A MATHEMATICAL MODEL FOR THE PATTERN OF COVID-19 POST-VACCINATION MORTALITY

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Abstract. In this article, we give a mathematical model for the pattern of post-vaccination mortality by using the Erlang distribution. This model is an analogue or generalization of Kiyoshi Itô's argument which describes radioactive decay.

Introduction

Fukushima et al. present a histogram [4, Figure 2] with the number of days from COVID-19 vaccination to death on the horizontal axis and the number of deaths on the vertical axis, based on a report from the Ministry of Health, Labour and Welfare (MHLW). Furthermore, we can find a similar histogram whose peak appears on the second day and then decreases in [12, Figure S1]. In the natural sciences, it is important to give mathematical interpretations to natural phenomena. For example, projectile motion and wave motion are mathematically described by parabolas and trigonometric functions, respectively. However, there are no mathematical explanation of the histograms above until now.

Here we give a mathematical interpretation or model for the histogram [4, Figure 2]. More precisely, this article suggests that the histogram can be approximated by the modified Erlang distribution. Note that the Erlang distribution of the parameters (n, λ) is a model in which small changes occur n times with a constant average incidence λ to cause a failure. When dealing with short-term deaths within 5 days, numerical computations indicate that the parameter n in the Erlang distribution is smaller than 5, which suggests sudden death of vaccine recipients.

This paper is structured as follows: Section 1 introduces some probability distributions based on [8, Chapter 2.5] related to this subject; Section 2 gives a review of Kiyoshi Itô's argument in [7, Chapter 3.4] and provides an analogue or generalization of his argument; Section 3 explains mathematically that the histogram [4, Figure 2] can be approximated by a modified Erlang distribution; Sections 4 and 5 explain the reason why Erlang distributions with $n = 3$ are chosen and its medical implications.

1. Associated distributions

An exponential distribution is a distribution in probability theory and statistics that describes, for example, the time intervals between events according to a Poisson process (a process in which events occur continuously, independently, and with a constant average incidence). Because of this property, the exponential distribution is often used as a model of random failure. The mean, mode, variance, probability density function, and

2010 *Mathematics Subject Classification.* Primary 62P10 and 92B05.

Key words and phrases. Model for the pattern of COVID-19 post-vaccination mortality, Erlang distribution.

cumulative distribution function of the exponential distribution with the parameter $\lambda > 0$ are as follows, respectively:

$$\frac{1}{\lambda}, \qquad 0, \qquad \frac{1}{\lambda^2}, \qquad \lambda e^{-\lambda x}, \qquad 1 - e^{-\lambda x}, \qquad (x \geq 0).$$

It is known that for n random variables $X_1, \ldots, X_n$ which are independent from each other and follow the exponential distribution of parameter λ, the sum of these random variables $S_n = X_1 + \cdots + X_n$ follows the Erlang distribution with the parameters (n, λ). Therefore, the Erlang distribution of the parameters (n, λ) is a model in which small changes occur n times with a constant average incidence λ to cause a failure. Clearly, the Erlang distribution of $(1, \lambda)$ is an exponential distribution with a parameter λ. The mean, mode, variance, probability density function, and cumulative distribution function of the Erlang distribution with the parameters (n, λ) are as follows:

$$\frac{n}{\lambda}, \qquad \frac{n-1}{\lambda}, \qquad \frac{n}{\lambda^2}, \qquad \frac{\lambda^n}{(n-1)!} x^{n-1} e^{-\lambda x}, \qquad 1 - e^{-\lambda x} \sum_{l=0}^{n-1} \frac{(\lambda x)^l}{l!}, \qquad (x \geq 0).$$

Since the Erlang distribution considers the failure with respect to a continuous time course, we consider discrete cases such as the first day, the second day, etc. From the cumulative distribution function of the Erlang distribution, the probability of small changes n times by day k, where n and k are natural numbers, is given by

$$1 - G(n, \lambda, k), \qquad G(n, \lambda, k) := e^{-\lambda k} \sum_{l=0}^{n-1} \frac{(\lambda k)^l}{l!}.$$

