Covid-19 Versus Monkeypox-2022: The Silent Struggle of Global Pandemics

Huber Nieto-Chaupis(✉)

Universidad Autónoma del Perú, Panamericana Sur Km. 16.3 Villa el Salvador, Lima, Peru
hubernietochaupis@gmail.com

Abstract. The theorem of Bayes is applied in a straightforward manner to investigate if Covid-19 and Monkeypox 2022 can coexist together. According to realistic scenarios and global data it was verified that Covid-19 is a kind of main pandemic whereas Monkeypox can be accepted a mini pandemic with a low lethality and a short period of existence. This would suggest that two global pandemics might not coexist at same time from the fact that people would acquire a disease belonging to all those pandemics with a strong capabilities of geographical translation and stability at long periods. From simulations, it is seen that Covid-19 would remain against Monkeypox that exhibits a noteworthy capability to produce infections but a weak lethality.

Keywords: Covid-19 · Monkeypox · Pandemic modeling

1 Introduction

At May 2022, it has been witnessed the apparition of the so-called Monkeypox virus (to be called along this paper Mkpx-22 in shorthand) [1–3] whose origin would be in central Africa [4,5]. According to global data, Mkpx-22 has bee aggressive at the very beginning showing high rates of infection basically in central Europe, mainly in England, Spain, Portugal, and reaching USA. The representative time evolution has been identified to be exponential:

$$N(t) = n_0 t^{\ell}, \tag{1}$$

as seen at Mkpx-22 in May 2022. However, as any pandemic, it will have to shown either capabilities or weakness. This can be seen in the second derivative of Eq. 1

$$\frac{d^3 N(t)}{dt^3} = n_0 \ell(\ell - 1)(\ell - 2)t^{\ell-3}. \tag{2}$$

Clearly, a interesting case is when $\ell = 2$ that convert to a polynomial that falls down in time. To guarantee this then Eq. 1 can be written as:

$$N(t) = \frac{n_0}{\ell - 2} t^{\ell}, \tag{3}$$

Y. Chen et al. (Eds.): BICT 2023, LNICST 512, pp. 91–100, 2023.
https://doi.org/10.1007/978-3-031-43135-7_9

for $\ell > 2$. In this manner more than a polynomial evolution, the number of infections is also depending on the characteristics of virus to take humans as potential host as for example the case of Covid-19 [6,7]. Thus, this paper has opted to apply the well-know Bayes theorem to identify if there is coexistence of Covid-19 and Mkpx-22. The direct usage of Bayes equation might not be enough to find evidences between these two global pandemics. In this manner, it was explored closed-form solutions for the probabilities. Thus, the well-known diffusion equation could be the one that models the spatial propagation of virus in pandemic. The rest of this paper is as follows: In Sect. 2 are formulated all required probabilities. In Sect. 3, the probability of confirmation is derived. In Sect. 4, the direct confrontation between Covid-19 and Mkpx-22 is done. Finally, the conclusion of paper is presented (Fig. 1).

