

# A human-fish model under COVID-19 disease incidence

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## SUMMARY

Based on the original Fish-Human Model, this investigation demonstrates the relation between fish and human under the influence of a disease transmissible disease in human such as COVID-19. The infective disease (COVID-19 as example) spreads among interacting groups, causing demographic changes among three categories of people. (S: susceptible, I: infected, R: recovered). This model is universal enough to be applied for different transmission diseases, since several common features of infectious diseases are considered.

The main results concern the analysis of local and global stability, the transmission features of common infectious diseases. A transmissible disease may cause a series of population mobility among different human categories, varying demographical factors such as birth/death rate and infection/recovery rate. In the following paragraphs, a more specific description about those will be demonstrated.

## 1. THE MODEL

Predation between man and fish has long been a concerned and controversial topic for demographic changes in biomathematical literatures. Additionally, mathematical epidemiology also plays a significant part in present medical science research, successfully simulating the population changes under the outbreak of different infectious disease. Recently an increasing number of research and experiments have been held to study demographic topics in the crossing field of mathematical epidemiology and biology. Along this research direction, many models combining the influence of natural population growth and transmissible diseases have been proposed, which could deal with more complicated environment in human reality. Based on Professor Mainul's instructional guidance, a new model has been introduced by us in this investigation, considering fish and man's population growth and the SIR disease model, to study the relation between human and fish.

More specifically, we consider predator-prey model and SIR model (S: susceptible, I: infected, R: recovered), in which the disease can be transmitted among people. In the epidemic system, the  $S$ ,  $I$ ,  $R$ ,  $x$  and  $y$  represent, respectively, the numbers of susceptible, infected, recovered people fish number and total population. To analyze this situation more specifically, now we classify it into two categories: when there exist people and there does not exist people, the reason will be discussed in the following paragraphs.

We assume that the new-born groups belong to the susceptible population at birth, for the coronavirus

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does not transmit between generations to next generations. And the birth rate is proportionate to the consumption rate of fish eaten by human (the amounts of fish eaten by all human at unit time), and the ratio of fish consumption and birth rate of human is  $e$ , called the conversion factor. The eating (consumption) rate of fish also follow the law of mass reaction. Furthermore, we assume that the recovered people have gained immunity, thus are impossible to infected again.

The model is general enough to encompass a wealth of ecosystems, especially a large number of examples of how transmissible diseases affect populations around the global areas, since many common factors of a classical transmissible disease have been considered and calculated.

### Model 1

Letting  $m$  denote the eating rate of fish by human,  $\lambda$  and  $\beta$  represent, respectively, the transmission efficiency of virus (the average number of contacts per person per time) and the rate of human being infected after contacting with human infected.  $\mu_n$  and  $\mu_i$  represent the natural death rate and death rate of human infected,  $\mu$  is rate of death to each group of humans. As for fish,  $r$  means birth rate,  $k$  is carrying capacity of environment of fish.  $A$  and  $B$  are positive constants and  $e$  is the conversion factor. View of the above assumptions the model takes the following form:

$$\frac{dS}{dt} = \frac{emxy}{Ax + B} - \frac{\lambda\beta SI}{y} - \mu_n S - \delta S$$

$$\frac{dI}{dt} = \frac{\lambda\beta SI}{y} - \mu_i I - \gamma I$$

$$\frac{dR}{dt} = \delta S + \gamma I - \mu_n R$$

$$\frac{dx}{dt} = rx \left(1 - \frac{x}{k}\right) - \frac{mxy}{Ax + B}$$

Model (1): there exist people

### Model 2

When the situation of no people exist is considered, Model (1) can be further simplified, which is shown below. The first three ODEs are omitted, we only discuss the ODE for fish:

$$\frac{dx}{dt} = rx \left(1 - \frac{x}{k}\right)$$

## 2. PRELIMINARIES

### 2.1. The SIR model

This model can simulate the behaviour of the number of people in the three groups at the period of epidemic.  $S$  represents the number of susceptible people. At the beginning of the epidemic, the number of susceptible people decreases as the number of infected people ( $I$ ) increases. Gradually the number of recovered ( $R$ ) people increases. some susceptible people remain uninfected. However, some missing part is also missing, such as creating new susceptible people by being born and the removal of susceptible, infected, and recovered people who die.

## 2.2. Basic properties

In this subsection we investigate some preliminary but relevant properties of the dynamical system and stability.