Since the probability of small changes n times on day k is obtained by subtracting the probability of small changes n times by day $k-1$ from the probability of small changes n times by day k, the probability of small changes n times on day k can be expressed as:

$$G(n, \lambda, k-1) - G(n, \lambda, k).$$

For $k \leq x < k+1$, let

$$\eta(n, \lambda, x) := G(n, \lambda, k-1) - G(n, \lambda, k), \qquad \theta(n, \lambda, x) := 1 - G(n, \lambda, k).$$

Then, a distribution in which the probability density function is $\eta(n, \lambda, x)$, that is, whose cumulative distribution function is $\theta(n, \lambda, x)$, and both the probability density and the cumulative distribution functions are 0 when $x < 1$, is called a modified Erlang distribution.

2. Itô's argument

In this section, we summarize and generalize Itô's argument appeared in [7, Chapter 3.4]. Let $N(t)$ the number of radioactive atoms at time t. Then, the radioactive decay or exponential decay is described by the following differential equation

$$\frac{d}{dt} N(t) = -\alpha N(t), \qquad N(0) = N,$$

where α is a disintegration constant (or exponential decay constant). As Kiyoshi Itô pointed out, the number $N(t)$ is always an integer, namely, $N(t)$ is a discontinuous function. However, it is well-know that any discontinuous function is non-differentiable. Hence, this argument is not mathematically rigorous.

To avoid this non-differentiability, Itô discussed as follows. Let $p(t)$ the probability that each atom survives (does not decay) until time t. Then we have

$$\frac{d}{dt}p(t) = -\alpha p(t), \qquad p(0) = 1.$$

By solving the differential equation, we have

$$p(t) = e^{-\alpha t}.$$

Assign number to each atom and let $X_n(t) = 1$ or 0 based on whether the atom n survives or not by time t. Then the total number of surviving atoms $N(t)$ by time t is the stochastic process expressed as

$$N(t) := \sum_{n=1}^{N} X_n(t).$$

By taking the means of both sides of the equation, we obtain

$$\mathrm{E}\big(N(t)\big) = \sum_{n=1}^{N} \mathrm{E}\big(X_n(t)\big) = \sum_{n=1}^{N} p(t) = Np(t) = Ne^{-\alpha t}.$$

Let N be sufficiently large. Then, the numbers $N(t)$ and $\mathrm{E}(N(t))$ are very close to each other according to the law of large numbers [1, Section 22] if we ignore the extremely small probability. Kiyoshi Itô (known as the founder of so-called Itô calculus) said that

> In the former argument, we forcibly applied theory of ordinary differential equations. However, we can consider naturally the latter argument in theory of probability. Moreover, the later argument is much closer to the truth in the position on the scientific understanding of radioactive decay.

Next, we consider an analogue or generalization of his argument. Recall that $p(t)$ is the probability that each atom does not decay until time t. We define $q(t)$ by the probability that each atom decays until time t. Then, clearly we have

$$q(t) = 1 - p(t) = 1 - e^{-\alpha t}.$$

It should be noted that the right hand side of the formula above coincides with the cumulative distribution function of the exponential distribution with the parameter α. Let $Y_m(t) = 1$ or 0 based on whether the atom m decays or not by time t. Then the total number of decayed atoms $M(t)$ by time t is the stochastic process given by

$$M(t) := \sum_{m=1}^{M} Y_m(t).$$

Taking the means of both sides of the equation above, we obtain

$$\mathrm{E}\big(M(t)\big) = \sum_{m=1}^{M} \mathrm{E}\big(Y_m(t)\big) = \sum_{m=1}^{M} q(t) = Mq(t) = M\big(1 - e^{-\alpha t}\big).$$

Therefore, the exponential distribution is a mathematical model of the radioactive decay.

Now we consider the case 500 atoms has an exponential decay constant α and 200 atoms has an exponential decay constant β. Let $Y_m(t) = 1$ or 0 based on whether the atom m with the disintegration constant α decays or not by time t and let $Z_n(t) = 1$ or 0 based on whether the atom n with the disintegration constant β decays or not by time t.