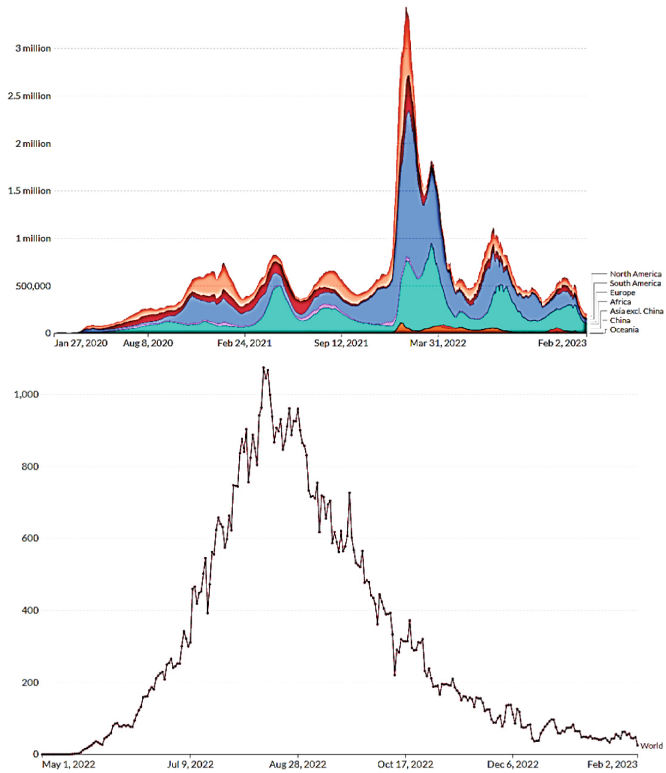

Fig. 1. Up: The global curve of infections for Covid-19 [8] and (Down) Mkpx-22 showing well-marked quantitative as well as qualitative differences. Data from [9]. Clearly Covid-19 imposes onto Mkpx-22 because the permanent intercontinental diffusion [9].

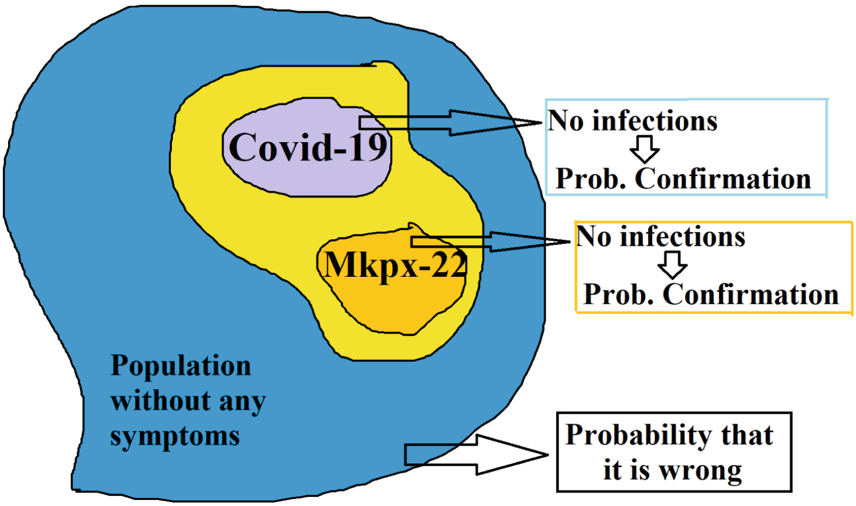

Fig. 2. Idea of paper: by knowing the rate of infection by Covid-19 and Mkpx-22, then emerges the question: What is the probability at a time t that a certain number of people acquires either Covid-19 or Mkpx-22 when both pandemics are superimposed each other? What is the implications about the confirmations for getting one of them if are true of wrong?.

2 Formulation of Probabilities

Consider a country with N_{TOT} the total number of habitants under the arrival of a first pandemic it is Covid-19 [10] and after a time (one or two years) there is evidence of arrival of a second pandemic: Mkpx-22 (see Fig. 2 above). Therefore there is time by which the pandemics are superimposed each other. In this time the fraction of people with symptoms like the ones of Covid-19 n_{SCV} and this fraction is seen as a probability p_{CV}:

$$p_{\mathrm{CV}} = \frac{n_{\mathrm{SCV}}}{N_{\mathrm{TOT}}}. \tag{4}$$

Same idea is used to characterize the ones under the suspect of having Mkpx-22:

$$p_{\mathrm{MK}} = \frac{n_{\mathrm{SMK}}}{N_{\mathrm{TOT}}}. \tag{5}$$

Now the it is noteworthy to add the probability that confirm that each suspect has absolutely the virus. Thus, for both Covid-19 and Mkpx-22 these confirmation probability are written as [11]:

$$p_{\mathrm{CCV}} = C(p_{\mathrm{CV}}) \tag{6}$$
$$p_{\mathrm{CMK}} = C(p_{\mathrm{MK}}). \tag{7}$$

In parallel, it should be noted that the ones that are healthy and do not present not any symptom either Covid-19 or Mkpx-22 is also a fraction and define by:

$$p_{\mathrm{HE}} = \frac{n_{\mathrm{HE}}}{N_{\mathrm{TOT}} - n_{\mathrm{SCV}} - n_{\mathrm{SMK}}}. \tag{8}$$

