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A Computer System Based on Neural Network and Rules System Based for Find an Optimum Mix of Vaccine or Drugs for mRNA Like Covid-19 Virus and Other Pathologies

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Abstract— *The aim of the present work is to give the percentage of different existing vaccines and associated to the respective mRna virus that can create a cocktail thanks to the knowledge of their percentage; this will be possible thanks to the use of a computer system based of a neural network; a base of knowledge useful for of the system, is necessary the cooperation of two scientific figures who work in different fields: the first is the doctor and the second one an expert of information technology whose collaboration will be able to transfer the knowledge to the system that will be presented below. We have to underline the process of approaching to an unknown object as a virus never seen before, whose we know only certain characteristics. So we can say that the process of approaching to a virus can used as a base of reasoning to join the information technology with the clinical expert as every observation can be contradicted immediately or can be put on hold about certain reasoning but it can be transferred in a production rules that take an operative form useful to suggest numerically the I/0 to the neural network system. The two figure can argue and will arrive to know each other and focus the useful aspect of the system after a series of reasoning where not everyone will be scientifically acceptable; we can accept also discussion as long as it will be considered that all can be useful.*

Keywords—*Artificial Intelligence, Data Collection, Expert System, Information Technology, Pandemic, Variants.*

I. Introduction

The most interesting aspect of this work is the fact that the COVID-19 has been an unknown virus over all it was for people who had to represent the basic knowledge; this aspect is due to the fact that is unknown as a biologic object but also referred to the interaction it has with the external world and the various districts of the host body (human in this case) that can help to build a collection of reasoning that will lead the involved scientific figures, and not only, to deepen the knowledge; at this step, thank to its emergence from the microcosm and its sudden appearance in the civil and scientific world we are able to speculate till discussion from esoteric meditation place.

II. First Blande Conjecture

In a pandemic and beyond, the first considerations that can be made in a process of approaching an etiological agent such as a virus are geographical and or environmental ones. Some different ways of proceeding with an environmental survey will be described [1]-[7] without the need for completeness and exhaustiveness but only to describe a completely personal and even imaginative cognitive process.

Continuing to move forward for a good purpose we would like to know the following information about COVID-19:

- we know how it responds to the electromagnetic field and/or geographic position in the Heart?
- its behavior in the water? Does it have polarities?
- we have an accurate and non-artistic external rendering?
- a chromatographic exam?
- a mass spectrometric exam to know if it's have iron and where?
- we have information about his content and where he is located inside?

If we are in the place with high density of patients in an alleged pandemic (red zone, such as town considered individually) and there are patients who use interferon for exampled; this drugs could provide references to the mayor who in turn could inquire about them state of health and could intertwine with the positive to COVID-19 or his recovery or not. The knowledge of patients who also take other antiviral drugs and the number of patients who have also become ill with COVID-19 should be high, low or zero, gives an important indication of the usefulness of administering interferon to COVID-19 patients. The possible low number of COVID-19 patients using interferon is certainly a very important data. These data are within reach of the authorities and obtaining statistical information is quite immediate, trivial and low-cost in terms of resources even if a neural and/or recognition (even of the possible time series) would be useful [14]-[27]. The geographical position and the pandemic incidence could be related to certain anthropogenic actions.

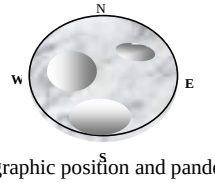

Fig. 1. Geographic position and pandemic incidence.

From the images seen on the web and on TV, COVID-19 has an apparently symmetrical shape up to the outer surface

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with "types of lipids" that come out in a non-symmetrical way even if approximately radially. We should try the incidence with the geographic position.