Then the radioactive decay of these 700 atoms are described by the following stochastic process given as

$$\sum_{m=1}^{500} Y_m(t) + \sum_{l=1}^{200} Z_l(t).$$

By taking the means of the stochastic process above, we have

$$\sum_{m=1}^{500} \mathrm{E}\big(Y_m(t)\big) + \sum_{l=1}^{200} \mathrm{E}\big(Z_l(t)\big) = 500\big(1 - e^{-\alpha t}\big) + 200\big(1 - e^{-\beta t}\big).$$

Therefore, we can handle the case when two types of atoms are mixed by modifying Itô's argument. Obviously, there is no need to limit the types of mixed atoms to two types, namely, there is no problem with any number of types.

3. Mathematical model for patterns of post-vaccination mortality

Recall that the Erlang distribution of the parameters (n, λ) is a model in which small changes occur n times with a constant average incidence λ to cause a failure and the Erlang distribution of $(1, \lambda)$ is an exponential distribution with a parameter λ. Consider a model in which a small change occurs in the body after vaccination, and death occurs after n instances of the change. Then the probability $p(t)$ that each vaccine recipient will die by time t can be considered to follow the Erlang distribution as discussed in Section 1, and is derived as follows:

$$p(t) = 1 - e^{-\lambda t} \sum_{l=0}^{n-1} \frac{(\lambda t)^l}{l!}.$$

Note that the right hand side of the formula above is the cumulative distribution function of the Erlang distribution with the parameters (n, λ). Clearly, the above equation describes the situation in continuous time, while Figure 2 in [4] shows the discrete time in days on the horizontal axis. Therefore, it is necessary to use a modified Erlang distribution. In summary:

The percentage of people who die after vaccination causes a change at the rate λ and the number of changes reaches n **by** day k can be approximated by the **cumulative distribution function** of the modified Erlang distribution with the parameters (n, λ).

This statement is equivalent to the following:

The percentage of people who die after vaccination causes a change at the rate λ and the number of changes reaches n **on** day k can be approximated by the **probability density function** of the modified Erlang distribution with the parameters (n, λ).

This leads us to believe that the histogram [4, Figure 2] is approximated by the modified Erlang distribution. This can be validated by the following numerical computation. First, we divide [4, Figure 2] into short-term mortality (within 5 days), medium-term mortality (6 to 15 days), and long-term mortality (16 to 30 days), and assume that each of these follows the modified Erlang distribution with parameters $(3, 1.48)$, $(3, 0.50)$, and $(3, 0.22)$. Then their probability density functions are as follows. The blue circles, orange squares, and green rhombus correspond to the modified Erlang distribution (MED) with the parameters $(3, 1.48)$, $(3, 0.50)$, and $(3, 0.22)$, respectively (*Figure* 1).

As this graph shows, death within 5 days is also associated with intermediate or long-term mortality. For this reason, although the numbers of short-term, medium-term, and

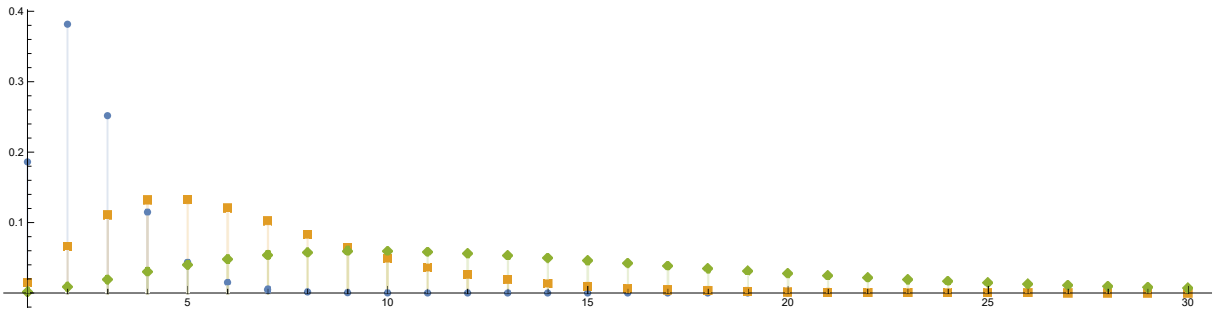


Fig. 1. MED with parameters $(3, 1.48)$, $(3, 0.50)$, and $(3, 0.22)$, $1 \leq k \leq 30$