If it is a probability then the probability of the “Non-Healthy” is given by:

$$p_{\mathrm{NHE}} = 1 - p_{\mathrm{HE}} = 1 - \frac{n_{\mathrm{HE}}}{N_{\mathrm{TOT}} - n_{\mathrm{SCV}} - n_{\mathrm{SMK}}}. \tag{9}$$

The negation that Eq. 8 is false becomes the probability that the existence of a number of non-healthy is wrong. Thus, the probability that p_{NHE} is wrong p_{WHE} is given by a function of this p_{NHE}:

$$p_{\mathrm{WHE}} = W(p_{\mathrm{NHE}}). \tag{10}$$

In virtue to Eq. 4–10 the Bayes theorem will be used [12]. Thus the conditional probabilities are all those that are contemplating a possible infection due to either Covid-19 or Mkpx-22. In this manner the Bayes theorem is adjusted to the following question: What’s the probability that at least a number of people have got the infection either Covid-19 or Mkpx-22 at the same period? To answer this the Bayes probability reads:

$$B = \frac{p_{\mathrm{CV}}C(p_{\mathrm{CV}}) + p_{\mathrm{MK}}C(p_{\mathrm{MK}})}{p_{\mathrm{CV}}C(p_{\mathrm{CV}}) + p_{\mathrm{MK}}C(p_{\mathrm{MK}}) + (1 - p_{\mathrm{HE}})W(p_{\mathrm{NHE}})} \tag{11}$$

3 Construction of Confirmation Probability from Trigonometrical Bayes Theorem

When one talk about According to data, cases of Mkpx-22 it has been propagated very fast particularly in central Europe in May 2022. In contrast to Covid-19, geographic propagation of Mkpx-22 [13,14] has exhibited to be continental in the sense that the first infections have been registered in central Europe, while Covid-19 has go ut from Wuhan, China at December 2019. Thus the spatial propagation becomes relevant.

3.1 Propagation of Confirmed Cases

It is again used the Bayes theorem as follows: For example if $\mathbf{S}^2$ the prior probability of having the virus at the normalized distance $\mathbf{S}$ as well as $(\frac{\mathbf{X}}{2})^2$ the posterior probability of getting the infection at $\mathbf{X}$ (with $\mathbf{X}$ also another normalized distance) with these definitions the Bayes’s probability with obvious values ranging between 0 and 1, can be written as the square of a sinusoid function either Sin or Cos for instance:

$$\mathrm{Cos}^2\theta = \frac{\mathbf{S}^2}{\mathbf{S}^2 + \left(\frac{\mathbf{X}}{2}\right)^2}. \tag{12}$$

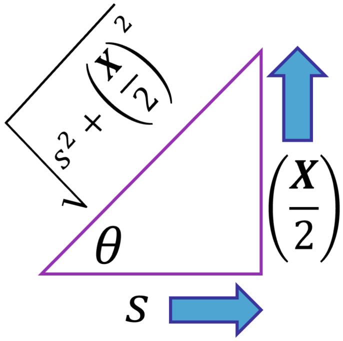

Fig. 3. Bayes's Path: For any traveler containing the virus at a time t and after of having moved S the subsequent step is random with a 50% of chance to go up or continue.

Under an inversion of roles so that one has in a similar manner as above:

$$\mathrm{Sin}^2\theta = \frac{\left(\frac{\mathbf{X}}{2}\right)^2}{\left(\frac{\mathbf{X}}{2}\right)^2 + \mathbf{S}^2}. \tag{13}$$

It should be noted that both $\mathbf{X}$ and $\mathbf{S}$ are denoting spatial displacement of confirmed cases. It leads to define a rectangle triangle as the one sketched in Fig. 3 that explains the origin of distance for an infected traveler: Fig. 3 can be explained as follows: at a given time a traveler containing the infection has been displaced from rest to $\mathbf{S}$, just there the traveler has two options: (i) continue along the path or (ii) follow a perpendicular direction reaching to $\mathbf{X}$. Because the traveler has two options then the perpendicular path has a 50% of probability. Thus the segment at the triangle is written as $\frac{\mathbf{X}}{2}$. Of course it is a single event, in other words that fact that one has a rectangle triangle forming an angle θ it is a random event. In another event one can have ϕ with a value less than $\pi/2$.

