

SIMULATION AND VISUALIZATION OF THE GENERALIZED FORMULATION OF THE BIOMECHANICAL DYNAMICS OF INFECTED PERSON AND TREATMENT STRATEGIES

¹Egboro S. A., ²Imah M. O., ¹Osafire E. O., ¹Enaibe E. A. and ^{2,3,*}Akpojotor G. E.

¹Department of Physics, Federal University of Petroleum Resources, Effurun, Nigeria

²Department of Physics, Delta State University, Abraka, Nigeria

Abstract

The purpose of our study here is to formulate the generalized biomechanical equation controlling the characteristic wave of the host which is the infected person: characteristic wave here means a wave that has all the wave characteristics of the source wave. The characteristic wave of the generalized biomechanical dynamics of the infected person is obtained by superposing the characteristic wave of the external agent (disease or poison collected designated as parasite here) on the healthy person. Therefore, the generalized equation can be used to obtain the characteristics of the wave of an infected person which are important to develop treatment strategies for the various infections. To demonstrate the importance of such data, we design and code a programme in Python for simulating and visualizing the generalized biomechanical equation as the characteristic wave of the host in various waveforms to mimic the superposed waves and then renormalized them into sinusoidal waveform that is characteristic of a healthy man as the possible treatment strategies. The motivation and path for actualization of our proposal is then discussed.

1.0 Introduction

Communicable diseases commonly referred to as infectious diseases are disorders caused by organism such as parasites, viruses, bacteria and, fungi. Some examples of these infectious diseases are Coronaviruses, Diphtheria, Ebola, Flu, Hepatitis, Hib, HIV/AIDS, HPV, chickenpox, Measles, Tetanus, Whooping Cough, Zika and so on are a fact of life. The AIDS epidemic, the recent SARS epidemic, recurring influenza pandemic (Fauci, 2001; Rogers, 2020; Jong and Stevens, 2021). Since time immemorial, these infectious diseases have not only been burden to human health but have been causing disabilities and even deaths as well as periodically threatened the survival of entire human race (Brachman, 2003; Holmes et. al., 2017; Akpojotor et. al., 2020). During this time, modeling of these infectious diseases has been growing. In particular, there is growing number of modeling techniques to study the dynamics of the spread of infectious diseases and possible strategies to curb them because direct experimental study on the spread of a disease hence how to curb it among humans is not ethical (Ming et al, 2016).

Modeling is an attempt to mimic reality in a controlled scenario (Akpojotor et. al., 2010; Akpojotor, 2014). A mathematical model is a representation of a system or scenario using mathematical concepts and languages to gain qualitative and/or quantitative understanding of some real-world problems and to predict future behaviour (Karen et al, 2016). However, Akpojotor (2014) asserted that in physics, a model can be conceived as a simple and well understood phenomenon or system designed to represent and explain a complex and not well understood phenomenon or system. Models are being

*Correspondence Author: Akpojotor G.E., Email: akpogea@delsu.edu.ng, Tel: +2349033636059

used to address an ever-expanding number of diseases and public health questions (Knight et. al., 2016; Kretzschmar, 2020) as well as to explore the importance of biological and ecological details on disease transmission (Grassly and Fraser, 2008), biological and physical dynamics of the disease (Enaibe and Idiodi, 2013; Enaibe and Omosede, 2013; Enaibe et. al, 2013) and possible treatments (Maziarz, and Zach, 2020). Thus modeling infectious diseases depends most often on the approach of the problem which in turn determines the type of model, mathematical or physical.

In general there are two approaches to modeling infectious diseases. The first is the modeling of infectious diseases as a tool to study the mechanisms by which diseases occur, spread and become pandemic in order to evaluate strategies to control an epidemic and possibly to predict and even checkmate future course of an outbreak (Daley and Gani, 2005; Ivorra et. al., 2014; Ivorra et. al., 2015; Kucharski et al., 2020). Therefore the goal of the mathematical description in this approach is to predict the equilibrium state in which there are no new infections, which means that the spread has stopped (Huo et. al, 2016; Nave et. al., 2020). Therefore, the optimal state is equilibrium stability of the transmission..