long-term deaths in [4, Figure 2] are 457, 220, and 66, respectively, we assume that 319 people follow MED$(3, 1.48)$, 226 people follow MED$(3, 0.50)$, and 168 people follow MED$(3, 0.22)$, where MED(n, λ) is the modified Erlang distribution with the parameter (n, λ). Namely, we consider the stochastic process

$$\sum_{j=1}^{319} X_j(t) + \sum_{l=1}^{226} Y_l(t) + \sum_{m=1}^{168} Z_m(t), \tag{♭}$$

where $X_j(t) = 1$ or 0 based on whether a person j, which follows MED$(3, 1.48)$, is dead or not by time t, $Y_l(t) = 1$ or 0 based on whether a person l following MED$(3, 0.50)$ is dead or not, and let $Z_m(t) = 1$ or 0 based on whether a person m following MED$(3, 0.22)$ is dead or not by time t. By taking the means of the stochastic process above, we have

$$\begin{aligned} &\sum_{j=1}^{319} \mathrm{E}\big(X_j(t)\big) + \sum_{l=1}^{226} \mathrm{E}\big(Y_l(t)\big) + \sum_{m=1}^{168} \mathrm{E}\big(Z_m(t)\big) \\ &= 319\theta(3, 1.48, t) + 226\theta(3, 0.50, t) + 168\theta(3, 0.22, t), \end{aligned} \tag{♯}$$

where $\theta(n, \lambda, t)$ is the cumulative distribution function of MED(n, λ) defined in Section 1. Note that (♭) and (♯) are close to each other by the law of large numbers if we ignore the extremely small probability (see Section 2). Furthermore, since the attributes of vaccinated people differ depending on their age and the presence or absence of underlying diseases, it is natural that the duration of death differs. In other words, when the same medicine is administered to uniform experimental animals, it is not necessary to choose three disintegration constants as above, and it is sufficient to specify one disintegration constant. The reason for setting $n = 3$ will be explained in the next section. The orange line below represents the line from [4, Figure 2], and the blue line represents the line from

$$319\theta(3, 1.48, t) + 226\theta(3, 0.50, t) + 168\theta(3, 0.22, t), \tag{⋆}$$

where $\eta(n, \lambda, t)$ is the probability density function of MED(n, λ) (*Figure* 2).

Note that the mean squared error between the blue line and the orange line is 16.9174..., the average absolute error is 2.61089..., the coefficient of determination is 0.984028..., the adjusted coefficient of determination (see [3, Chapter 7]) is 0.979862.... When the day of vaccination and the second day are excluded, the mean squared error is 8.84202..., the mean absolute error is 1.98385..., the coefficient of determination is 0.984771..., the adjusted coefficient of determination is 0.98042....

In [4, Figure 2] (see Reference data 1), it can be seen that similar graphs are obtained when only the data reported on May 26, June 9, June 23, July 7 and July 21 are used, in