3.2 Probability as Rate of Infection

Consider Fig. 3 in a generalized manner so that the probabilistic number of infections $\mathbf{n}$ that have been displaced of 0 to $\mathbf{X}$ can be written now as:

$$\mathbf{n} = \frac{\mathbf{S}^2}{\mathbf{S}^2 + \left(\frac{\mathbf{X}}{2}\right)^2}. \tag{14}$$

In order to introduce the time it is easy to verify that on can rewrite Eq. 14 when $\mathbf{S}^2 \Rightarrow 4\mathbf{S}^2 t/t$:

$$\mathbf{n} = \frac{4\mathbf{S}^2 \frac{t}{t}}{4\mathbf{S}^2 \frac{t}{t} + \left(\frac{\mathbf{X}}{2}\right)^2}. \tag{15}$$

Once the infections are propagating inside a geographical area then one can invoke to diffusive equations with capabilities to describe diffusion of infections [15,16]. In such sense, it is noteworthy to introduce a kind of diffusive parameter that can be written as:

$$\gamma = \frac{\mathbf{S}^2}{t}. \tag{16}$$

With this Eq. 15 is rewritten as:

$$\mathbf{n} = \frac{4\gamma t}{4\gamma t + \mathbf{X}^2} = \frac{4\gamma t}{4\gamma t\left(1 + \frac{\mathbf{X}^2}{4\gamma t}\right)}. \tag{17}$$

It should be noted that $4\gamma t$ has equal units than $\mathbf{X}^2$ so that at the approximation dictated by $(\frac{\mathbf{X}^2}{4\gamma t})^\ell \approx 0$ if only if $\ell \geq 2$. Then in Eq. 17:

$$\mathbf{n} = \frac{4\gamma t}{4\gamma t\left(1 + \frac{\mathbf{X}^2}{4\gamma t} + \frac{\mathbf{X}^4}{16\gamma^2 t^2}\right) + ...} = \mathrm{Exp}\left(-\frac{\mathbf{X}^2}{4\gamma t}\right). \tag{18}$$

Actually one can multiply to $\mathbf{n}$ by $\sqrt{4\pi\gamma t}$ so that solving for $\mathbf{n}$ one arrives to:

$$\mathbf{n}(\mathbf{X}, t) = \frac{1}{\sqrt{4\pi\gamma t}}\mathrm{Exp}\left(-\frac{\mathbf{X}^2}{4\gamma t}\right), \tag{19}$$

that is actually direct solution of the well-known diffusion equation.

$$\frac{d\mathbf{n}}{dt} = \gamma\frac{d^2\mathbf{n}}{d^2\mathbf{X}}, \tag{20}$$

with γ the diffusion coefficient. The standard solution is given by:

$$\mathbf{n}(x, t) = \frac{1}{\sqrt{4\pi\gamma t}}\mathrm{Exp}\left[-\frac{\mathbf{X}^2}{4\gamma t}\right]. \tag{21}$$

Thus, Eq. 21 is interpreted as the probability of having $\mathbf{n}$ infections at the time t from an distance $\mathbf{X}$. Turning now to Fig. 3 one has that $\mathrm{Tan}\theta = \frac{\mathbf{X}}{2s} \Rightarrow \mathbf{X} = 2s\mathrm{Tan}\theta$, so that Eq. 21 can be generalized to one depending on the angle θ as:

$$\mathbf{n}(\theta, t) = \frac{1}{\sqrt{4\pi\gamma t}}\mathrm{Exp}\left[-\frac{s^2\mathrm{Tan}^2\theta}{\gamma t}\right], \tag{22}$$

with θ a random angle. It is emphasized the randomness of angle θ from the fact that there is not any knowledge about the route of infections once the pandemic has started. The case for calculating the probability of fatality can be modeled to a good level of approximation through the well-known theorem of Bayes [17] that states the estimation of a posterior probability $P(h|d)$ depends on the prior one $p(h)$ and $P(D) = \sum_Q P_Q(D)$ with $P_Q(D)$ the probability of having prior data that will be observed for Q cases or scenarios. In this manner the conditional probability of Bayes is given as:

