)K_{1}(1-r)w_{1}}{A_{3}A_{7}}, w_{8} = \frac{-(\beta_{1}w_{4}+\beta_{2}w_{5}+\beta_{3}w_{6}+\beta_{4}w_{7})}{A_{8}}, w_{9} = \frac{-\alpha_{1}w_{8}}{A_{9}}, w_{10} = \frac{-\alpha_{2}w_{8}}{A_{10}}, w_{11} = \frac{-(\theta_{1}w_{9}+\theta_{2}w_{10})}{A_{11}},$$

$$= \frac{-(\delta_{1}w_{11}+\delta_{2}w_{12}+\delta_{2}w_{12}+\delta_{2}w_{12}+\delta_{2}w_{12}+\delta_{2}w_{12}+\delta_{2}w_{12}}{A_{10}}, w_{11} = \frac{-(\theta_{1}w_{9}+\theta_{2}w_{10})}{A_{11}},$$

$$w_{12} = \frac{-s_1 w_{11}}{A_{12}}$$
, $w_{13} = \frac{-s_2 w_{11}}{A_{13}}$, $w_{14} = \frac{-s_3 w_{11}}{A_{14}}$, $w_{16} = \frac{-(\xi_1 w_{12} + \xi_2 w_{13} + \xi_3 w_{14})}{A_{16}}$

 $w_{17} = w_{18} = w_{19} = 0$ with w_1 as a free vector.

Since all our A_1 to A_{19} are all negative, it follows that;

$$\begin{split} w > 0, w >$$

 $v = \underline{\qquad}, \qquad \frac{-\beta_4 v_8}{A_7}, v_8 = \frac{-(\alpha_1 v_9 + \alpha_2 v_{10})}{A_8}, v_9 = \frac{-\theta_1 v_{11}}{A_9}, v_{10} \qquad \frac{-(\theta_2 v_{11} + \rho v_{15})}{v} \qquad v = \underline{\qquad}, v$ Computations $\frac{-(\lambda v_4 + K_2(1-\lambda)v_5)}{A}, v_3 = \frac{-(\sigma v_6 + K_3(1-\sigma)v_7)}{A} \qquad v = and v \quad is a free vector.$ Of a and b (Bifurcation Coefficients)



 $\begin{aligned} \frac{\partial}{\partial x_4} \frac{d}{\partial x_4} \frac{\partial}{\partial x_1} &= -\frac{m_1}{N}, \frac{\partial}{\partial x_4} \frac{f_4}{\partial x_{14}} = -\frac{m_1}{N}, \frac{\partial}{\partial x_4} \frac{f_4}{\partial x_{16}} = -\frac{m_4}{N}, \frac{\partial}{\partial x_4} \frac{f_4}{\partial x_{19}} = -\frac{m_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_5 \partial x_{11}} &= -\frac{m_5}{N}, \frac{\partial^2 f_5}{\partial x_5 \partial x_{14}} = -\frac{n_1}{N}, \frac{\partial^2 f_5}{\partial x_5 \partial x_{16}} = -\frac{n_4}{N}, \frac{\partial^2 f_5}{\partial x_5 \partial x_{19}} = -\frac{n_3}{N}, \\ \frac{\partial^2 f_6}{\partial x_6 \partial x_{11}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{12}} = -\frac{e_2}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{14}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{16}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x \partial x_{14}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{16}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x \partial x_{10}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x \partial x_{12}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x \partial x_{11}} + \frac{e_1 + e_1}{\partial x_4 \partial x_{12}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{19}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{12}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} &= -\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} + \frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_5}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} &= +\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_3}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} &= +\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_4}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_5}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} &= +\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_1}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = -\frac{e_5}{N}, \\ \frac{\partial^2 f_5}{\partial x_6 \partial x_{11}} &= +\frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = \frac{e_5}{N}, \frac{\partial^2 f_5}{\partial x_6 \partial x_{10}} = \frac{e_5}{N}, \\$

 $\Rightarrow b < 0$ (since v w = 1 and N cannot be negativ.) a = b < 0 (since v w = 1 and N cannot be negativ.) a = b < 0 (since v w = 1 and N cannot be negativ.) a = b < 0 (since v w = 1 and N cannot be negativ.) a = b = 0 (since v w = 1 and N cannot be negativ.)

0.Otherwise, the system exhibits a forward bifurcation. Since, a < 0 and b < 0 we then conclude that the system exhibits a forward bifurcation. Forward bifurcation means that the EVD - free equilibrium point is locally asymptotically stable for R < 1 and unstable for R > 1. And it also means that the EVD - Infection equilibrium point is locally asymptotically stable for R > 1 and unstable for R < 1. This implies that the control of the Ebola Virus Disease in the population is independent of the number of those that are initially infected by the disease and the virus will be eliminated in the population when R < 1. This also means that the disease cannot overtake (invade) the population when R < 1 and it is possible to have global asymptotical stability of both equilibria ^[21].