The earliest account of mathematical modeling of spread of disease was carried out in 1760 by Daniel Bernoulli, who created a mathematical model to defend the practice of inoculating against smallpox (Hethcote, 2000). Modeling vector-borne infectious diseases such as Dengue fever, West Nile Virus, Lyme disease, and malaria was first carried out by Sir Ronald Ross in his study of malaria transmission in 1916 and subsequent models for other kinds of diseases followed. Recently, researchers have developed various mathematical models that describe the evolution of the Coronavirus in the populations of various countries (Kucharski et al., 2020).

The second approach is the modeling of infectious diseases as a tool to study the biomechanical dynamics of these diseases in order to possibly find strategies for their treatments (Waziri and Makinde, 2012; Enaibe and Idiodi, 2013; Enaibe and Omosede, 2013; Enaibe et. al, 2013; Weickenmeier et. al., 2018; Lindley, 2018;). The modeling strategy here is to first delineate the biological behaviour of the presence of the disease in the host who is the infected person. Thereafter, the physical description of this biological behaviour is designed so that it can be theoretically formulated. In other words, the model should possess the domineering properties of the system that it is supposed to represent (Akpojotor, 2014) which can be infected person with disease (Enaibe and Idiodi, 2013; Enaibe and Omosede, 2013; Enaibe et. al, 2013) or even a poisoned person as demonstrated with the Schrodinger cat (Akpojotor, 2020).

In the case of infected person, Enaibe and co-workers the aforementioned literature have done a number of studies of the HIV/AIDS infection. The biological behaviour from clinical literature is to consider the virus to be feeding on the active cells and in the process weakens the immune system of the host. The physical description of this scenario is to consider it as the superposition of the virus vibration on the host vibration and the resultant superposed wave describe the infected person. Thus the principal physical property of both the host and the parasite is that they are living matter and therefore possess vibrations. In the reductionist approach of physics, all matter, living and non-living, are made of atoms. For example, an average adult human male of 70 kg is estimated to be made up of about 7×10^{27} atoms (Helmenstine, 2019). A common property of atoms is that they are constantly vibrating. Therefore, in their pilot study, Enaibe and Idiodi (2013) considered the human heart as a transducer of this vibration so that the blood stands as a means of conveying this vibration to all units of the human system. The theoretical formulation of this physical description of the dynamic mechanical wave characteristics of HIV/AIDS in the human blood circulating system is the formulation of the constitutive carrier wave equation (CCWE) on the basis of the vibratory dynamic components of the human (host) parameters and those of the HIV (parasite) parameters in the pilot study (Enaibe and Idiodi, 2013). The most influential parameter of the CCWE is the multiplicative factor λ whose physical range varies from the onset of the effect of the disease till the host biological system ceases to exist.

In an independent study, Akpojotor (2020) demonstrated that the part of poisoning the Schrodinger cat can be modeled as simple harmonic oscillator (SHO). The purpose of the modified Schrodinger cat experiment (MSCE) was to mimic an ideal measurement in quantum mechanics following the recent experiment by Pokorny et. al. (2020) on tracking the dynamics of a naturally occurring ideal measurement process with enticing results. The biological behaviour of the modified Schrodinger cat is that the poison it inhales will distort its heart beat. Therefore, the effect of the varying the amount of poison vile with time can be determined from the heart rate of the cat depending on its mass. The physical description is that the heart rate can directly be measured by the heart pulse which in turn can be measured by the fingers to be a vibration that can be conceived simply as a to and fro movement. Therefore, movement of the heart of the cat can be considered as a simple harmonic motion (SHM). Thus the theoretical equation of the SHO is adopted to be the poisoning part of the Schrodinger Cat Experiment: this equation is a homogenous second order differential equation of the heart pulse with constant coefficients as the domineering parameters: one of these parameters is the amount of poison denoted as λ because it affects the normal flow of the blood in the heart hence the heart beat.

Quickly, lets explain further how λ emerges in the SHO equation. In the theoretical formulation of the SHO, λ is the damping constant in the linear damping force due to the connection of the bob to a snapshot. Thus the SHO equation can be

envisage as the product of the superposed damping force on the normal SHO which in the case of the MSCE, it is the wave of the poison being superposed on the normal wave of the heart beat of the cat. The resultant superposed wave will have the characteristic wave of the poisoned cat; characteristic wave here means a wave that has all the wave characteristics of the source wave. This physical scenario can be extrapolated to poisoning of man. Therefore, in general, the effect of the external agent such as poison or disease on the host can be determined from the characteristic wave of the host so that λ can be used to monitor these effects from the onset till the host heart pulse stops. This is known as quenching of the host characteristic wave which is the death state.