$$P = \frac{P(h|d)}{\sum_Q P_Q(D)}. \tag{23}$$

4 Covid-19 Versus Mkpx-22

To normalize the probabilities, the constant $1/\sqrt{4\pi}$ is applied. The probability that $\mathbf{n}(t)$ is confirmed at time t reads for Covid-19 and Mkpx-22 respectively as:

$$\mathbf{C}_{\mathrm{CV}} = \frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[-\frac{x_0^2}{4\gamma t}\right] \tag{24}$$

$$\mathbf{C}_{\mathrm{MK}} = \frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[\frac{x_0^2}{4\gamma t}\right] \tag{25}$$

$$p_{\mathrm{NHE}} = 1 - p_{\mathrm{HE}} = 1 - \frac{N}{\sqrt{\gamma t}}e^{\left[-\frac{x_0}{4\gamma t}\right]} \tag{26}$$

It should be noted that apart that $\mathbf{n}(t)$ is expressing the instantaneous number of infections, the normalization through the constant N makes it acquire values between 0 and 1, so that $\mathbf{n}(t)$ now can describe probabilities. This is inserted for each case of Master Equation Eq. 11 that can be explicitly written by:

$$P_{\mathbf{B}} = \frac{\left(p_{\mathrm{CV}}\frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[-\frac{x_0^2}{4\gamma t}\right] + p_{\mathrm{MK}}\frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[\frac{x_0^2}{4\gamma t}\right]\right)}{\left(p_{\mathrm{CV}}\frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[-\frac{x_0^2}{4\gamma t}\right] + p_{\mathrm{MK}}\frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[\frac{x_0^2}{4\gamma t}\right]\right) + \left(1 - \frac{N}{\sqrt{\gamma t}}\mathrm{Exp}\left[-\frac{x_0}{4\gamma t}\right]\right)W(p_{\mathrm{NHE}})} \tag{27}$$

One can see that all variables can be known. Particular attention is paid onto the ones given by p_{CV} and p_{MK} that are denoting the fractions of all those that are exhibiting symptoms. The spatial variable x_0 is nominal, γ is an input that can be roughly calculated to priori from global data. N the normalization constant, and $W(p_{\mathrm{NHE}})$ the probability by which discards the scenario where the healthy people is apparent and there is a latent risk that all of them are carrying the virus. In order to illustrate Eq. 27 in Fig. 4 a bivariate plot has been done. In one hand Eq. 27 with solely Covid-19 and on the other side the possible behavior of Mkpx-22. Thus, by using Wolfram [19] the smooth density histograms are depicted. Because it exhibited a fast up at the number of infections, the associate function follows t^{ℓ} with ℓ an integer number ≥ 2. In Fig. 4 are seen the ellipses corresponding to the Covid-19 risk and in a minor extent the ones belonging to Mkpx-22. Thus, as specified above, these distributions of probabilities are denoting in an explicit manner the number of infections. Thus, in left one can see that the small ellipse is losing a certain volume of infections, fact that is interpreted as the absorption of infections by the Covid-19 pandemic, and leaving a reduce ellipse. A similar case happens in middle plot where the Mkpx-22 transfers some infections to big ellipse governed by Covid-19. In right-side panel, the Mkpx-22 cases becomes to be separated and their infections although might back again as seen at May-2022, the plot is telling to us the although Mkpx-22 has a small fatality ratio, the people with Mkpx-22 symptoms although are released from Mkpx-22, some or all of them might to pass from a recovery state from having Mkpx-symptoms.

