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Considerations regarding COVID vaccines and excess deaths

Discussion about COVID vaccines and excess deaths in Japan

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The COVID vaccine administered in Japan since April 2021 is an mRNA (messenger ribo nucleic acid) vaccine. This type of vaccine was put to practical use for the first time during the current pandemic. It was specially approved to minimize the emergency situation, and long-term safety has not been verified. This paper discusses the medium- to long-term safety based on changes in the number of excess deaths.

The COVID vaccine that has been inoculated in Japan since April 2021 is based on an mRNAÿmessenger ribo nucleic acidÿmethod. The method was put into practical use for the first time during this pandemic.

Special approval was granted to minimize the emergency situation. However, long-term safety has not been verified yet.

This paper approaches long-term safety from changes in the number of excess deaths.

Keywords: excess deaths, COVID, vaccine, neural network, descriptor evaluation

1. Exceed the number of deaths

We will analyze the relationship between the number of excess deaths in Japan from 2000 to 2023 [1] and COVID vaccination. The analysis starts on January 9, 2000, and ends on September 24, 2023. The time scale is the number of elapsed weeks (eWK, an integer value) from January 9, 2000. Figure 1 shows the change in the number of excess deaths in Japan.

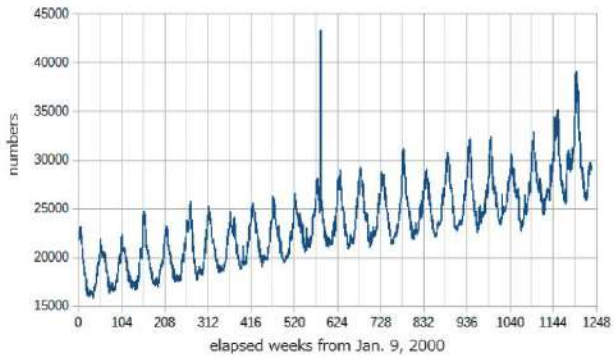

Figure 1. Excess deathsÿmortalityÿin Japan.

The isolated peak in **Figure 1** is 2011/3/13 (583 [eWK]). This was due to the Great East Japan Earthquake. This peak is unrelated to vaccination and reduces the accuracy of the analysis as an "outlier," so it is replaced with the average value for the weeks before and after.

The start date for vaccination in Japan is April 1, 2021 (1108 [eWK]). First, we remove **the linear increase component (due to aging) in Figure 1 in the eWK = [0, 1108] interval .**

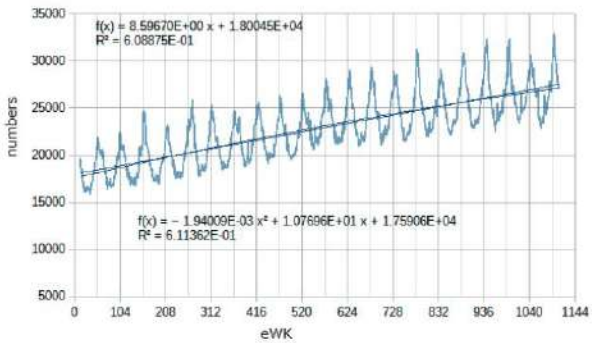

Figure 2. Monotonically increasing function bias of excess deaths.

The linear approximation of the function of the increase component is f(x)ÿ8.6x+1.8E4. (Hereafter, ×10^4 will be written as E4, and the symbol "^" represents a power.) The difference with the quadratic function approximation is minute.

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2. Average temperature

The number of excess deaths is calculated by subtracting the number of estimated deaths from the number of deaths [2]. There are several methods for estimation. The Farrington algorithm of the CDC (Centers for Disease Control and Prevention), the Euro MOMO* network
The FullMOMO model is often used. Its formula is given in reference [2].

*ÿEuroMOMO is a European mortality monitoring activity, aiming to detect and measure excess deats related to seasonal influenza, pandemics and other public health threats. Looking at the change in the number of deaths after estimation processing, it is difficult to deny
the existence of seasonal fluctuations. Since seasonal fluctuations are reflected in the average temperature, we will calculate the average temperature in Japan.

The most populous municipalities are Tokyo's wards, Yokohama, Osaka, Nagoya, Sapporo and Fukuoka have a combined population of 22.2 million.

The ratios are 0.4388, 0.1703, 0.1241, 0.1051, 0.0890, and 0.0727. **Figure 3 is obtained** by downloading weekly temperatures from past weather data from the Japan Meteorological Agency [3] and calculating the average temperature in Japan using the ratios as weights .

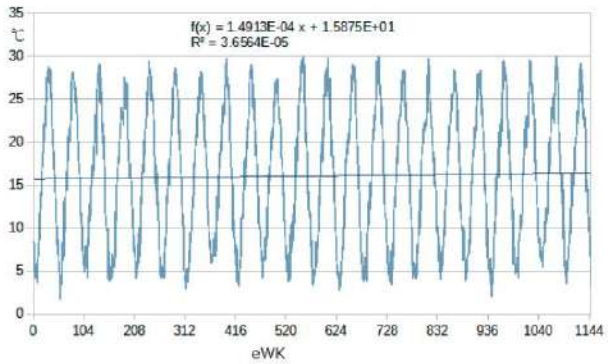

Figure 3. Average temperatures of Tokyo, Yokohama, Osaka, Nagoya, Sapporo, & Fukuoka from 2000 to 2023.