It is easy to observe that the λ in the SHO modeling of poisoned Schrodinger cat in Akpojotor (2020) has one to one correspondence with the λ in Enaibe and co-workers CCW modeling of the HIV/ AIDS infected person. They both represent the effect of the poison and disease respectively on the host with time. Therefore they capture the window period which is the time for the effect of the poison or disease to manifest to quench the wave form of the host so that the amplitude is zero. The implication of this observation opens the possibility that the CCW equation can be generalized not only for infectious diseases but also to account for animal including man's poisoning of any kind just as the SHO equation can be generalized not only for poisonings but also to account for animal including man's infectious diseases of any kind. It is important to point out that this generalized CCW equation will have a one to one correspondence with the generalized SHO equation. The reason is that the physics used in both modeling techniques is the same: the host (man or any other animal) is made of atoms that their vibrational dynamics can be depicted as a normal characteristic sinusoidal waveform while the disease (living matter) and poison (non-living matter) to be collectively named simply as parasite are also made of atoms and therefore have their own vibrational dynamics. The basic assumption in developing both modeling techniques is that the parasitic vibration when superposed on the host vibration will yield the resultant generalized CCW equation or generalized SHO equation.

The world in general is still suffering from the challenges of various infectious diseases as well as all kind of poisoning. The current COVID-19 pandemic has affected the entire world so much that it is often said that it has created a new global normal. The COVID-19 however, is a localized human infectious disease unlike the HIV/AIDS which is a non-localized disease: 'localized' here means it affects only specific parts of the body while 'non-localized' means it affects all parts of the body. The implication is that the HIV/AIDS studies of Enaibe and co-workers have been on a non-localized disease. Therefore there is need to extend their approach to localized diseases such as the COVID-19, tuberculosis, gonorrhoeal, leprosy and others. Further, the approach can also be extended to poisons' effects on humans. Thus such extended approach can be considered as a generalized physical model to study the biomechanical behaviour of these diseases which will provide data to strategize treatment for these diseases as well as future diseases. The purpose of our study here is to formulate the generalized constituted carrier wave equation and the generalized SHO equation as generalized formulation of the biomechanical dynamics governing the characteristic wave of the host. This will be done in Section 2. The application of the generalized formulation to the Coronavirus family including the COVID-19 is an ongoing project. However, to galvanize interest in this entire project, we will also demonstrate here one of the significance of the project: how the understanding of the physics of the biomechanical dynamics of the infectious diseases or poisons in the host opens the possibility to strategize future treatments for them. This will be done by using simulation and visualization of a superposed wave forms mimicking the characteristic wave of the host and them renormalized as the treatment into healthy person characteristic sinusoidal waveform with normal modes in Section 3. This will be followed by a summary and a conclusion in Section 4.

2,0 Generalized theoretical formulation

As stated in the preceding section, a model in physics can be conceived as a simple and well understood phenomenon or system designed to represent and explain a complex and not well understood phenomenon or system (Akpojotor, 2014). The modeling strategy is to first delineate the biological behaviour of the presence of the parasite in the host who is the infected person. Thereafter, taking into account the domineering properties of the system that it is supposed to represent, the physical description of this biological behaviour is designed so that it can be theoretically formulated. As stated above also, the physical description effects of any parasite on the host is to consider it as the superposition of the parasitic vibration on the host vibration and the resultant superposed wave describe the characteristic wave of the infected person.

2.1 Generalized constitutive carrier wave equation

To mathematically formulate the physical description of an infected person with a parasite let us, adopt the approach of Enaibe and Idioidi (2013) by considering wave defined by the non - stationary displacement vectors representing the healthy person characteristic wave, y_n whose propagation depends on the inbuilt raising multiplier $\beta (= 0, \dots, 1)$

$$y_n = a\beta \cos (\vec{k}\beta.\vec{r} - n\beta t - \varepsilon\beta) \tag{2.1}$$

and the parasite characteristic wave, y_p with a multiplicative factor or an inbuilt raising multiplier λ_n ($n = 0,1,2,\dots, \lambda_{\max}$) :

$$y_p = \beta\lambda_n \cos (\vec{k}'\lambda_n.\vec{r} - n'\lambda_n t - \varepsilon'\lambda_n) \tag{2.2}$$

where all the symbols retain their usual meanings.