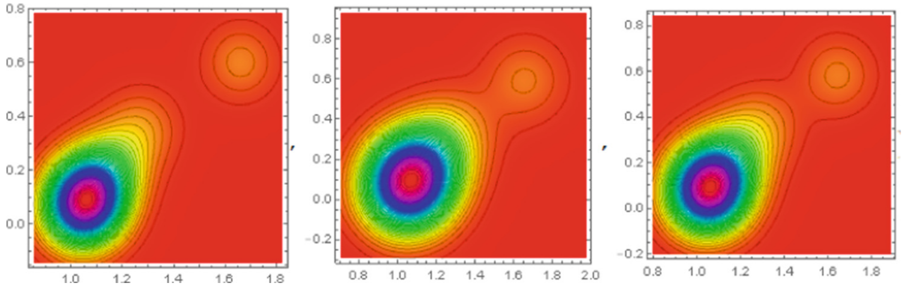

Fig. 4. The smooth density histogram [19] for a probability distribution function following Eq. 27 and one dictated by the polynomial t^{ℓ} in according to the very beginning of Mkpx-22. The ellipses begins to be closer each other.

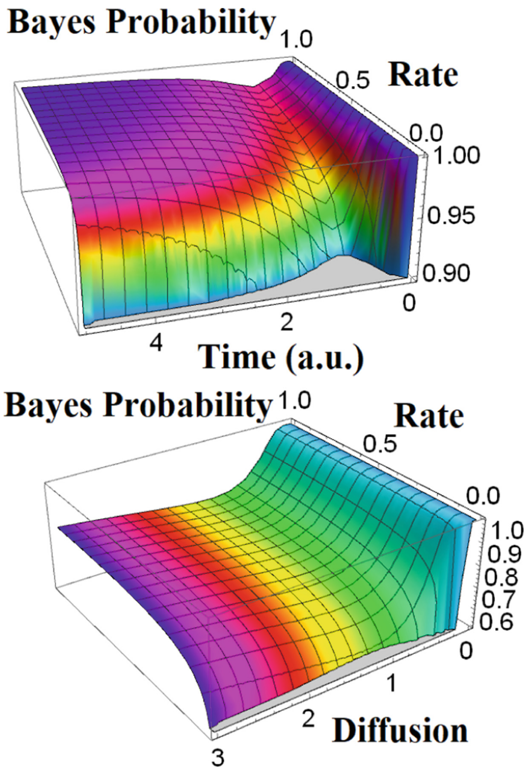

Fig. 5. The probability of Bayes as function of "Rate" and time (up) as well as "Rate" and the diffusion constant. In both cases the arrow is indicating the characteristic of Mkpx-22 and Covid-19. Here it is noted the infections and probabilities for the case of Covid-19 remain in its 50% of getting the virus [19].

In Fig. 5 up panel, the case of Eq. 27 when $p_{\mathrm{CV}} = p_{\mathrm{MK}} = u$ thus Eq. 27 is actually a 3D surface $P_{\mathbf{B}}(u, t)$. Thus the variable u defined as "Rate" is varied between 0 and 1. The highest value means that Covid-19 establishes a scenario of pandemic (first and second wave for example) and for the lowest values, it is clearly indicating the apparition of Mkpx-22. Thus for example, the reader can see the arrow is indicating the lowest values of "Rate" and for short periods, the Bayes probability Eq. 27 falls to the smallest values of that. It is actually of Mkpx-22 that only would emerge for short periods as seen at May 2022 at the very beginning at UK, Spain and Portugal. On the other side, one can see that Covid-19 keeps up to a 50% of lethality as seen in 3D plot. In down panel the case when Eq. 27 is plotted as function of "Rate" and diffusion constant. The arrow is indicating that for small rates and small diffusion constant the Bayes probability is also small. Although it is associated to Mkpx-22 one can also assume that this scenario encompasses well to Covid-19 in the sense that the Bayes probability is opting for small values as a response to the end of wave of pandemic but always by keeping at least a 50% of probability for getting the infection even in the case of having received a certain number of shots (vaccinations).