Another method certainly imaginative and not without contraindications emerges following the hypothetical geometric and morphological identification of COVID-19 and the possible interaction with ferromagnetic elements close to its external surface; the nano-robotic agent codiv-19 should have about a size of 500[*nm*] [13] while a piece of iron crystal that can be considered a Weiss domain 10^{-6} [*cm*] [2] or about a size that makes always hope that it can be achieved (a magnetically controlled, protein-enzyme-coupled nano robotic agent). Considering that we can also have a contrast agent that brings iron (better ferromagnetic) of comparable size with a few Weiss domains, such as a soot, immersed before deposition in broth with many different proteins (including fungi) that bind to the virus. it amplifies the ferromagnetic properties and the patient's transition to *NMR* (nuclear magnetic resonance) could reduce its vitality. By depositing the ferromagnetic soot in the areas of interest, the union of the virus with ferromagnetic pieces that excited by the magnetic field could act on the virus.

Another way that certainly not without aspects to clarify is to understand if there is a fungus (and which of its enzymes) frequent in the mammal that is immune to it and by lengthening any broth; or better make a broth-herbal tea prepared at around 75° [C] (not being sure that the variety contained is preserved in this way) based on local infusions such as: proteins, mushrooms, enzymes and spores ... (very difficult to experiment in the immediacy of the pandemic). -- Observing [3] we can ask ourselves what advantage could be obtained by locally administering hydrogen peroxide (to be evaluated if it is better if heavy, ozone, or some isotope of interest) could measure whether a reduction in the viability of the virus is obtained.

In order to make the covid-19 harmless or less aggressive or rather its spikes or its membrane, where polarities are present; a polar-headed sphingomyelin [4]-[5] or a sphingolipid (such as Normast® 600 sublingual from Epitech Group®). The length and polarity of Normast® or other supplements are likely to interact with COVID-19 and its "polarity" and "length" reducing the ability of the tips to penetrate the cell membrane due to both polar attraction and presence of sphingomyelin which reduces the spaces necessary for penetration through the membrane.

III. NEUROVAX, A NEURAL NETWORK AND RULES BASED SYSTEM FOR IDENTIFIED A OPTIMUM COCKTAIL OF EXISTING VACCINES OR/AND DRUGS

In the following pages, is present an application with neural networks ruled based system that are able to provide the optimal drug cocktail able to weaken the "virus" is reported. Given the latest news on the English, African, Indian, Omicron and so on variants and for those to come of COVID-19, it is noted that the ability to indicate the cocktail on said increases and that the greater the number of variants in inputs entered (obviously pre-treated), greater are the system's abilities to weaken the virus. It seems an abstruse and delusional idea, but it is an idea and sometimes like now there is no time to embellish it in form. And if sooner you share the better is it [8]-[12]. Thanks to the use of neural networks, rules based system the known data can be used to train it. The basic idea is to use known vaccines on mRNA of known viruses (even non-coronavirus) to train a multilayer perceptron back propagation neural network with "delta" learning rule. As in the following figure.

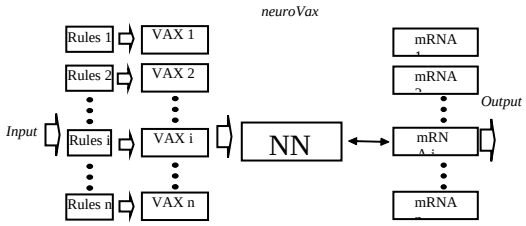

Fig. 2. Vaccines or type of specific drug pre-treatment whit rules for have a kind of input like a mRNA too.

Once system trained, she is presented with the "vaccine" and/or drugs whit Rules based filter and NN give a percentage virus affected and which traits of mRNA affected and in what percentage of the different inputs used she gives the [6] as a cocktail:

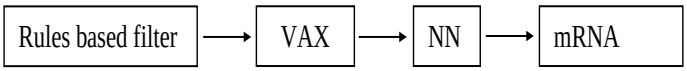

Fig. 3. Block diagram of *neuroVAX*.

IV. TOOLS AND METHODS

The main difficulties are finding the input patterns 1,2, .. n and their representation, or rather the representation of knowledge. It can also be challenging to find the typical neural architecture as an extrapolating or classical interpolating time series [18].