6. Global Stability of the EVD - Free Equilibrium Point

To prove the global stability for the EVD - free equilibrium, we construct a Lyapunov function for which we have the following theorem;

Theorem 3

For global asymptotic stability, the system at EVD - free equilibrium point is globally asymptotically stable if $R_E \le 1$. Proof:

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To show global asymptotic stability of the system (4) at EVD - free equilibrium we consider the following Lyapunov function stated as;

*G S***, *S***, *S***, *S***, *S***, *S***, *E***, *E***, *E***, *I***, *I***, *I***, *R***, *D***, *S***, *E***, *I*** =

$$\begin{pmatrix} & & & & & \\ & & & & \\ & -S^{**} - S^{**} \log \frac{S^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} - s_v^{**} \log \frac{s_v^{**}}{S} \end{pmatrix} + \begin{pmatrix} s_v - s_v^{**} \log \frac{s_v^{**}}$$

Evaluating the derivatives of G at EVD-Free equilibrium we have;

$$\frac{dG}{dt} = \left(\frac{S+S^{**}}{s}\right)\frac{dS}{dt} + \left(\frac{S_{v}+S_{v}^{**}}{s_{v}}\right)\frac{dS_{v}}{dt} + \left(\frac{S_{u}+S_{u}^{**}}{s_{u}}\right)\frac{dS_{u}}{dt} + \left(\frac{S_{vc}+S_{vc}^{**}}{s_{vc}}\right)\frac{dS_{vc}}{dt} + \right)$$

$$\left(\frac{S_{vn}+S_{vn}^{**}}{s}\right)\frac{dS}{dt} + \left(\frac{S_{uc}+S_{uc}^{**}}{s}\right)\frac{dS_{u}}{dt} + \left(\frac{S_{ur}+S_{un}^{**}}{s}\right)\frac{dS_{un}}{dt} + \left(\frac{S_{vr}+S_{v}^{**}}{s}\right)\frac{dS_{vr}}{dt}\right)$$
Substituting the equations of the model into (8) and evaluating we have;

$$\frac{dG}{dt} = \left(1 + \frac{s^{**}}{s}\right)(P) - \frac{(s+s^{**})^{2}}{s}\left(\mu + r + K_{1}(1-r)\right) + \left(1 + \frac{S_{v}^{**}}{s}\right)r(S + S^{**}) - \frac{(S_{v}+S_{v}^{**})^{2}}{s}\left(\mu + \lambda + K_{2}(1-\lambda)\right)_{+}\right)$$

$$1 + \frac{S_{u}^{**}}{s}\left(K_{1}(1-r)(S + S^{**}) - \frac{(S_{u}+S_{u}^{**})^{2}}{s}\left(\mu + \sigma + K_{3}(1-\sigma)\right) + \left(1 + \frac{S_{vc}^{**}}{s}\right)\sigma(S_{v} + S_{v}^{**}) - \frac{(S_{vc}+S_{vc}^{**})^{2}}{s}\left(\mu\right)$$

$$(9) + \left(1 + \frac{S_{vn}^{**}}{s}\right)K_{2}(1-\lambda)(S_{v} + S_{v}^{**}) - \frac{(S_{vn}+S_{vn}^{**})^{2}}{s}\left(\mu\right)\left(1 + \frac{S_{uc}^{**}}{s}\right)\sigma(S_{u} + S_{u}^{**}) - \frac{(S_{uc}+S_{uc}^{**})^{2}}{s}\left(\mu\right)$$

$$(+) + \left(1 + \frac{S_{vn}^{**}}{s}\right)F_{2}(1-\lambda)(S_{v} + S_{v}^{**}) - \frac{(S_{vn}+S_{vn}^{**})^{2}}{s}\left(\mu\right)\left(1 + \frac{S_{uc}^{**}}{s}\right)\sigma(S_{u} + S_{u}^{**}) - \frac{(S_{uc}+S_{uc}^{**})^{2}}{s}\left(\mu\right)$$

$$(+) + \left(1 + K(1-\sigma)(S + S)\right) + S$$

Collecting the positive and negative terms of (9) we have the following expression; $\underline{\quad} = U - N$