The average temperature is also increasing slightly. The linear approximation function is f(x) = 1.5E-4 x+16.0. This slope is not corrected.

3. Comparison of excess mortality and mean temperature fluctuations

The linear growth function of the excess deaths before vaccination is extrapolated to eWK = [1108, 1237] and subtracted from the excess deaths. This predicts the background of excess deaths in the absence of vaccination.
ing.

There is an extrapolated measurement for the average temperature. Since there is an "inverse correlation" in which the number of excess deaths decreases when the temperature is high, we set scaled_T = 251-(T-16). The coefficient 251 is a parameter for overlaying the graphs. This is how we obtain Figure 4.

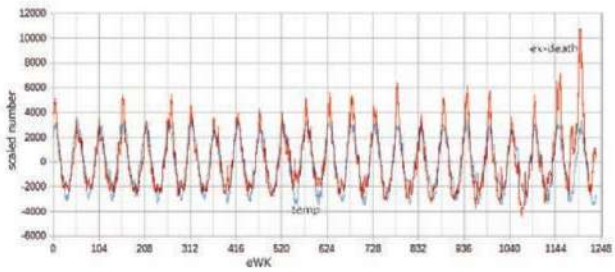

Figure 4. Corrected excess deaths by the bias coming from population aging; and A curve obtained by subtracting the average temperature of five major cities from a constant.

The correlation between the two curves in Figure 4 is R^2 = 0.72. This correlation value cannot be ignored. Plot the squared value of the difference between the two curves with eWK on the horizontal axis to see when the difference began to widen.

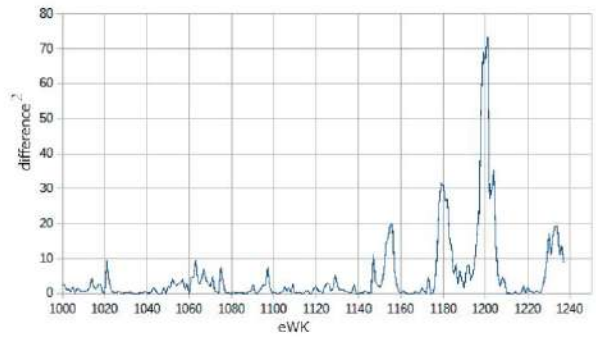

Figure 5. Square of the difference between both curves in Figure 4 on 1000-1237 ÿeWKÿperiod.

From Figure 5, the difference between the two, or the increase in the number of excess deaths, begins after eWK = 1140, 2021/11/14, 7.5 months after the start of COVID vaccination.

4. Multivariate Functions

4.1 Definition

Let us consider a multivariate function that connects cause and effect. Let the time series causal phenomenon be f(x) and the result be g(x). x is the elapsed time and is a discrete value, so we will write it as x(i).

In the case of multiple causes, it is {fv(x), v = 1, 2, ...}. If J(fv(x), v = 1, 2, ...) = g(x) using the function J(), it may be a "function that connects cause and effect." If the functional form is unknown, the correlation may be coincidental (correlation does not imply causation).

Therefore, we search for a function that links the average temperature and the excess mortality.

The function J() is different for each individual cause rather than being equally related to multiple causes. Since there is more freedom in the case

where v = 1, 2, … }, we write {Jv{fv(x)}, v = 1, 2, … }
= g(x). In the following, we write Jv{fv(x)} = Fv(x).

The Jv() function is a nonlinear function, but the magnitude relationship,

We must hold that fv(x(i)) < fv(x(j)). Among such functions is the sigmoid function. We will use it here.

Fv(x(i); w, y) = 1/[1+exp{-w(x(i)+y)}], (1) The sigmoid function has two parameters (w, y).
Determine the properties of the shape, where v ÿ v'. Next, define a function J() that integrates {Fv(x)}.
J(Fv(x),v=1,2...;m(v))ÿÿvm(v)Fv(x)+const. (2) "m(v)" is the weight applied to the function value Fv(x), and formula (2) is a linear combination. This weight is a scalar coefficient in formula (2), but in long-term time series data it may be a vector coefficient {m(v;i)}. In long-term phenomena, it is difficult to imagine that the ratio of multiple causes remains unchanged.

4.2 parameters decision

Determine the parameters that define the function form.
Let E be the square of the difference.
E = ÿ{g(x)-J(Fv(x),v = 1,2...; m(v))}^2 dx, (3) is partially differentiated with respect to parameters {w,y,m(v), const} so that ÿE = 0 (a stationary value). This operation is forward/back-propagation learning [4] of a 3-layer (Perceptron type-) neural network (NN).

NNs have input and output, and the input data is called descriptors and the output data is called teaching data. In equation (1,3), the descriptors are {fv(x)} and the teaching data is {g(x)}.