### *Proposition 1 Jacobian matrix and equilibrium stability*

Jacobian matrix is the matrix of all its first-order partial derivatives and its determinant is referred to as the Jacobian determinant. The Jacobian matrix represents the differentiation of  $f$  at every point where  $f$  is differentiable. An equilibrium point is a constant solution to a differential equation. By evaluating the Jacobian matrix at each of the equilibrium points of the system, it can discuss equilibrium stability. If the eigenvalues of the Jacobian determinant all have real parts that are negative, then the system is stable near the stationary point. If at least one of the real parts is positive, then the point is unstable.

### *Proposition 2 Routh–Hurwitz stability criterion*

Given a real polynomial, it is stable if and only if the sequence of determinants of its principal submatrices are all positive. For the application of this article all four roots have negative real part if and only if all the elements of leading principal minors of the matrix are positive. A tabular method can be used to determine the stability when the roots of a higher order characteristic polynomial are difficult to obtain. For an  $n$ th-degree polynomial:

$$a_0\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0$$

## 2.3. Equilibria

The ordinary differential equations have the following six Equilibrium points, since we firstly slightly transform the equations into the form of factorization:

$$0 = \frac{emxy}{Ax+B} - \frac{\lambda\beta SI}{y} - \mu_n S - \delta S$$

$$0 = \frac{\lambda\beta SI}{y} - \mu_l I - \gamma I = I \left( \frac{\lambda\beta S}{y} - \mu_l - \gamma \right)$$

$$0 = \delta S + \gamma I - \mu_n R$$

$$0 = rx \left( 1 - \frac{x}{k} \right) - \frac{mxy}{Ax+B} = x \left( r \left( 1 - \frac{x}{k} \right) - \frac{mxy}{Ax+B} \right)$$

Based on the equation above, we divide the solution of equilibrium into two occasions. The first one is when the population  $y=S+I+R$  is equal to 0 and the other is not. The previous occasion will be discussed first.

### *Equilibrium for Model 2 (Equilibrium $E0$ and $E1$ )*

By solving the only equation of Model 2, we have  $E0=0$  and  $E1=k$ .

### *Equilibrium for Model 1*

As for the second occasion where  $S+I+R$  is different from 0, there will be 4 possibilities based on the 4 given equation above.

### *Equilibrium $E2$*

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Case(i):  $I = 0$  and  $x = 0$ , it gives the result  $S=I=R=x=0$ , which contradicts to the statement above.

### Equilibrium E3

Case(ii):  $I = 0$ ,  $r\left(1 - \frac{x}{k}\right) - \frac{mxy}{Ax+B} = 0$ , it also can be divided into two occasions with  $x = k$  or  $x =$

$$\frac{B\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}{me\left(\frac{\mu_n^2}{\delta} + 2\mu_n + 1\right) - A\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}.$$

### Equilibrium E4

In the first occasion,  $x = k$ ,  $S=I=R=0$  makes a contradiction to the given requirement,  $S+I+R$  is different from 0. Thus, it only remains one occasion as  $I = 0$  and, in this case, we have another equilibrium point E4:

$$S = \frac{\frac{B\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}{me\left(\frac{\mu_n^2}{\delta} + 2\mu_n + 1\right) - A\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}}{\mu_n + \delta} \left(1 - \frac{\frac{B\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}{me\left(\frac{\mu_n^2}{\delta} + 2\mu_n + 1\right) - A\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}}{k}\right)$$

$$I = 0$$

$$R = \frac{\frac{B\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}{me\left(\frac{\mu_n^2}{\delta} + 2\mu_n + 1\right) - A\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}}{\frac{\mu_n^2}{\delta} + \mu_n} \left(1 - \frac{\frac{B\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}{me\left(\frac{\mu_n^2}{\delta} + 2\mu_n + 1\right) - A\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}}{k}\right)$$

$$x = \frac{B\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}{me\left(\frac{\mu_n^2}{\delta} + 2\mu_n + 1\right) - A\left(\frac{\mu_n^2}{\delta} + \mu_n\right)(\mu_n + 1)}$$

### Equilibrium E5

Finally, when

$$0 = \frac{emx(S + I + R)}{Ax + B} - \frac{\lambda\beta SI}{S + I + R} - \mu_n S - \delta S$$