$$U = \left(1 + \frac{S^{**}}{s}\right)(P) + \left(1 + \frac{S^{**}}{s}\right)r(S + S^{**}) + \left(1 + \frac{S^{**}}{s}\right)K_{1}(1 - r)(S + S^{**}) + \left(1\frac{S^{**}}{s}\right)\lambda(S_{v} + S^{**}_{v}) + \left(1 + \frac{S^{**}}{s}\right)K_{2}(1 - \lambda)(S_{v} + S^{**}_{v}) - 1 + \frac{S^{**}}{s}\right)\sigma(S_{u} + S^{**}_{u}) + \left(1 + \frac{S^{**}}{s}\right)K_{3}(1 - \sigma)(S_{u} + S^{**}_{u}) - 1 + \frac{S^{**}}{s}\right) + \left(1 + \frac{S^{**}}{s}\right)K_{3}(1 - \sigma)(S_{u} + S^{**}_{u}) - 1 + \frac{S^{**}}{s}\right) + \left(1 + \frac{S^{**}}{s}\right)K_{3}(1 - \sigma)(S_{u} + S^{**}_{u}) - 1 + \frac{S^{**}}{s}\right) + \left(1 + \frac{S^{**}}{s}\right)K_{3}(1 - \sigma)(S_{u} + S^{**}_{u}) - 1 + \frac{S^{*}}{s}\right)K_{3}(1 - \sigma)(S_{u} + S^{*}_{u}) - \frac{S^{*}}{s}\right)K_{3}(1 - \sigma)(S_{u} + \frac{S^{*}}{s}\right)K_{3}$$

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If U < N, then ____ will be negative definite along the solution path of the system. This means that ____ < 0 and ___ = 0 only at EVD – Free equilibrium point. This according to LaSalle's invariant principle implies that the EVD - free equilibrium is globally asymptotically stable.

7. Numerical Simulations

Using MATLab software the numerical simulations of the EVD model was performed in order to see the effect of all our incorporated control measures when combined and what history the fractional order model will give us at different values of alpha which is the order of the fractional order model. The model was implemented using the population of Liberia which was estimated to be 4396554 in the year 2014 ^[23]. We then estimate our initial conditions and parameter values as follows; S (0) = 4396521, I (0) = 33, D_u(0) = 24, E_O(0) = 74, E (0) = 0, E_T(0) =

 $\begin{array}{l} 0, \ I_i \left(0 \right) = 9, \ I_T \left(0 \right) = 0, \ I_N \left(0 \right) = 0, \ R \left(0 \right) = 0, \ S_v \left(0 \right) = 1758608, \ S_u \left(0 \right) = 2637913, \ S_{vc} = 527582, \ S_{vn} \left(0 \right) = 1231026, \\ S_{uc} \left(0 \right) = 1582748, \ S_{un} \left(0 \right) = 1055165, \ S_r \left(0 \right) = 6000, \ E_r \left(0 \right) = 0, \ I_r \left(0 \right) = 0 \end{array}$

Parameter	Values	Source	Parameter	Values	Source	Parameter	Values	Source
S			S			S		
Р	422	[23]	α	0.07143	[17]	ρ	0.0314862	[27]
Λ	100	Assume	α	0.02741	Assume	ξ	0.2443	Assume
		d			d			d
μ	0.000024657	[23]	θ	0.08333	[22]	ω	0.5	Assume
	5							d
μ	0.08	Assume	θ	0.014	Assume	${\Phi}$	0.6	Assume
		d			d			d
r	0.05	[10]	J	0.10518	[17]	ξ	0.3110	Assume
				6				d
K	0.895	Assume	J	0.17	[27]	q	0.5	Assume
		d						d
K	0.765	Assume	S	0.2257	[17]	т ,т ,т	0.03,0.00003,0.01,0.0003,0.00	Assume
		d				,т ,т	3	d
Κ	0.886	Assume	S	0.25	[30]	e , e , e	0.07,0.00007,0.0001,0.0007,0.	Assume
		d				, e , e	007	d
λ	0.02	Assume	S	0.148	Assume	n, n, n,	0.04, 0.00004,	Assume
		d			d	n , n	0.001,0.0004,0.004	d
σ	0.07	Assume	ξ	0.11386	[17]	<i>t</i> , <i>t</i> , <i>t</i> ,	0.09, 0.00009,	Assume
		d				t,t	0.0002,0.0009,0.009	d
τ	0.06	[27]	ξ	0.0901	[27]			

Table C: Model Parameter Values



Results

Now, with the initial values and fixed parameter values in Table C, the numerical solutions for our model at different values of alpha (α) = 0.01, 0.1,0.7 and 1, the results obtained from MATLab computer software are shown in Figure 2, Figure 3 and Figure 4 as follows;



Figure 2: Susceptible Human and Animal Populations

Figure 2: The simulation graph showed the graphs of the susceptible human and animal populations within 60 days. It showed that the susceptible human population decreased with time but never got to zero. The vaccinated and unvaccinated populations both increased initially and the unvaccinated population reduced drastically with time while the vaccinated did not. The susceptible vaccinated and unvaccinated condom users and non condom users populations all decreased with

time but the susceptible unvaccinated non condom users population decreased the most and faster also while the susceptible vaccinated condom users population decreased the least and slower. The susceptible animal population decreased with time but did not get to zero. The graph shows that as the value of alpha is being increased the fractional order solution tends to the integer order solution as for each population.