Due to the nature of the sigmoid function, calculations within the NN are performed in the [0,1] interval. A scaling operation using min- and max-values between the external data is required.
NN has a feature generation function called learning.
One of the learning methods is back-propagation (BP).
BP has two steps: forward- and back-propagation.

5. Neural Network Feature Generation

The forward-propagation function of neurons in each layer of the NN is shown below. •Layer 1: Scales the input data {x} to the interval [0.1,1].
The last neuron in the first layer has no input and always outputs 1. This is called a bias neuron.

•Second layer There is a 1:1 correspondence between the neurons in layers 1 and 2 (this is not an actual NN, but a constraint introduced to investigate the relationship between the descriptors and the training data). The last neuron in the second layer is also a bias-neuron. The input of the neuron in the second layer is the output of the corresponding neuron in the first layer and the bias-neuron. This value is multiplied by the connection weight WIj (the suffix "I" is the number of the neuron in the first layer, and "j" is that of the neuron in the second layer). WIj can take positive or negative values. The initial value of WIj is a uniform random number in the interval [-0.3, 0.3].

The number of outputs from the first layer neurons that are input to the second layer neurons is two. The two outputs are added together. The sum is transformed using a sigmoid function, where a nonlinear transformation is performed that preserves the magnitude relationship.

•Layer 3 There is one neuron in layer 3.
The input is all the outputs of the second layer neurons. This connection is Wjk (k is limited to 1). The initial value of Wjk is also a uniform random number. The sum of these is taken, and this becomes the output (Out) of the neuron. If the input data {x} is a vector, Out is also a vector. To explicitly state that it is a vector, we write {x(i)}, {Out(i)}.

The BP function of neurons in each layer of the NN is shown below. •Layer 3 The output of the neuron in the third layer, Out, and {g(x)} = vector scaled to the interval [0,1] are written as {TE(i)}.

Therefore, the difference vector, {w(i)} = {Out(i) - TE(i)} can be defined.
The end of learning is ÿi{w(i)^2} < threshold value (~0.01). To achieve this, the Wjk connection between the second and third layers is also a vector.
From now on, we will write it as {Wjk(i)}.
{Wjk(i)} ÿ {Wjk(i)-eps*(Out(i)-TE(i))*Hj(i)}, (4) where “eps” is a parameter and a small value of about 0.1.
Hj(i) is the j-th neuron in the second layer.
The connections between the neurons are compensated for by the difference.

The formula for the second layer BP is ÿHj(i)ÿWjk(i)*Hj(i)*{1-Hj(i)}, (5) {WIj(i)}-->{WIj(i)-epsh*ÿHj(i)*XI(i)}, (6) The term Hj(i)*{1-Hj(i)} is the differential form of the sigmoid function.
XI(i) is the output of the “I”th layer neuron. “epsh” is This is a small parameter.
Equations (4-6) are the steepest descent method damped with the eps and epsh parameters. This is because the direction of the steepest descent method is not necessarily correct in the early stages of learning.
When NN learning is ÿE<1.0E-5, {g(x(i))} = {Out(i)} using forward propagation alone without BP. When ÿE<1.0E-2, {g(x(i))} ÿ {Out(i)} using forward propagation alone. In this case, BP is added to the calculation of {Out(i)}. This means that the NN output error is renormalized. This calculation method is called 1-step prediction. This NN is a constrained version of the original Perceptron's fitting function.

Therefore, one-step prediction may be the goal.
The purpose of this NN is to visualize the effect of fitting a group of neurons to a changing phenomenon on the time-varying parameters, thereby verifying the validity of the descriptors.

6. Descriptive nature of average temperature data

We test whether the NN can calculate the number of excess deaths using only the average temperature data as a descriptor.

The output of the NN {Out(i)} and the teaching data {g(x)} are shown in Figure 6.

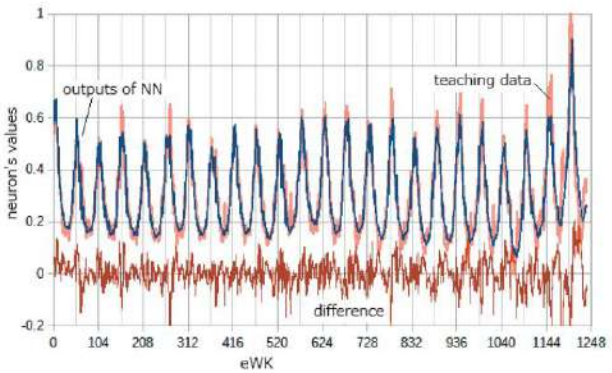

Figure 6. Testing whether NN calculates excess deaths, when the descriptor is an average temperature.

In Figure 6, the calculated values within the NN are plotted as is. As can be seen, the NN reproduces the excess mortality to a certain extent using only average temperature data. The increase in the excess mortality on the right side of the figure is the effect of the 1-step prediction of BP. However, the accuracy decreases after eWK = 1144.