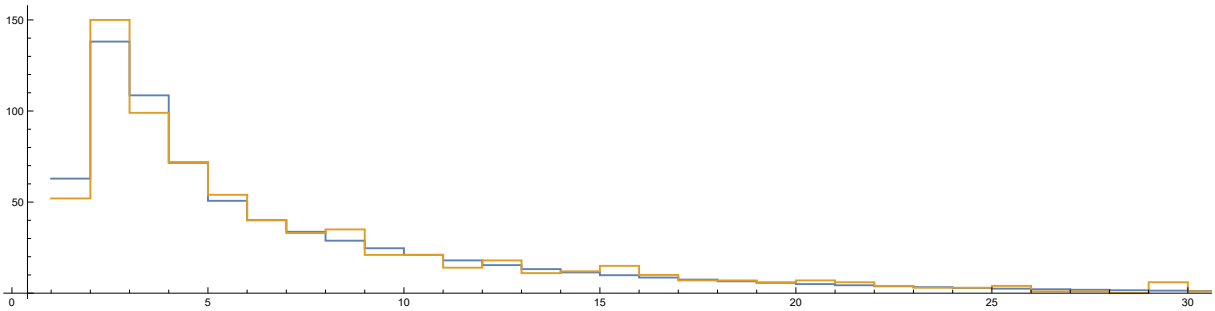


Fig. 2. Comparison of ($\star$) with [4, Figure 2], $1 \leq k \leq 30$

which the peak appears on the second or third day and then decreases. It is reasonable to suspect that $\lambda = 1.48$, the rate at which vaccine-induced changes occur, is too high. However, this is because the histogram [4, Figure 2] was originally provided based on the "Summary of Events Reported as Death after COVID-19 Vaccination" published by MHLW, and it is inevitable that the population had a high rate of small changes caused by the vaccination. In [4, Figure 2], there is a possibility that some recipients were recorded as "dead on the second day after vaccination if death was confirmed the morning after the day of vaccination". Furthermore, if the vaccine was administered in the evening and the recipient died the next morning, less than 24 hours had passed since vaccination. Hence, there is a large difference between deaths recorded on the first day and the second day.

We can find a similar histogram whose peak appears on the second day and then decreases in [12, Figure S1] (see Reference data 2). In addition, similar graphs are obtained when only the data caused by BNT162b2 Vaccine and mRNA-1273 vaccine. Furthermore, we can find a similar shape in [2, Figure 1] with the number of days from COVID-19 vaccination to symptom on the horizontal axis and the number of patients of with myocarditis in Korea on the vertical axis. Therefore, this phenomenon is not unique to post-vaccination mortality in Japan, but is expected to occur in many side effects from COVID vaccine all over the world (see also [12, Figure and Figure S2]).

4. Reasons and medical implications for Erlang distributions with $n = 3$

The Weibull distribution, rather than the Erlang distribution, is frequently used in survival time analysis. The basis for using the Weibull distribution as a failure model is the "weakest link model", but judging from papers [4] and [5], it seems that this does not apply to deaths after vaccination. In the first place, the weakest link model [15] applies to the phenomenon that "a chain breaks when one of its rings breaks". But if there were an organism with such a mechanism, that organism would be unable to survive due to its weakness, and it will become extinct immediately. Namely, the principles of survival of living organisms and industrial products are fundamentally different. Life forms that follow the Erlang distribution such that "even if there is a single change, they can carry out life activities, but die due to the combination of several changes" are more prosperous than those that follow the Weibull distribution, such that "a single failure causes the entire function to stop". It should be noted that the above idea of "accumulation of changes" has long been known as the Knudson hypothesis [9] in cancer research. The probability density function of the Erlang distribution may be very similar to that of the Weibull

distribution. However, the Erlang distribution is better suited for analyzing deaths after vaccination due to the above-mentioned "principle of life."

Next, we show that $n = 3$ is optimal. First, consider the short-term deaths from days 1 to 5. The number of deaths during this period was 52 on day 1, 150 on day 2, 99 on day 3, 72 on day 4, and 54 on day 5, for a total of 427 deaths. Define the sequences $F(n, \lambda_1, k)$ and $f(k)$ by

$$F(n, \lambda, k) := G(n, \lambda, k-1) - G(n, \lambda, k),$$
$$f(1) = 52, \quad f(2) = 150, \quad f(3) = 99, \quad f(4) = 72, \quad f(5) = 54,$$

where $G(n, \lambda, k)$ is given in Section 1. Consider $\lambda \in \mathbb{R}$ and $n \in \mathbb{N}$ with $\lambda > 0$ and $1 \leq n \leq 100$ such that