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Figure 3: Exposed, Infectious, Recovered and Dead Unburied Human Populations

Figure 3: The simulation graphs showed the graphs of the human exposed and infectious populations with the recovered and dead unburied populations over a period of 60 days. It showed that the exposed population drastically increased from initial time and got to its peak before 10 days before the population reduced with time. The exposed treated and quarantined populations both increased also before they decreased but the exposed quarantined population increased the most. The infectious populations also increased and later decreased with time but the infectious isolated population increased the most while the infectious not treated population increased the least. The recovered and dead unburied populations both increased initially, got to their peaks and decrease with time but the recovered population increased the most. Then also as the value of alpha is being increased the fractional order solution tends to the integer order solution as for each population.



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Figure 4: Exposed and Infectious Animal Population with all the Populations at alpha = 0.01 Figure 4: The simulation graphs showed the exposed and infectious animal populations with the entire human and animal populations at alpha = 0.01 within a period of 7 days. It showed that the exposed and infectious animal populations both increased and got to their peaks before both of them decreased but the exposed animal population increased the most. It also showed that some of the populations experienced a chaotic motion at alpha = 0.01 within the first 7 days. This shows that at this value of alpha the system is unstable.

Discussion

In integer or classical order calculus, the operations are focused mainly at the integers while fractional order calculus is actually a more generalizes type of calculus which puts into consideration every real number, that is $\alpha > 0$. The fractional order model of a system can be compared to the integer order model of the system especially when $\alpha \rightarrow 1$. Fractional calculus may improve the understanding of biological processes because fractional differential equations can see past events of the system being considered. At $\alpha = 1$, fractional order solution becomes inter order. The numerical simulations for different values of alpha with their corresponding effects on the disease spread in the population shows that the fractional order model is sensitive to the value of α which is the order of the fractional model. This means that the fractional order Ebola Virus Disease transmission dynamics model can help in predicting the spread of the virus in the population in time.

The graph of each population, Figure 2, Figure 3 and Figure 4 shows that as the value of alpha is being increased, the value of the fractional order solution (alpha = 0.1 and alpha = 0.7)gets closer and closer to the integer order solution (alpha = 1) as expected. At alpha = 0.01 (Figure 4) the graph showed that some of the populations experienced a chaotic motion within the first 7 days. Chaos is something related to physics. If a physical system contains many input parameters and the behavior becomes sensitive to even small changes in inputs then such system is chaotic in nature. Chaotic systems are unstable which means that a small parameter in the model can change the equilibrium



points and this change the solution trajectories to a chaotic behavior that is difficult or impossible to determine in a precise way.

8 Conclusion

In this study, the general epidemiology of the Ebola Virus Disease is considered and we formulated a fractional order model for the dynamics of Ebola Virus Disease detailed with recent developments in the area of the disease. This is to help see what happened at those times that the integer order model of the disease could not capture. The effective reproduction number for the model was computed and estimated to be less than one and used in the stability analysis of the equilibrium points of our model. The EVD- Free equilibrium of the model was found to be locally asymptotically stable as long as $R_E < 1$, which means that the disease would be eliminated from the system within a short period of time when our control measures are well implemented. The EVD - Infection equilibrium was also found to be unstable when $R_E < 1$ and exhibits a forward bifurcation near $R_E = 1$. This means that the control of the virus in the population is independent on the number of the individuals initially infected. The disease will be eradicated from the population with all our control measures put in place since our $R_E < 1$. Finally, the numerical simulations of the model was carried out using MATLab computer software which showed that our fractional order model of the dynamics of Ebola Virus Disease can produce interesting results. The numerical simulation result confirmed that with all our control measures strictly implemented that the disease will die out of the population within a short time and that the fractional model helped show the previous activities of the disease. With these obtained results we believe we have added to the transmission dynamics of Ebola Virus Disease by using fractional derivatives of order alpha. Acknowledgement None

Authors Contributions

All authors contributed in writing the manuscript, interpreting the findings and approved the final version for publication. Conflict of Interests The authors declare that there is no conflict of interests regarding the publication of this paper. Availability of data and materials The data and materials used in this work are all available on request.

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