The object that we should recognize is a sequence of bases of the *mRNA* of the virus that distinguishes it, or rather the NN should do it in our place or the statistical systems. The steps we can take for now go in two directions: the first is the recognition of parts of the genetic code and see if they are an important signature of the virus that allows their recognition; it is our opinion would require a long human work of optimization with numerous and not too big of NN; the second direction that seems to us to be more adequate and useful for the moment is an NN back-propagation with a number of inputs equal to or less than an order of magnitude of the size of the number of bases of the *mRNA* under consideration, for example 10, 9 , 8, ... inputs if the bases considered in sequence are 100 for example.

Since genetic information is redundant in the optimization phase, the number of Input nodes can be reduced. Since the two chains are similar, we can initially give:

$$Input_{RN} \leq \frac{n_{basi}}{10}, \quad (5.2) \qquad Input_{RN} \cong Output_{RN} \tag{1}$$

The presentation of the I/O to the network can be done by dividing the chains of the *mRNA* into a number equal to the number of inputs and outputs respectively considering an

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approximately 20% of overlap between one input considered and the next in the chain sequence. The size of the input or output vector can be taken as (2):

$$Dim_{I/O}^{NN} = Dim_{VAX/MaxRNA}^{RNA} \quad (2)$$

This presentation can be made either sequentially or randomly, it would not be bad to compare them. Suppose we have a basket of "n" $mRNA_{VIR}$ of as many viruses (mRNA or other genetic material) and the respective vaccines. We divide the sequences into array and $mRNA_{VIRi}$ which $mRNA_{VAXi}$ in turn will be normalized and the frequency of the bases examined in order to develop the production rule for normalization. The nitrogenous bases that constitute the mRNA are Adenine (A), Guanine (G), Cytosine (C) and Uracil (U). In the figure below Fig. 4 we represent an example of a production rule in the case that the frequency of the bases are:

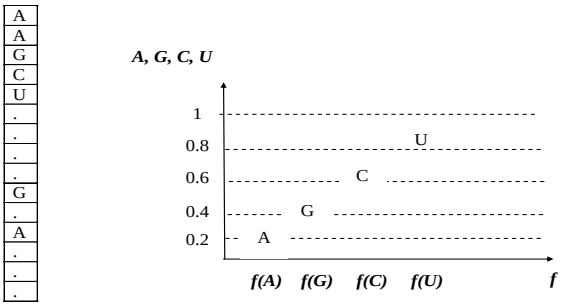

Fig. 4. i-th decomposition of the n virus-vaccines found in the basket. For this simulation we think you need a not too rich basket and a very powerful calculator.

Regarding normalization, although the data from the production rule are normalized with Matlab® [24], it is a good idea to normalize anyway.

A. Data Generation

The data used in this work have been generated on the basis of the information found on the *WEB* and from those present in the bibliography. The most important aspects of the elements covered are:

- length of the *mRNA* chain of COVID-19 that is 32,000 bases, a high enough number that allows the *neuroVAX* system to not lose generality in the event that another problem were to be faced;
- variety of bases, equal to four, contained in each of the bases possessed by the *mRNA* chain under examination;
- size and architecture of the neural network chosen and linked to the most suitable type of learning;
- number of vaccines (or drugs) and viruses (or etiological factors of known pathologies);

and in particular: 10 vaccines and associated viruses training, validation and also 10 test vaccines without coupled viruses. A very important aspect to describe is related to the dimensions in terms of calculation for home computers. In fact, it was necessary to reduce the dimensions of the various components and some parameters internal to the use of the NN and in particular some are described in the following table:

TABLE 1. Possible data simulation of COVID-19.

	BASES	GENES	I/O NN
Effettive	32.000	Known >1000 bases	> 320
Simulate	320	32 bases	32

Regarding the scanning of the base chain (excessive for home computers) by the neural system, choices had to be made for debugging and to make the recognition platform usable as described in the figure below.