$$\sum_{k=1}^{5} \big(427F(n, \lambda, k) - f(k)\big)^2$$

is minimal. Then, we can find $n = 3$ by "FindMinimum" implemented in Mathematica 13.0. Let $f(k)$ be the number of deaths on the k-th day and assume $a_1 + a_2 + a_3 = 713$ by the fact that the total number of deaths over 30 days is 713. Under the condition $n = 3$, we can find the real numbers a_1, a_2, a_3 and the real numbers $\lambda_1, \lambda_2, \lambda_3$ that minimize

$$\sum_{k=1}^{30} \left(\sum_{j=1}^{3} a_j F(n, \lambda_j, k) - f(k) \right)^2$$

by using the"FindMinimum" command in Mathematica 13.0. Then we obtain

$$(a_1, a_2, a_3) = (318.895..., 225.653..., 168.452...),$$
$$(\lambda_1, \lambda_2, \lambda_3) = (1.48468..., 0.497776..., 0.21803...).$$

Therefore, in Section 3, we assume that

$$(a_1, \lambda_1) = (319, 1.48), \quad (a_2, \lambda_2) = (226, 0.50), \quad (a_3, \lambda_3) = (168, 0.22).$$

In the preceding discussion, it has been assumed that death occurs after a change occurring n times, but the above discussion has shown that the optimal value of n is 3. That is, when dealing with short-term deaths within 5 days, it would be expected that n may be greater than 3, but not greater than 10. This has significant implications: death from three changes means a dramatic worsening of the condition, which suggests sudden death. In fact, the 28-year-old man described in [5] died suddenly of myocardial rhabdomyolysis 5 days after the second vaccination. Furthermore, it is reported in [11] that a 14-year-old girl died suddenly of fatal multi-organ inflammation 2 days after the third dose of the BNT1262b2 mRNA COVID-19 vaccine (see also [6, Table 1 and Figure 4]). Therefore, this mathematical model is highly rational.

5. Zeta function universality and Akaike information criterion

The universality of the Riemann zeta function $\zeta(s)$ is the remarkable property of $\zeta(s)$ to approximate arbitrary non-vanishing holomorphic functions arbitrarily well. A mathematically precise statement of universality for $\zeta(s)$) is as follows. Let K be a compact subset of the vertical strip $D := \{s \in \mathbb{C} : 1/2 < \Re(s) < 1\}$ such that the complement of K is connected. Let $f(s)$ be a continuous function on K which is analytic on the interior of K and does not have any zeros in K. Then for any $\varepsilon > 0$,

$$\liminf_{T\to\infty} \frac{1}{T} \mu\left(\left\{ \tau \in [0, T] : \max_{s\in K} \big|\zeta(s + i\tau) - f(s)\big| < \varepsilon \right\} \right) > 0,$$

where μ denotes the Lebesgue measure on the real numbers (e.g. [14, Thereom 1.9]). As a corollary of the universality theorem above, we have the following (see [13, Theorem 2]). Put $Z_1(s) := \Re\zeta(s)$ and $Z_2(s) := \Im\zeta(s)$, where $\Re z$ and $\Im z$ are the real and imaginary parts of a complex number z, respectively. Let $\mathcal{K}$ be a compact subset of the strip D without interior and with connected complements. Let $g_1(s)$ and $g_2(s)$ be continuous functions on $\mathcal{K}$. Then for any $\varepsilon > 0$,

$$\liminf_{T\to\infty} \frac{1}{T}\mu\left(\left\{\tau \in [0,T] : \max_{j=1,2}\max_{s\in\mathcal{K}}\left|Z_j(s+i\tau) - g_j(s)\right| < \varepsilon\right\}\right) > 0.$$

The inequality above implies that any continuous function on a closed interval can be approximated by $\zeta(s+i\tau)$, $\Re\zeta(s+i\tau)$ or $\Im\zeta(s+i\tau)$ arbitrarily well if we chose only one suitable parameter $\tau \in \mathbb{R}$.