5 Conclusion

In this paper, the usage of Bayes theorem has been directly for testing in the case that two pandemics can coexist simultaneously. According to simulations, it has been verified in terms of probabilities, the Covid-19 is stable against Mkpx-22 fact that makes us to suppose that for capabilities to be scattered geographically, Covid-19 can remains in time, while Mkpx-22 although it is more diffusive, its lifetime as global pandemic is short as seen in global data. Simulations, have demonstrated that while Mkpx-22 ends in a full cycle, Covid-19 is indicating the end of a wave as experienced along 2020–2022. This would constitute the main argument to claim that Covid-19 still will manifest more pandemics, whereas Mkpx-22 or another pandemic would be active for short periods (months but not years), confirming that Covid-19 is the main pandemic whereas the other ones, are solely mini pandemics with seasonal apparition.

References

1. Petersen, E., et al.: Human Monkeypox: epidemiologic and clinical characteristics, diagnosis, and prevention. Infect. Dis. Clin. North Am. **33**(4), 1027–1043 (2019)
2. Kluge, H., Ammon, A.: Monkeypox in Europe and beyond - tackling a neglected disease together. Euro. Surveill. **27**(24), 2200482 (2022)
3. Kumar, S., et al.: Human Monkeypox outbreak in 2022. J. Med. Virol. **95**, e27894 (2022)
4. Kozlov, M.: Monkeypox outbreaks: 4 key questions researchers have. Nature **606**, 238–239 (2022)
5. Vandenbogaert, M., Kwasiborski, A., Gonofio, E., et al.: Nanopore sequencing of a Monkeypox virus strain isolated from a pustular lesion in the Central African Republic. Sci. Rep. **12**, 10768 (2022)

6. Tian, H., et al.: An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China. Science **368**, 638–642 (2020)
7. Chakraborty, I., Maity, P.: Covid-19 outbreak: migration, effects on society, global environment and prevention. Sci. Total Environ. **728**, 138882 (2020)
8. Mathieu, E., et al.: Coronavirus Pandemic (COVID-19) (2020). Published online at OurWorldInData.org. https://ourworldindata.org/coronavirus
9. Roser, M., Mathieu, E., Spooner, F., Dattani, S., Ritchie, H., Roser, M.: Mpox (Monkeypox) (2022). Published online at OurWorldInData.org. https://ourworldindata.org/monkeypox
10. Nieto-Chaupis, H.: Pandemic of Covid-19 as global entropy: when Shannon theory fits to-date data of new infections. In: 2021 International Conference on Electronic Communications, Internet of Things and Big Data (ICEIB), pp. 298–301 (2021). https://doi.org/10.1109/ICEIB53692.2021.9686434
11. Nieto-Chaupis, H.: Identifying second wave and new variants of Covid-19 from Shannon entropy in global pandemic data. In: 2021 Fifth World Conference on Smart Trends in Systems Security and Sustainability (WorldS4), pp. 289–293 (2021). https://doi.org/10.1109/WorldS451998.2021.9514017
12. Gaglione, D., et al.: Adaptive Bayesian learning and forecasting of epidemic evolution-data analysis of the COVID-19 outbreak. IEEE Access **8**, 175244–175264 (2020). https://doi.org/10.1109/ACCESS.2020.3019922
13. Alakunle, E., Moens, U., Nchinda, G., Okeke, M.I.: Monkeypox virus in Nigeria: infection biology, epidemiology, and evolution. Viruses **12**(11), 1257 (2020)
14. Kumar, N., Acharya, A., Gendelman, H.E., Byrareddy, S.N.: The 2022 outbreak and the pathobiology of the Monkeypox virus. J. Autoimmun. **131**, 102855 (2022)
15. Jin, T., Xiong, J.: Singular extinction profiles of solutions to some fast diffusion equations. J. Funct. Anal. **283**(7), 109595 (2022)
16. Anacleto, M.A., Brito, F.A., de Queiroz, A.R., Passos, E., Santos, J.R.L.: Diffusive process under Lifshitz scaling and pandemic scenarios. Phys. A **559**, 125092 (2020)
17. Chan, G.M., et al.: Bayes' theorem, COVID19, and screening tests. Am. J. Emerg. Med. **38**(10), 2011–2013 (2020)
18. Liu, Y., Yangyang, Yu., Zhao, Y., He, D.: Reduction in the infection fatality rate of Omicron variant compared with previous variants in South Africa. Int. J. Infect. Dis. **120**, 146–149 (2022)
19. https://www.wolframalpha.com/