$$0 = \frac{\lambda\beta S}{S + I + R} - \mu_I - \gamma$$

$$0 = \delta S + \gamma I - \mu_n R$$



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 $R=$ 

$$\begin{aligned}
 x = & \left[ \begin{aligned} & \left( \frac{\beta\lambda(\gamma+\mu_I) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right) \left( -\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n \right) (\delta+\mu_n)(\gamma+\mu_I) \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right)^2}{\left( \frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma \right) (\beta\lambda-\gamma-\mu_I)} + \frac{\beta\lambda-\gamma-\mu_I}{\beta\lambda-\gamma-\mu_I} \right) \right] \\ & + B \left[ \begin{aligned} & \left( \frac{\beta\lambda(\gamma+\mu_I) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right) \left( -\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n \right) (\delta+\mu_n)(\gamma+\mu_I) \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right)^2}{\left( \frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma \right) (\beta\lambda-\gamma-\mu_I)} + \frac{\beta\lambda-\gamma-\mu_I}{\beta\lambda-\gamma-\mu_I} \right) \right] \\ & - A \left[ \begin{aligned} & \left( \frac{\beta\lambda(\gamma+\mu_I) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right) \left( -\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n \right) (\delta+\mu_n)(\gamma+\mu_I) \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right)^2}{\left( \frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma \right) (\beta\lambda-\gamma-\mu_I)} + \frac{\beta\lambda-\gamma-\mu_I}{\beta\lambda-\gamma-\mu_I} \right) + em \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right)^2 \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right)^2 \right] \\ & + k \left[ \begin{aligned} & \left( \frac{\beta\lambda(\gamma+\mu_I) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right) \left( -\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n \right) (\delta+\mu_n)(\gamma+\mu_I) \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right)^2}{\left( \frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma \right) (\beta\lambda-\gamma-\mu_I)} + \frac{\beta\lambda-\gamma-\mu_I}{\beta\lambda-\gamma-\mu_I} \right) + em \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right)^2 \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right)^2 \right] \\ & + m \left( \frac{\gamma+\mu_I}{\beta\lambda-\gamma-\mu_I} + 1 \right) \left( \frac{-\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \mu_n}{\frac{\delta(\gamma+\mu_I)}{\beta\lambda-\gamma-\mu_I} + \gamma} + 1 \right) \end{aligned} \right]
 \end{aligned}$$

### 3. ANALYSIS OF THE DYNAMICS OF THE EQUILIBRIUM POINTS

#### Analysis of Model 2

Now we still firstly discuss the simplified model (2).

For  $E_0(0)$ , we have  $Y(S, I, R) = Y(0)$ , there is no human alive. For the fish model,  $X(0) \rightarrow 0$ , but this point is unstable. Near this point, the non-negative solutions of  $Y$  that start in are bound, with the independence of the initial conditions. Clearly, while  $t = 0$ , we can get  $X \rightarrow 0$  and  $E_0(0)$  is unstable.

For  $E_0(K)$ , we have  $Y(S, I, R) = Y(0)$ , and it supposes that the fish of this species will die out at  $t = k$ . This point is stable because the right-hand side of the above inequality is bounded and the population of fish is independent of the human conditions. Hence, we can find the  $t > 0$  which implied that this point is stable.

#### Analysis of Model 1

For the  $E_2(0,0,0,0)$  equilibrium point, the Jacobian matrix of this point has at least one eigenvalue  $(\lambda[-\mu_n, r, -\delta - \mu_n, \lambda\beta - \gamma - \mu_I])$  that has a negative real part and at least one has a positive real part ( $r > 0$ ), the equilibrium is a saddle point and it is unstable. So it deduces that  $E_2(0,0,0,0)$  is an unstable point.

$E_3$  : At equilibrium point  $E_3$ , using the Routh–Hurwitz stability criterion. We figure out the eigenvalues of

the jacobini matrix is  $\lambda[-r, \frac{-Ak\mu_n - B\mu_n + ekm}{Ak+B}, -\delta - \mu_n, \lambda\beta - \gamma - \mu_I]$ .  $\lambda$  is a positive constant number, while  $-r$ ,



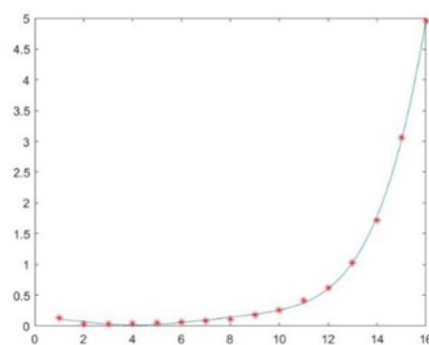


Figure (1)

The polynomial fitting to this figure is

$$y = 0.0000x^5 - 0.0013x^4 + 0.0133x^3 - 0.0493x^2 + 0.0322x + 0.1155$$

$\mu_i$ : Death rate of human infected can be influenced by age and time.

Research shows the relationship.