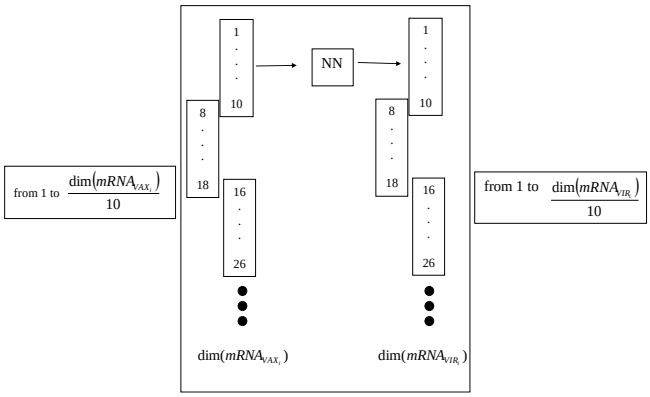

Fig. 5. Possible data simulation of mRNA array.

B. Data Organization for Features Extraction

Since there are many programming languages that offer professional tools for the calculations you want to carry out in this work such as Pyton® or Matlab® [24]; the choice fell on the latter due to the experience gained in applications of this type. Below are the nomenclatures of the patterns used in this work:

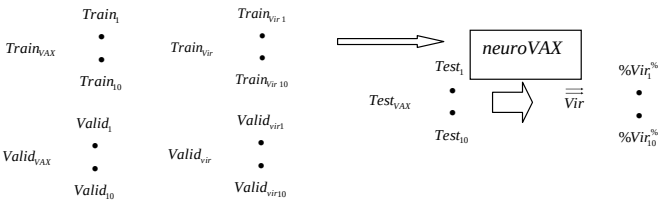

Fig. 6. Training e validation data, test and features extraction.

Fig. 6 shows the result of the simulation and each *Vir* vector has inside it in decreasing sense the percentages (and if desired also specific genome traits) of virus affected by the incoming vaccine.

C. Criteria for Selection Of Similarity

The lines below describe a method for assessing similarity with the system response for a vaccine (or cure) U_1:

$$Test_{VAX_1} \quad U_1 \rightarrow \quad U_1 - \begin{bmatrix} Train & \begin{bmatrix} 1 \\ \bullet \\ \bullet \\ 10 \end{bmatrix} \\ Valid & \begin{bmatrix} 1 \\ \bullet \\ \bullet \\ 10 \end{bmatrix} \end{bmatrix} \quad (3)$$

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Carrying out the formula (3) of this group of 20 *mRNAs* we put in order with a similarity criterion

$$(4)\qquad \min_i \left[U_i - \left[\begin{matrix} Train_i \\ Valid_i \end{matrix} \right] \begin{bmatrix} 1 \\ \bullet \\ \bullet \\ 10 \end{bmatrix} \right]$$

following the comparison, the results can be sorted thanks to this for loop:

$$(5)\qquad \begin{matrix} for\, i = 1:n \\ \min_{ik} \quad [U_i] - \begin{bmatrix} Train_i \\ Valid_i \end{bmatrix} \\ end \end{matrix}$$

we select 10 +10 Vir and you can order and associate them thanks to a look-up tabled as follows

$$(6)\qquad \begin{bmatrix} U_1 \rightarrow & \min \begin{bmatrix} T_{1k} \\ V_{1k} \end{bmatrix} & \begin{bmatrix} 1 \\ \bullet \\ \bullet \\ 10 \end{bmatrix} \\ & \bullet & \\ & \bullet & \\ U_{10} \rightarrow & \min \begin{bmatrix} T_{1k} \\ V_{1k} \end{bmatrix} & \end{bmatrix}$$

The performance of the learning system as shown in figures Fig. 8, 9 and 10, in fact the trend is consistent with the fact that the data were generated randomly.