We quickly point out that both β and λ_n which are the inbuilt multipliers are dimensionless and as the name implies, they are capable of gradually influencing the basic intrinsic parameters of both waves respectively with time.

Now in line with the physical design, let superposed Eqs.(2.1) and (2.2) to obtain the characteristic wave of the host y_h :

$$y_h = y_1 + y_2 = a\beta \cos (\vec{k}\beta.\vec{r} - n\beta t - \varepsilon\beta) + b\lambda_n \cos (\vec{k}'\lambda_n.\vec{r} - n'\lambda_n t - \varepsilon'\lambda_n) \tag{2.3}$$

Like in the related previous studies of Enaibe and co-workers in the literature, it can be shown after some lengthy mathematical process that the resultant superposed wave which is the CCWE that describes the superposition of the parasitic wave on the host wave will be

$$y_h = \sqrt{(a^2 - b^2\lambda_n^2) - 2(a - b\lambda_n)^2 \cos ((n - n'\lambda_n)t - (\varepsilon - \varepsilon'\lambda_n))} \times \cos ((\vec{k} - \vec{k}'\lambda_n).\vec{r} - (n - n'\lambda_n)t - E) \tag{2.4}$$

Eq.(2.4) describes the activity and performance of most physically active systems of the infected person

2.2 Generalized simple harmonic oscillator equation

Vibrating systems in general, can be categorized as linear systems whose motion is described by linear differential equations; and nonlinear systems whose motion is governed by nonlinear differential equations (Yang, 2001), For linear systems, many well-developed methods of vibration analysis are available, as the superposition principle is valid. The human heart vibration is a linear system and therefore can be described as free oscillation using the differential equation:

$$m\ddot{y}_n + \beta y_n = 0 \tag{2.5}$$

while the parasite on the on contrary is described by a damping force

$$\lambda_n \dot{y}_p \tag{2.6}$$

where all the symbols retain their usual meanings.

Again in line with the physical design, let us superposed Eqs.(2.5) and (2.6) to obtain the characteristic wave of the host y_h

:

$$m\ddot{y}_h + \lambda_n \dot{y}_h + \beta y_h = 0 \tag{2.7}$$

In principle, Eqs.(2.4) and (2.7) have one to one correspondence and are the generalized mathematical formulation of the biomechanical dynamics that governs the characteristic wave of the infected person.

3.0 Simulation and visualization simplified treatment design from data to be provided

Our simulation is based on the assumption that the characteristic wave of the infected person can have any incoherent waveform. Therefore, the treatment strategy will be to renormalize these various forms into the sinusoidal waveform which is the characteristic wave of a healthy person. The coding is done in Python using VPython, Numpy and Matplotlib libraries (Akpootor et. al., 2010) and is available on request to the corresponding author. The salient feature is that the superposed wave can be simulated to be in various waveforms by choosing the appropriate combinations for the switching values (x, y, z) and (x', y', z') as show in the extract from the programme below.

```
# Code for developing a superposed Function
step_fn_data = []
for i in arange(0, 15, 0.5):
    if math.fmod(i,2) == 0:
        switching_value = [x, y, z]
    else:
        switching_value = [x', y', z']
    step_fn_data.extend(switching_value)
d = curve(x = arange(-35,size(step_fn_data)- 40), y = step_fn_data)
d.color = color.red
```

In nature, this superposition of the λ_n and λ_p can be done by several complex techniques and therefore all these techniques will be depicted by a red box so that it become the source of λ_h in our simulation. Now in general, treatment is to improve the condition of the infected person and cure is when the condition has been completely improved which implies that the disease has been completely removed (Kolenchuk, 2019). There are very many and varied treatment techniques to cure infected diseases. So as we did for the superposition techniques, we will depict these treatments by a blue box so that it becomes the converter of λ_h into λ_n in our simulation. Our programme can be used to simulate various waveforms which are then renormalized into a normal sinusoidal waveform until the infected state is converted by the treatment into a cure state that is depicted with a green box as the source of the λ_n now in green colour. To demonstrate the visualization here, we have taken snapshots at three levels of treatments: at the onset of the treatment, when the effect of treatment is pronounced and when the treatment has resulted to cure as shown in Figure 1 wherein the λ_h is an M-shaped waveform. Figure 1(a) is a snapshot showing the y_h as it begins to be renormalized by the treatment into the y_n , Figure 1(b) is a snapshot showing the renormalizing of y_h into y_n increases with more treatment and Figure 1(c) is a snapshot showing that the y_h has been completely renormalized into y_n so that $y_h \Rightarrow y_n$ hence $y_h = 0$ which implies a cure. It is interesting to point out that our programme can be used to simulate and visualize the treatment of an infected dying state as shown in Figure 2 wherein y_h is simulated as an almost linelike waveform with fast decreasing characteristics of wave. The Figure 2(a) is a snapshot showing the y_h as it begins to be renormalized by the treatment into the y_n , Figure 2(b) is a snapshot showing the renormalizing of y_h into y_n as the treatment increases and Figure 2(c) is a snapshot showing that the y_h has been completely renormalized into y_n so that $y_h \Rightarrow y_n$ hence $y_h = 0$ which implies a cure. Finally, we simulate and visualize a healthy person that is vaccinated. In this case, the vaccination obliterate the characteristic wave of the parasite so that $y_n + (y_p = 0) \Rightarrow y_n$. In nature, this means the vaccination has made the healthy person to be immune to the parasite.