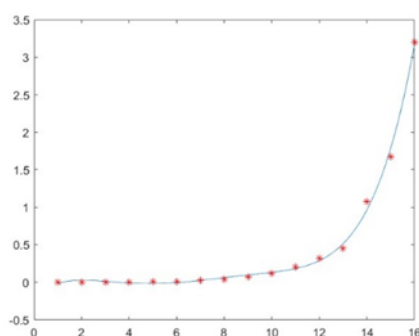


Figure (2)

The polynomial fitting to this figure is

$$y = 0.0001x^5 - 0.0019x^4 + 0.0232x^3 - 0.1264x^2 + 0.2860x - 0.1948$$

In general, we can see the tendency of  $\mu_n$  and  $\mu_i$  to age are Highly convergence. But possibility of the natural death rate is far less than the infected death.

A comparison figure from BBC shows the same conclusion.



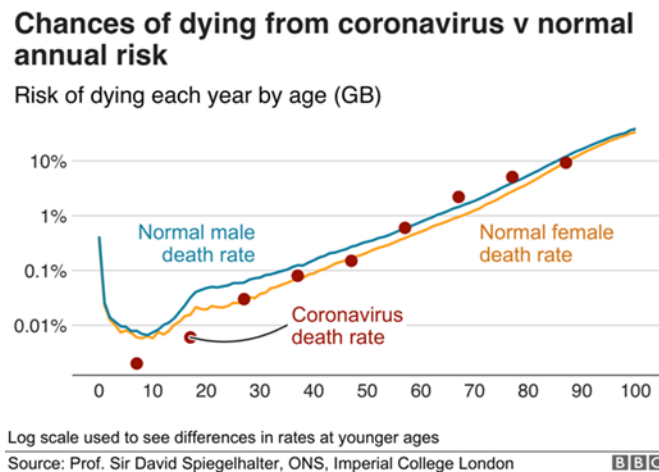


Figure (3)

This conclusion using the  $\mu_i$  to denotes the all death in infected group is available.

$\lambda$  and  $\beta$ :

To simulate the transmission of the virus among the people, we introduce  $\lambda$  (the average number of contacts per person per time) and  $\beta$  (the rate of being infected after contacting with human infected). The  $\lambda$  is directly related to the density of human. Many factors influence  $\beta$ , like temperature.

$R_v$  and  $R_s$ : the vaccine acceptance rate and effectiveness rate

Since it has been analyzed that by the WHO, COVID-19 vaccine can highly and effectively prevent the bacteria from invading human's body, thus we assume that an amount of people who has accepted vaccines has the antibody to fight against the disease, which can be treated equivalently as recovered people. We introduce the vaccine acceptance rate and effectiveness rate ( $R_v$  and  $R_s$ ), in which the amount of susceptible people transfers into recovered people can be calculated as follows:  $P = SR_v R_s$ .

Vaccine acceptance rates vary among global areas, and different kinds of vaccine has different effectiveness rates, which could be shown by the tracking links in appendix.

### Error analysis

Considering our model, the infection transformation is nonlinear, which is more realistic. However, it makes it hard to calculate the equilibrium point in the system. At the same time, we consider the effects of natural mortality and vaccination on the model and use the fish model to indicate the natural birth rate. And it makes our model richer than the traditional SIR model. However, as the number of people infected increases, the spread of the disease is suppressed through the implementation of epidemic prevention policies, which does not express in the model. Meanwhile, we assume that the natural mortality rates of susceptible and recovered persons are equal, but this does not correspond to the reality of the situation, as the disease can cause long-term damage to people's bodies. As the model becomes more complex, it will make the analysis of the model more difficult. We cannot analyze the system dynamics because it is too complex.

### Reference for vaccine figures

[https://www.who.int/docs/default-source/immunization/sage/2021/january/4-evidence-assessment5-jan-2021-final.pdf?sfvrsn=cf627b70\\_9](https://www.who.int/docs/default-source/immunization/sage/2021/january/4-evidence-assessment5-jan-2021-final.pdf?sfvrsn=cf627b70_9)

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[https://cdn.who.int/media/docs/default-source/immunization/sage/2021/february/3---sage\\_8-feb\\_evidence-assessment\\_azd1222\\_-final.pdf?sfvrsn=ce0bcfb1\\_8](https://cdn.who.int/media/docs/default-source/immunization/sage/2021/february/3---sage_8-feb_evidence-assessment_azd1222_-final.pdf?sfvrsn=ce0bcfb1_8)

[https://cdn.who.int/media/docs/default-source/immunization/sage/2021/april/2\\_sage29apr2021\\_critical-evidence\\_sinopharm.pdf](https://cdn.who.int/media/docs/default-source/immunization/sage/2021/april/2_sage29apr2021_critical-evidence_sinopharm.pdf)