V. CODE USED

The specific area is interdisciplinary and concerns information technology and medical clinic in response to the pandemic caused by the COVID-19 virus and its variants. Thanks to the random generation of COVID-19 mRNA, the potential of Neural Networks is highlighted in finding a similarity between existing vaccines and associated with the respective variants and their percentages to be dosed for an unknown variant to be proposed to clinicians who face the COVID-19; thanks to random generation of COVID-19 and their respective vaccines all represented by their mRNAs in the training, validation and testing phases [28]-[34].

A. How the Data Were Acquired

In the next lines we report the main characteristics of the hardware used:
Device name DESKTOP-H90KT1Q
Intel (R) Core (TM) i7-6700 CPU @ 3.40GHz 3.41 GHz processor
RAM installed 8.00 GB
Device ID 188A7097-E445-4D3E-8B72-697B037AE954
Product ID 00325-95978-85623-AAOEM
System type 64-bit operating system, x64-based processor

B. Description of Data Collection

The data used in the present work are three groups of six vectors of 32 bases (if desired also 32,000 with a Main Frame PC) rows and 1 column representing the mRNA vaccines of COVID19 type viruses where the bases have been randomly generated; and also three other groups of six vectors representing the virus under examination of known variants, and lastly an mRNA representing the unknown variant of COVID19.

All of these arrays have been normalized and pre-treated with specific MATLAB functions suitable to adapt the inputs to the learning algorithm chosen in this work. The learning algorithm is a multy layer perceptron Neural Network with Back Propagation learning algorithm.
Set parameters such as:
epochs = 300;
vettMax = zeros (32.1) +1;
vettMin = zeros (32.1);
PR = [vettMin '; vettMax '];
the function that generates the neural network with tansig activation function has been called and trainlm is a network training function that updates weight and bias values according to Levenberg-Marquardt optimization.
pattern = newff (PR ', [32 32], {' tansig '' tansig '},' trainlm ');
model = init (model);
model.trainParam.epochs = epochs;
model.trainParam.show = 10;
model.trainParam.goal = 0.000001;
model.trainParam.max_fail = epochs;
model.trainParam.min_grad = 1.0000e-30;
Once the neural network has been initialized, the training phase begins
model = train (model, IN.PN, OU.TN, [], [], VN);
Once the training is completed, it is simulated by presenting the test arrays as input
T = sim(model,vaxCOVID19norm(:,:));
the post processing consists in identifying the range where the difference with the criterion of similarity of the bases falls between the response of the system and those of the unknown variant:
VAX - COVID 19=0, bases are the same
VAX - COVID 19=-0.25 at 0 and 0 at 0.25, bases are not the same
VAX - COVID 19=-0.75 at -0.25 and 0.25 at 0.75 bases are not the same. The zeros of difference above give the similarity, the clinician should make a genomic metric, now let's consider only the zeros=0;

C. Value of the Data

- Recognize Genome traits and a possible use as a genomic sniffer
- Help to the clinician to find indications for dosages of any vaccines
- The proposed system with only 32 bases can be increased as the PC memory increases
- By changing the number 32 to 36 and with 36,000 (°) you can think of an application as a compass for space travel and more
- The scientific community can benefit from the workbench for other pathologies.

D. Data Description

This figure shows the standardized and randomly generated arrays, with dimensions of only 32 bases, to train, validate and

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finally test the response to an unknown variant called COVID 19

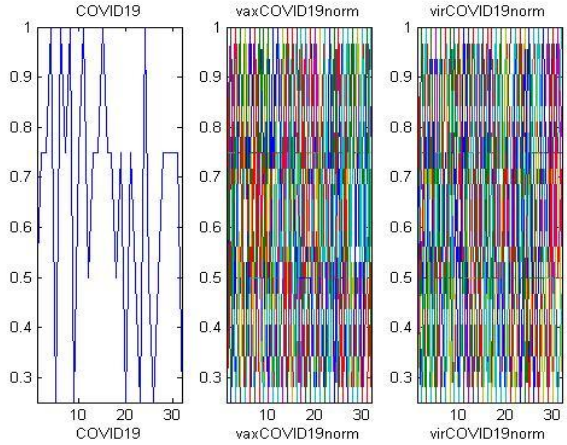


Fig. 7. Randomly generated arrays, with dimensions of only 32 bases, to train, validate and finally test called COVID 19.