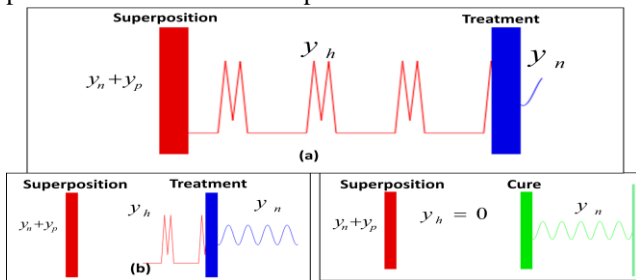


Figure 1: The snapshots of the superposition of the characteristic wave of a healthy person y_n and the characteristic wave of the parasite y_p resulting in an M-shape waveform as the characteristic wave of the infected person y_h which is then renormalized by treatment into the characteristic wave of a healthy person y_n . (a) A snapshot showing the fully resultant characteristic wave y_h as it begins to be renormalized by the treatment into the y_n (b) A snapshot showing the renormalizing of y_h into y_n increases with more treatment (c) A snapshot showing that the y_h has been completely renormalized into y_n which implies a cure.

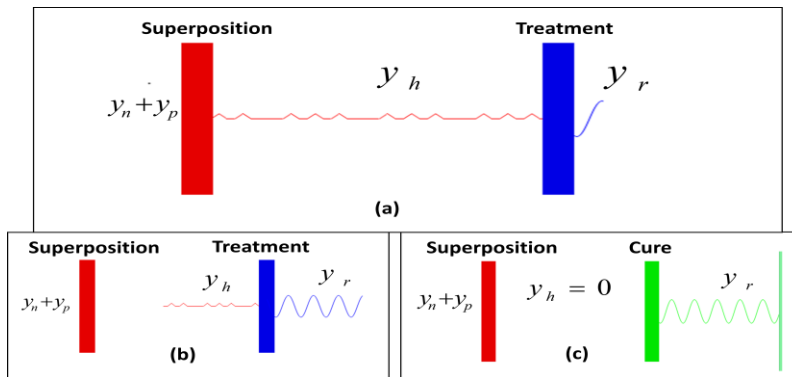


Figure 2: The snapshots of the superposition of the characteristic wave of a healthy person y_n and the characteristic wave of the parasite y_p resulting in an almost linelike waveform as the characteristic wave of the infected person y_h which is then renormalized by treatment into the characteristic wave of a healthy person y_n . (a) A snapshot showing the fully resultant characteristic wave y_h as it begins to be renormalized by the treatment into the y_n (b) A snapshot showing the renormalizing of y_h into y_n increases with more treatment (c) A snapshot showing that the y_h has been completely renormalized into y_n which implies a cure.

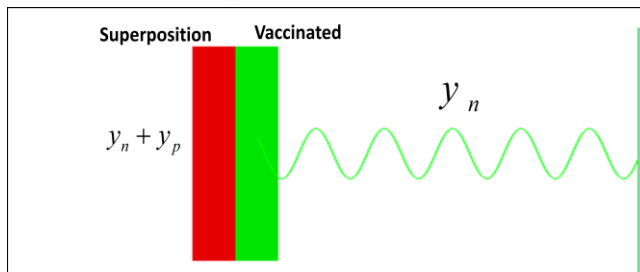


Figure 3: The snapshots of the superposition of the characteristic wave of a healthy person y_n and the characteristic wave of the parasite y_p in which the latter is obliterated by the vaccine so that y_n remains unaffected.