Figure 7 shows the changes in the values of {WIj(i)}, {bias-neuron's weight in 1st layer}, {Wjk(i)}, {bias-neuron's weight in 2nd layer} inside the NN .

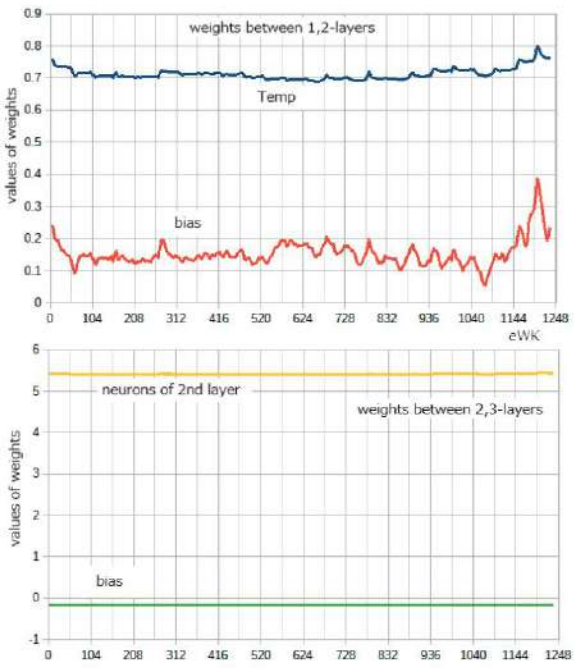

Figure 7. Changes of weights between 1,2-layers; and those of between 2,3-layers.

In the bottom of Figure 7, the weights in layers 2 and 3 are not dependent on changes in eWK. This is the behavior of the original weights in a NN.

In the top of Figure 7, the weights in layers 1 and 2 for both the average temperature and the bias neuron oscillate violently in

response to changes in eWK. This behavior indicates that the difference between the output Out(i) of the neuron in layer 3 and the teaching data is incorporated into the weights at BP. This is a typical one-step prediction.

Therefore, there is no significance in the agreement between the blue and red curves in Figure 6.

The upward curve of bias weights after eWKÿ1144 is

The eWKÿ{1,1144] section is flat, and the eWKÿ{1144,1237] section

This suggests the need for a "new" descriptor to rise in between.

7. Descriptive properties of average temperature data + bent straight line

Here, the horizontal line bends upwards at point Xp[eWK].

A line that curves like this is called a bent line. Xp is the parameter,

The calculation was performed with Xp = {1, 782, 1108, 1140} points. As a result, Xp = 1140 **was the best fitting. Figure 8 shows the difference between the NN output and the excess mortality rate. Figures 9 and 10** show the changes in the weights of the two descriptors and bias.

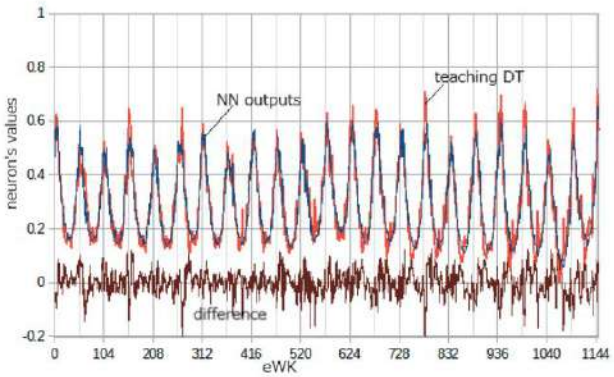

Fig u re 8. O n us e of 2 de scr iptor s , average temperature and a linear increasing function; plots of NN-simulation and excess-deaths.

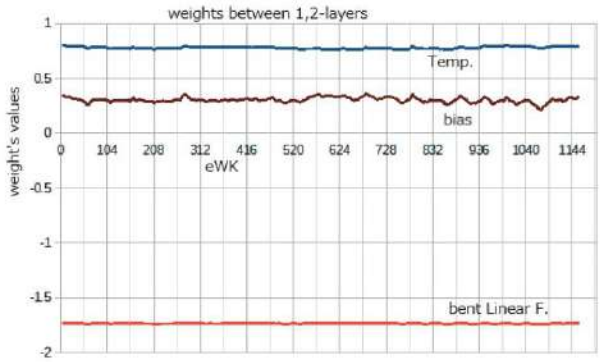

Figure 9. Weights between 1,2-layers.

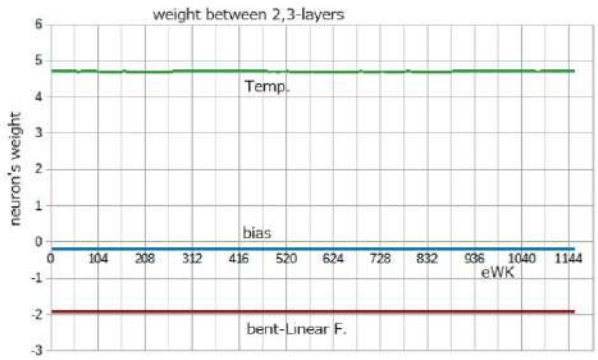

Figure 10. Weights between 2,3-layers.