Akaike Information Criterion (AIC) is an index for evaluating the quality of statistical models. AIC is used to "balance the complexity of the model with its goodness of fit to the data." For example, consider creating a model that statistically explains certain data. In this case, the more the number of parameters are increased, the better the fit with the data can be. However, on the other hand, it is forced to adjust to accidental fluctuations such as noise, so it does not match the same type of data. To avoid this problem, it is necessary to limit the number of modeling parameters, but it is difficult to determine how many parameters. AIC provides one solution to this problem. Specifically, it is said that in many cases, a good model can be selected by selecting the model with the minimum AIC. A precise definition of AIC is as follows (see [10, Chapter 6.4.1]). Let n be the number of data points in the data set, k be the number of parameters fitted plus one, and SSE be the least-squares error. Then the AIC value of the model is defined as

$$\mathrm{AIC} = 2k + n\log\frac{\mathrm{SSE}}{n}.$$

In Section 3, we approximate the data [4, Figure 2] (the orange line) by the function ($\star$) (the blue line). Now we approximate the data [4, Figure 2] by the Riemann zeta function $\zeta(s+i\tau)$, $\Re\zeta(s+i\tau)$ or $\Im\zeta(s+i\tau)$. Then, for any $\varepsilon > 0$, there exits $\tau \in \mathbb{R}$ such that $\mathrm{SSE} < \varepsilon$ according to the universality theorem above. Hence, for any $R > 0$, there exits $\tau \in \mathbb{R}$ such that

$$\mathrm{AIC} < -R.$$

It should be emphasized that one has $k = 2$ for any data if we approximate the data by $\zeta(s+i\tau)$ from the universality theorem. In addition, for AIC_C defined by [10, (6.5)], we have $k = 2$ and can find $\tau \in \mathbb{R}$ such that $\mathrm{AIC}_C < -R$. Therefore, if we judge a model based only on the shape of the graph and the number of parameters, approximation using the Riemann zeta function is optimal for any data. However, the approximation by $\zeta(s+i\tau)$ does not provide any medical interpretation of cases such as sudden death after vaccination discussed in Section 4. Hence, the shape of the graph itself is not important, but the background in which the graph was constructed is essential. Therefore, in this paper, we adopted the Erlang distribution based on the principle of life mentioned in the first half of Section 4.

Conclusion

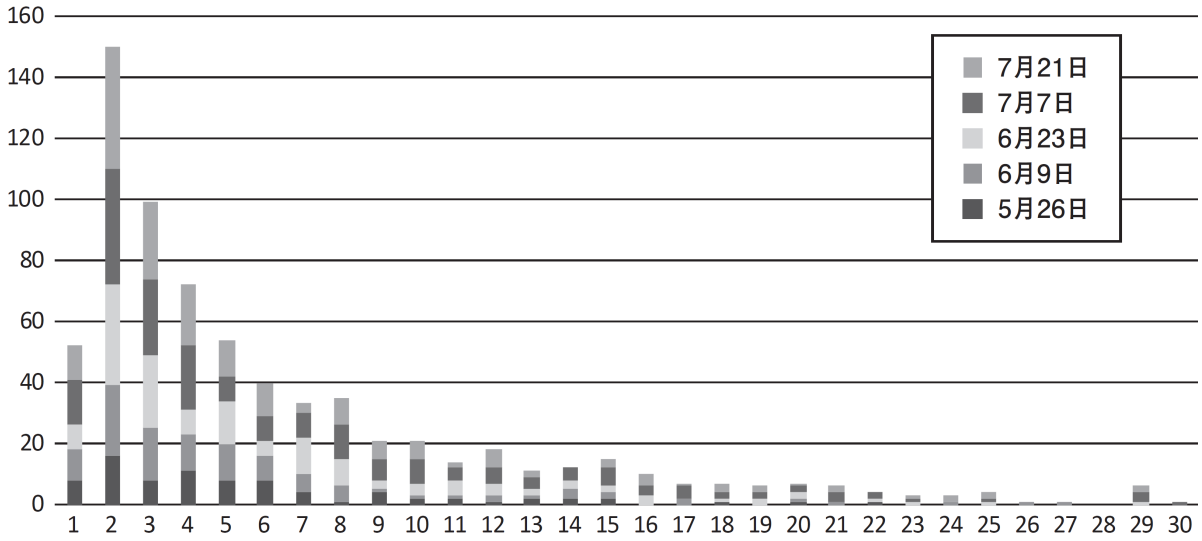
The modified Erlang distribution of the parameters (n, λ) is a model in which small changes occur n times with a constant average incidence λ to cause a failure. This article suggests that the histogram [4, Figure 2], can be approximated using the modified