Conclusion

We have subtly shown that the equation of the characteristic wave of an infected person from the previous studies of Enaibe and co-workers and equation of the characteristic of the poisoned Schrodinger cat in Akpojotor (2020) have one to one correspondence since they are both formulated from the superposition of the characteristic wave of the external agent (disease or poison) on the characteristic wave of the healthy person. Thus we pointed out here that the two formulations can be generalized to formulate the biomechanical dynamics of the an infected person. The data to be obtained are the wave characteristics of the healthy person, wave characteristics of the parasite which could be infectious disease or poison here and the wave characteristics of the infected person. The motivation is that the availability of these data on the biomechanical dynamics of the healthy person, parasite and infected person will be useful in designing treatment strategies. This again we subtly demonstrated by simulating and visualizing how the characteristic wave of the infected person mimicked in various waveforms which are then renormalized as the treatment strategies into sinusoidal waveform of a healthy person. It is pertinent to point out that the treatment strategies are vast and varied as they include both orthodox and unorthodox practices in general. We also demonstrated the use of vaccination to boost the immunity of healthy person using the snapshots in Figure 3. Therefore, the actualization of this study requires interdisciplinary contributions and is an ongoing project.

References

- [1] Akpojotor G. A. (2014) Nonlinear Dynamic Modelling and Visualization of the Phase Diagram of the High Temperature Superconducting Cuprates. *International Journal of Theoretical and Mathematical Physics* 4, 103-109.
- [2] Akpojotor G. E. (2020) Simulation and Visualization of the Predictable Parts of the Schrodinger Cat Experiment. American Physical Society (APS) March Meeting held April 18–21, 2020 was to hold at Washington D.C, USA but later changed to a virtual meeting due to the COVID-19 pandemic. <http://meetings.aps.org/Meeting/APR20/Session/Y14.7>. Videos of all online presentations can only be assessed by members of the APS. Request for video to the Author: akpogea@delsu.edu.ng.
- [3] Akpojotor G. E., Ehwerhemuepha L., Echenim M. and Akpojotor F. (2010), Modeling and visualization of some physics phenomena with Python simulations. *African Journal of Physics* Vol.3, 94-118.
- [4] Akpojotor G. E., Morka E., Jonathan A. M., Michael O. E., Egbojodu W. O., Okposo N. I., Okolugb B. C., Ogharanduku T. I., Okpara N., Odibo E., Ossiaugbo M. I., Ndakara E. O., Okinono O., Obi C. k., Owhe-Ureghe U. B., Tonukari N. J., Nmorsi O. P. G. and Egwunyenga A. O. (2020) Aspects of epidemiological study of COVID-19 pandemic: Perception and beliefs in Delta State. *Nigerian Journal of Science and Environment*, 18 (1), 281-295.
- [5] Brachman P. S. (2003) Infectious diseases: past, present, and future. *International Journal of Epidemiology* 32, 684–686.
- [6] Daley D. J. and Gani J. (2005). *Epidemic Modeling: An Introduction*. New York: Cambridge University Press.
- [7] Grassly N. C. and Fraser C. (2008) Mathematical models of infectious disease transmission. *Nat Rev Microbiol* 6: 477–487.
- [8] Enaibe E. A. and Idiodi J. O. A. (2013). The biomechanics of HIV/AIDS and the prediction of Λ . *The International Journal of Engineering and Science* 2, 43 – 57.
- [9] Enaibe E. A. and Omosede O. E. (2013) Energy Attenuation Mechanism of a Carrier Wave propagating in a Viscous Fluid. *Journal of Applied Physics* 4, 59 – 74.
- [10] Enaibe E. A., Omosede O. E. and Idiodi J. O. A (2013) Quantitative treatment of HIV/AIDS in the human microvascular circulating blood system. *International Journal of Computational Engineering Research* 3, 1 – 13.
- [11] Fauci A. S. (2001) Infectious Diseases: Considerations for the 21st Century, *Clinical Infectious Diseases* 32, 675–685.
- [12] Helmenstine A. M. (2019) Atoms in the Body, Retrieved on 10/03/2020 from <https://www.thoughtco.com/how-many-atoms-are-in-human-body-603872>
- [13] Hethcote H.W. (2000) The mathematics of infectious diseases. *Society for Industrial and Applied Mathematics* 42, 599–653.
- [14] Holmes K. K., Bertozzi S, Bloom B. R, et al. (2017). Major Infectious Diseases: Key Messages from Disease Control Priorities (3rd Edition.) In: Holmes K. K., Bertozzi S., Bloom BR, et al.(Editors) Major Infectious Diseases(3rd edition.) Washington (DC): The International Bank for Reconstruction and Development / The World Bank; Nov 3. Chapter 1. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK525197/> doi: 10.1596/978-1-4648-0524-0_ch1
- [15] Huo H. F., Chen R. and Wang X. Y. (2016) Modelling and stability of HIV/AIDS epidemic model with treatment. *Applied Mathematical Modelling* 40, 6550–6559
- [16] Ivorra B, Martinez-Lopez B, Sanchez-Vizcaino J. M. and Ramos A. M. (2014). Mathematical formulation and validation of the Be-FAST model for classical swine fever virus spread between and within farms. *Annals of Operations Research* 219(1), 25–47.
- [17] Ivorra B., Ramos A.M. and Ngom D. (2015) Be-CoDiS: a mathematical model to predict the risk of human diseases spread between countries—validation and application to the 2014 Ebola virus disease epidemic. *Bulletin of Mathematical Biology* 77(9), 1668–1704.
- [18] Jong E. C. and Stevens D. J. (2021) *Netter’s infectious diseases*. Elsevier.
- [19] Knight G. M., Dharan N.J., Fox GJ, Stennis N., Zwering A., Khurana R., Dowdy D. W.(2016) Bridging the gap between evidence and policy for infectious diseases: how models can aid public health decision-making. *Int J Infect Dis.* 42, 17–23.
- [20] Kolenchuk T. (2019) A Theory of Cure. https://www.researchgate.net/publication/338167157_A_Theory_of_Cure_-_Paper_-_Update_Dec_25_2019
- [21] Kretzschmar M. (2020) Disease modeling for public health: added value, challenges, and institutional constraints. *Journal of Public Health Policy* 41, 39–51.