The difference between the NN output and the excess mortality rate improves as the number of descriptors increases. The time series changes in the weights between the second and third layers are good, and the changes in the bias weights between the first and second layers have been improved. The renormalization of the results by BP has been reduced. The weights of the mean temperature and the broken line are at a satisfactory level.

This result is significant, unlike the "apparent goodness of agreement" in Figure 6. This simulation shows the possibility of the existence of a "bent straight line = an increase in excess mortality."

A hint for tracing this phenomenon in more detail lies in the complex group of peaks at the right end of the bias weight between layers 1 and 2. We will investigate this by expanding the time axis. 1049-1237 (2023/9/24) [eWK] is shown in Figure 11.

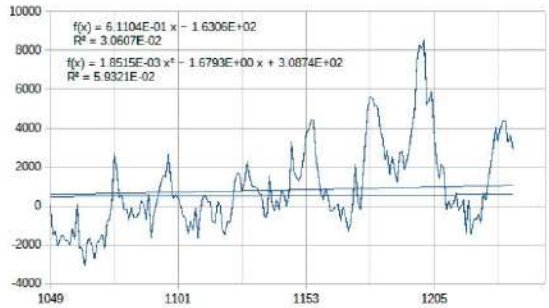

Figure 11. Difference between excess deaths and scaled average temperature for 1049ÿ1237 eWK. 2 approximated funct ions a re got from t he difference curve.

Figure 11 subtracts the increase in the mortality rate due to the aging of the population and the periodic changes in the average temperature.

Nevertheless, such waves exist and can be expressed as straight lines and quadratic curves. When we approximate it by, the mortality rate is rising. Let's investigate this.

8. Detailed COVID data

Daily changes in the number of COVID-19 cases, deaths, and vaccinations (fully vaccinated & booster) were published by region on Our Data World [5].

We downloaded the situation in Japan from February 21, 2020 to May 14, 2023. Based on that data, we analyzed the number of excess deaths. R.

If 2020/2/21 is elapsed day (eD) 0 [eD], 2021/2/21 is 1049.714 [eWK]. 2023/2/21 is 1096 [eD], 1206.286 [eWK].

Figures 12 to 14 show the daily changes in cases, deaths, vaccinated, and booster injections. The units are [people] and [ratio per population].

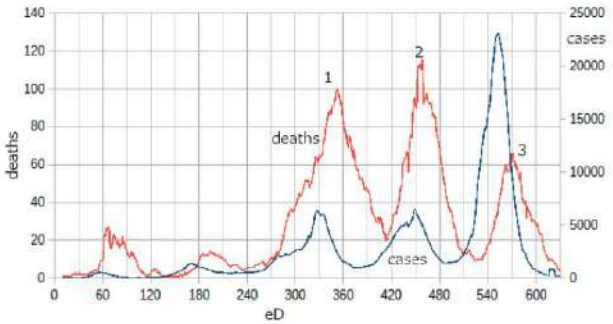

Figure 12. COVID cases and deaths in period, 0ÿ630 ÿeDÿ.

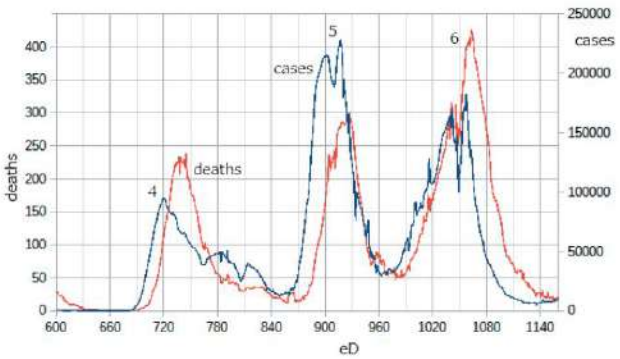

Figure 13. COVID cases and deaths in period, 600ÿ 1237 ÿeDÿ.

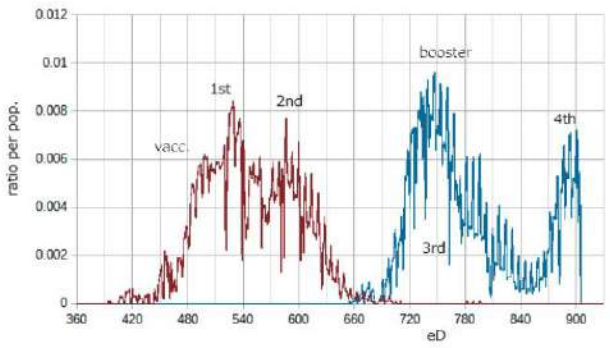

Figure 14. Fully vaccinated and booster injected persons in Japan.

The unit is the number of injected persons per populations.

Figures 12 and 13 show the status of COVID cases and deaths by elapsed days [eD] in two figures. Since the number of cases and deaths is different, the scale is divided into right and left. Typical peaks are numbered 1 to 6. Figure 14 **shows** the vaccination status of fully vaccinated and booster by eD. The scale is the ratio to the population.