Erlang distribution by appropriately dividing it into short-term mortality, medium-term mortality, and long-term mortality. Especially, for the short-term deaths within 5 days, the optimal value of n is 3, which suggests a dramatic worsening of the condition. Actually, some papers [5], [6], and [11] have reported sudden death after vaccination.

Acknowledgement. I would like to express my gratitude to Dr. Masanori Fukushima, Mr. Takayuki Kikuchi, Dr. Eiji Nakatani, and Dr. Tsutomu Nishimura for their very useful advice and comments in the Zoom meeting. The author was partially supported by JSPS grant 22K03276.

Compliance with Ethical Standards. The author has no conflicts of interest directly relevant to the content of this article.

Reference data 1: Histogram in [4, Figure 2]. The vertical axis is the number of deaths, and the horizontal axis is the number of days after vaccination (day 1 refers to the day of vaccination).



Reference data 2: Histogram in [12, Figure S1]. Number of reports of death per day following vaccination, by manufacturer, to Vaccine Adverse Event Reporting System (VAERS)-December 14, 2020–June 14, 2021 (day 0 refers to the day of vaccination).

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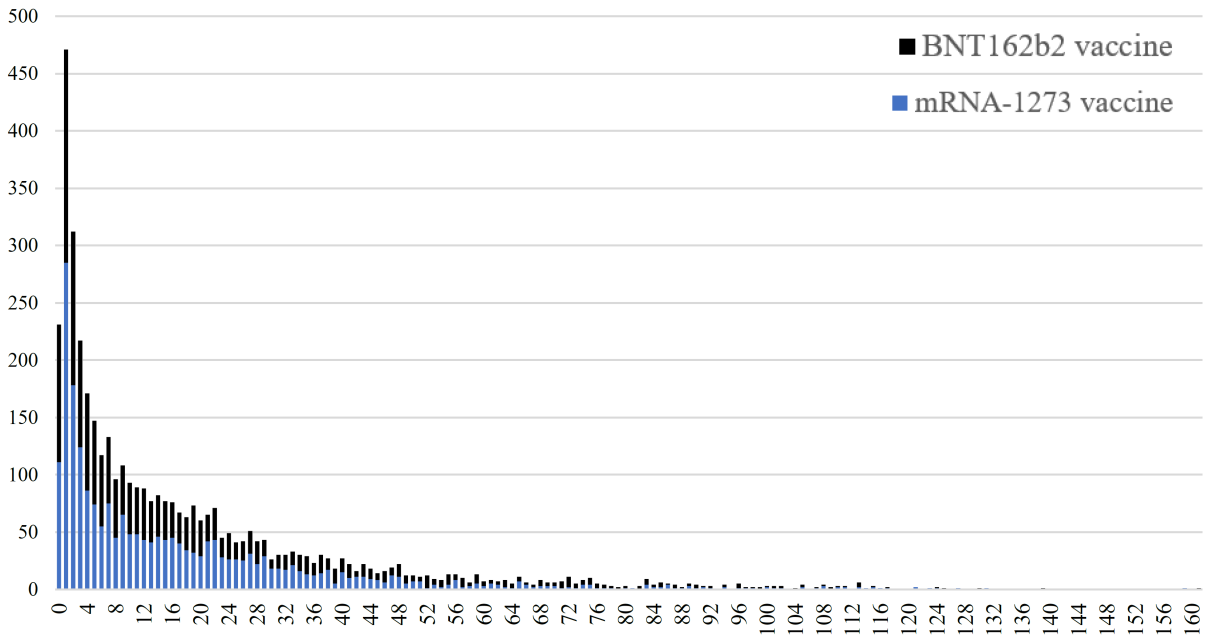

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