- [22] Kucharski A. J, Russell T. W, Diamond C., Liu Y., Edmunds J., Funk S., Eggo R. M., Sun F., Jit M, Munday J. D., Davies N., Gimma A., Van Zandvoort K., Gibbs H., Hellewell J., Jarvis C. I., Clifford S', Quilty B. J., Bosse N. I., Abbott S., Klepac P. and Flasche S. (2020) Early dynamics of transmission and control of COVID-19: a mathematical modelling study. *Lancet Infectious Diseases* 20(5):553–558.
- [23] Lindley D. (2018) A Physical Model for Neurodegenerative Disease. *Physics* 11, 104.
- [24] Maziarz M. and Zach M. (2020) Agent-based modelling for SARS-CoV-2 epidemic prediction and intervention assessment: A methodological appraisal. *Journal of Evaluation in Clinical Practice*. 26 (5): 1352–1360.
- [25] Ming R., Liu J., Cheung K. W. and Wan X. (2016). Stochastic modelling of infectious diseases for heterogeneous populations. *Infect Dis Poverty* 5, 107
- [26] Nave O., Hartuv I. and Shemesh U. (2020). Θ -SEIHRD mathematical model of Covid19-stability analysis using fast-slow decomposition. *PeerJ* 8:e10019. DOI 10.7717/peerj.10019,
- [27] Pokorny F., Zhang C., Higgins G., Cabello A., Kleinmann M. and Hennrich M. (2020) Tracking the Dynamics of an Ideal Quantum Measurement. *Phy Rev Lett* 124, 080401.
- [28] Rogers K. (2020) *Engineering Solutions for Epidemics and Pandemics*. The Rosen Publishing Group, Inc, New York.
- [29] Yang B. (2001) *Theory of vibration: Fundamentals*. Academic Press. doi:10.1006/rwvb.2001.0112.
- [30] Waziri A.S. and Makinde O.D. (2012) Mathematical modelling of HIV/AIDS dynamics with treatment and vertical transmission, *J. Appl. Math.* 2 (3) 77–89 .
- [31] Weickenmeier J, Kuhl E. and Goriely A. (2018) Multiphysics of Prionlike Diseases: Progression and Atrophy. *Phys. Rev. Lett.* 121, 158101.