From the normal distribution-like changes in Figure 14, it is believed that the vaccine is effective from 480 + 21 = 501 [eD] onwards.

Comparing peaks 2 and 3 in Figure 12, the deaths/cases in peak 3 are smaller than those in peak 2. This shows that the vaccine is effective in preventing severe illness.

From Figure 13, the period from 630 to 690 [eD] seems to be the end of COVID. However, after that, a rapid increase in cases is seen up to 720 [eD]. The second peak of fully vaccinated is ~600 [eD]. This suggests that the vaccine is effective for ~90 [eD]. The induced IgG antibodies may be decreasing, but it seems that the antibody production function remembered in B cells is not working, or the SARS-CoV-2 virus is mutating quickly, making the antibodies ineffective.

Booster vaccinations are not usually given 720-600 = 120 [eD] after a fully vaccinated person. If vaccinations are given frequently with the same antigen (the third vaccination initially used the same antigen as the second vaccination, and then a vaccine for mutant strains was used), the IgG subset that shows affinity to the antigen, IgG4 antibodies, will increase, making it difficult to completely eliminate the pathogen. However, in reality, booster vaccinations were given.

Since the Booster rapidly increases antibodies after vaccination, the deaths value of peak 4 after 720 [eD] should be suppressed, but not as much as peak 3. This is thought to be a mutation of the SARS-CoV-2 virus.

9. Relationship between COVID deaths and excess deaths by NN

The number of COVID deaths is at most ~450 on the left scale of Figure 13. The peak value of the excess deaths after removing population aging and seasonal fluctuations is ~8000 from Figure 11.

Therefore, it may seem strange to use COVID deaths as a descriptor of the excess deaths. Since severe COVID patients consume a lot of medical resources, it has a significant impact on the treatment of non-COVID patients. With that in mind, in this paper, COVID deaths is used as a descriptor of the negative impact on Japan's medical system. Figure 15 shows the two NN descriptors, COVID deaths, linear function, and teaching data.

The time scale is [eD], and the vertical scale is the neuron value. From this figure, we can see that there is a shape similarity between COVID deaths and teaching data. The correlation is calculated to be R^2 = 0.34. The two are shifted by ~30 [eD]. Although there is a similarity, the two cannot be considered to have the same properties.

Figure 16 shows the results of learning 40k times with the NN in Section 5.

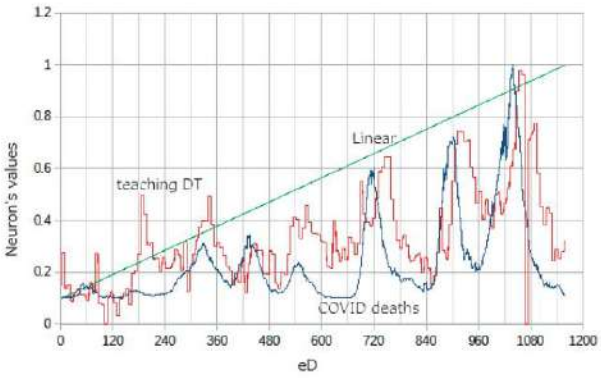

Figure 15. Descriptorsÿinputsÿlearned by NN and the trainingÿteachingÿ data.

vinegar.

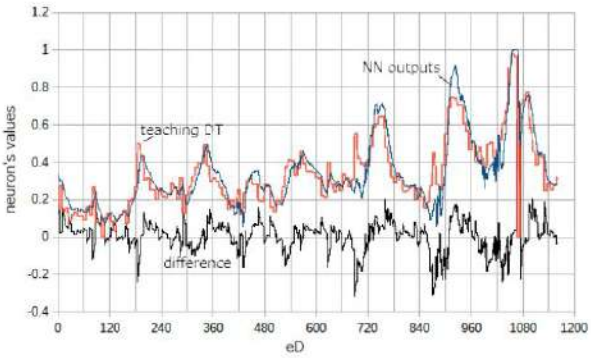

Figure 16. NN-outputs after 40k learnings; the teaching data, and difference.

It is possible to approximate the NN output to the teaching data by introducing a linear function into the descriptor. We investigate where this agreement comes from by tracking the time series changes in the weights between each layer of the NN.

Figures 17 and 18 show the change in weights between the 1,2- and 2,3- layers. In Figure 17, the fluctuations in weights are small before 660 [eD], and the descriptors are significant. After 660 [eD], the weights fluctuate for COVID deaths, Linear, and Bias at each peak of 4, 5, and 6. The situation at each peak appears to be different. The weight of Linear rises in a step-like manner. In Figure 18,

there is almost no fluctuation in the descriptors. There is a slight increase in the weight of Linear.

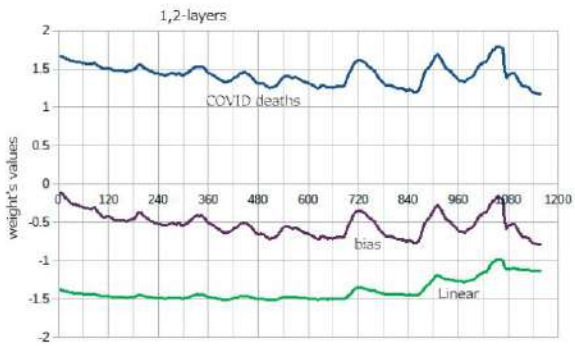

Figure 17. Changes of weights between 1,2-layers.

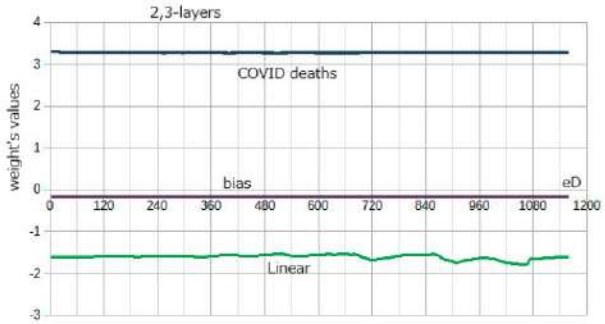

Figure 18. Changes of weights between 2,3-layers.

varies for each peak.

We believe that the change in the linear descriptors at each peak indicates the difference in the degree of strain on the medical system. The product of the weights in Figures 17 and 18 times the function value is the effect on the excess deaths of the linear component. Since the weights do not cancel out the increase in the function value, the number of excess deaths will continue to increase in the future. Let us consider what the linear component is.

10. Effectiveness of vaccines

From COVID cases and deaths data, we estimate the vaccine's effectiveness in preventing severe disease (this vaccine does not strengthen the IgA system and does not prevent initial infection). It is said that the vaccine is effective from the 21st day after full injection. As time passes, the induced IgG antibodies decrease. The half-life of antibodies was initially said to be 8 months, but it has gradually become shorter and is now 90 days. If we use this to calculate the effectiveness of the vaccine from Figure 14, it does not match the actual deaths curves in Figures 12 and 13. The discrepancy is that the deaths curve rises even though IgG antibodies should remain. Even if we change the exponential function to Gaussian, it does not match. As a result of trials, we set the effective period to a (convex) function with a value of 1 for [21, 90] days and a value of 0 for other days. The idea is that after three months, the mutant strain will become dominant and the induced antibodies will be ineffective. The vaccine effectiveness function is Veff(x), x[eD], and Calc.1 Deaths(x)ÿ case(X)*{1- k*Veff(x)}, ÿ7ÿ

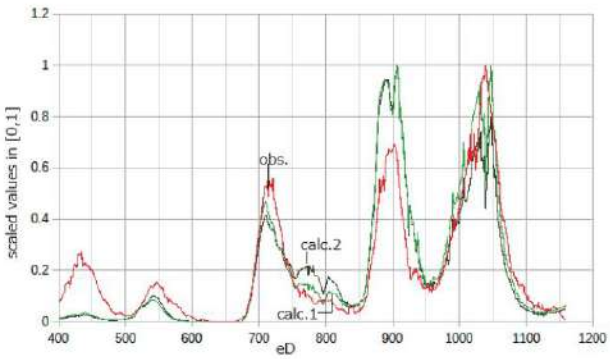

Figure 19. Comparison with calculated and observed deaths curves. Whole curves are scaled inÿ0,1ÿ.

Calculations were performed with k = {0.1, 0.35, 0.5, 0.7, 1} and X = x-14.

Calc.2 Deaths(x)ÿcase(X)*k2, k2ÿ0.005. The ÿ8ÿ best match was obtained with

Calc.1 & kÿ0.5. This is shown in Figure 19. The correlation between the two curves in Figure 19 is R^2ÿ0.864. Initially, the effectiveness of the vaccine was said to be kÿ0.9 to 0.95. In clinical practice, there may be differences in that level.

The vaccine's effectiveness in preventing severe disease was observed up to 1100 [eD]. R.

However, the difference from when the fixed rate in Calc.2 was multiplied by the cases (R^2 = 0.859) was small. This indicates that the treatment also worked to prevent the disease from becoming severe. We will investigate this using NN.

The descriptors are COVID cases, vaccine effectiveness (equation (7)), and bias (a constant value is substituted for "no change in treatment" during this period). The period 400 to 500 [eD], when the vaccine does not work well, and 1100~ [eD], when there is insufficient data, are "effectiveness ~ small value ~ bias". The NN during that period cannot distinguish between vaccine effectiveness and treatment. Figures 20 and 21 are interpreted taking this property into account.

Both the NN descriptors and the treatments suppressed the number of deaths. it is conceivable that.

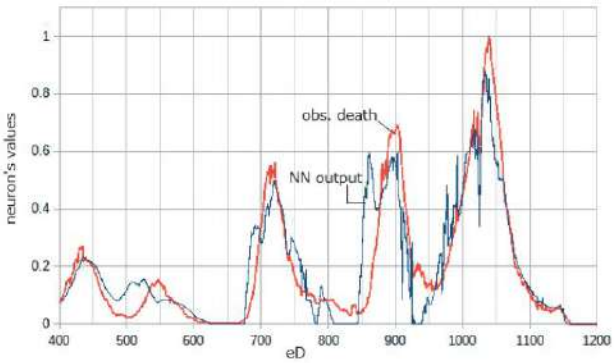

Figure 20. COVID deaths calculated by cases and vaccination effectsÿeq.ÿ7ÿÿ and medical treatments.

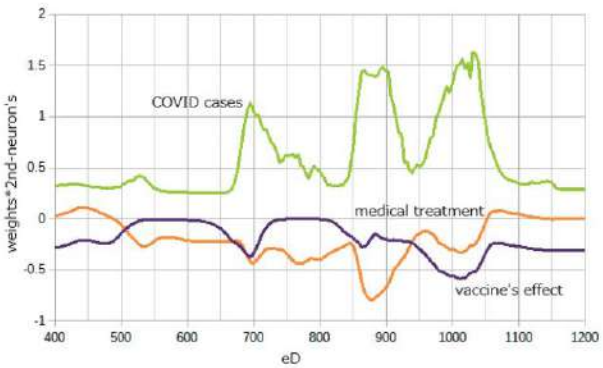

Figure 21. Changes in effects of descriptors on the number of deaths over time. The reliability is in 500ÿ1100ÿeDÿperiod.

11. Side effects of vaccines

11.1 Japan's situation in 2024/1

In Japan, the side effect of the vaccine is defined as anaphylactic shock immediately after vaccination, and does not apply to symptoms 7 days or later after vaccination. There is no concept of mid- to long-term side effects of COVID mRNA vaccines. However, some clinicians are increasingly suspicious of the effects of the mRNA vaccine on the heart and vascular circulatory system, the central to peripheral nervous system, autoimmune diseases, and rapidly progressing cancers. Globally, a considerable number of researchers have published papers [6] on the mid- to long-term side effects of mRNA vaccines.

11.2 The Side-Effect Hypothesis

From here on, this is the author's hypothesis. The mid- to long-term would be the effects after the 90-day validity period of the vaccine. Looking at a paper on HPV vaccine side effects [7], there is an example of an effect occurring 35 months later. In the discussion in Section 3, this is 7.5 months. Therefore, it is assumed that symptoms will appear after 180 days.

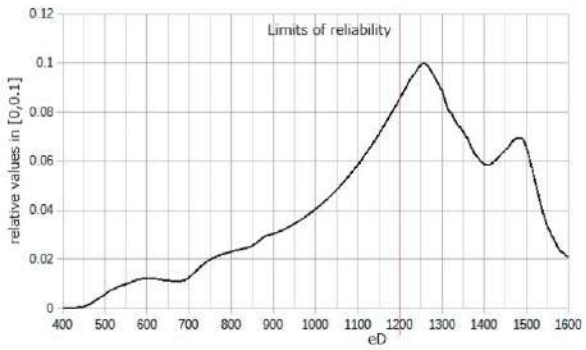

Figure 22. An assuming function of vaccine side effects; The effects is maximum at 180 days after the injection. Side effect increases exponentially until the maximum day; and the effect decreses exponentially after the maximum.

Calculation method for **Figure 22 :** A = -Ln(0.5)/180, f(t) = Cut{exp(-A|t-180|)}, (9) The Cut(t) function multiplies the argument by 1 when 90<t<360, and by 0 otherwise. Equation (9) is integrated for each vaccination date. The function in Figure 22 is called the expected side effect function. If the half-life is longer than 180 [eD], the function will be flatter and increase more slowly. Based on the shape of the increase in the function value, we believe that this may be the Linear component in Section 9.

12. Summary

Among the mRNA COVID-19 vaccines administered in Japan Long-term safety was discussed based on the number of excess deaths.

It is true that excess deaths have increased in the last two years. This is thought to be due to the strain on medical resources caused by the Besides that, there is something else hidden that is unclear as the cause of the long-term almost linear increase. A hypothesis was put forward and discussed in Section 11. Future steady data collection will be necessary.

Since the COVID pandemic, interest in viruses has increased, but to understand viruses, it is necessary to know their relationship with cells. As an introductory book, we recommend [8, 9]. With modern technology, viruses can be chemically synthesized. Viral genome editing is an existing technology. It is also possible to design an mRNA amplification system that does not produce virus particles, and a replicon vaccine that uses this system has been approved. Such edited mRNA can be encapsulated in lipid nanoparticles and delivered to cells in the body. Research into medium- to long-term safety is progressing.

do not have.

13. Literature

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Appendix:It is true that the number of excess deaths has increased over the past two years. This is thought
to be due to the strain on medical resources due to
COVID.

Other than that, a long-term almost linear increase part
is,
the cause is not clear; i.e., something is hidden.
To detect the hidden one, we analyze the excess
mortality curve excepted linearly increasing bias using
Fourier-transformation.

We find small 2-waves in the background, whose periods of 4 to 6 years. The 1st-wave represents an increase in the number of excess influenza deaths in
2018-2019;

The 2nd is larger, and it is recent two years wave, whose peak will be in the future.