The next three figures show the learning curves in relation to the "epochs" performed.

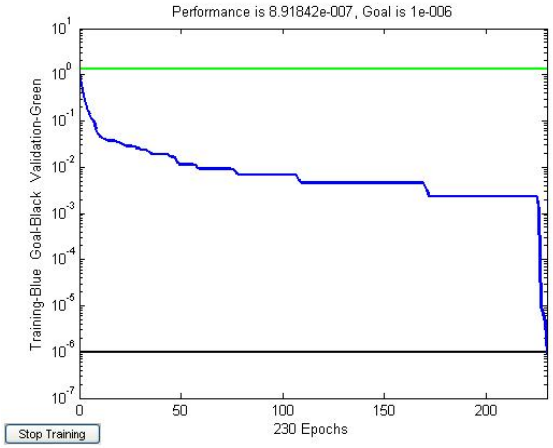


Fig. 8. Training curve after 200 epoch.

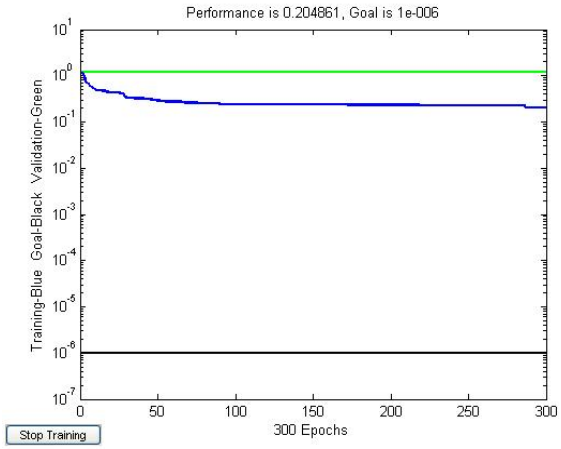


Fig. 9. Training curve after 300 epoch.

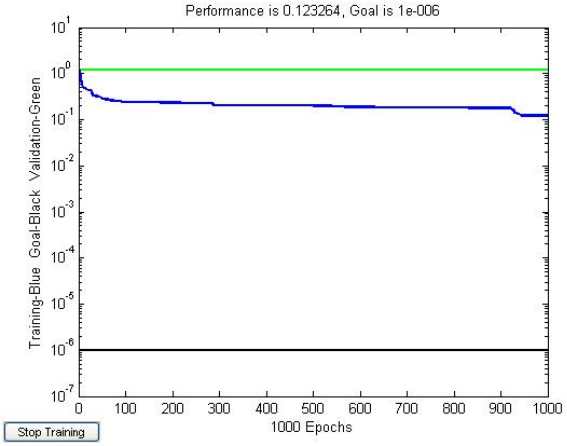
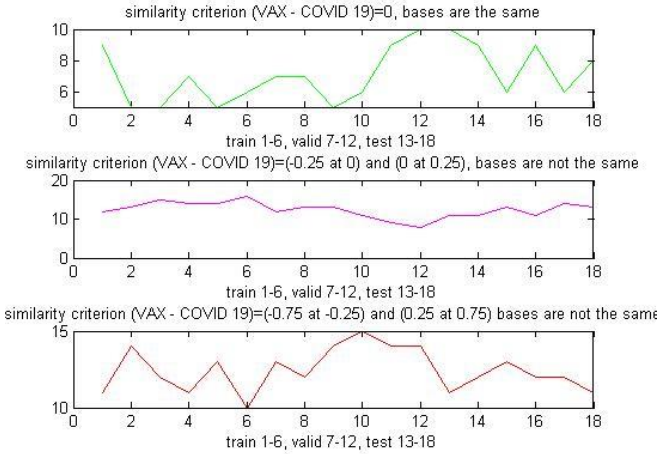
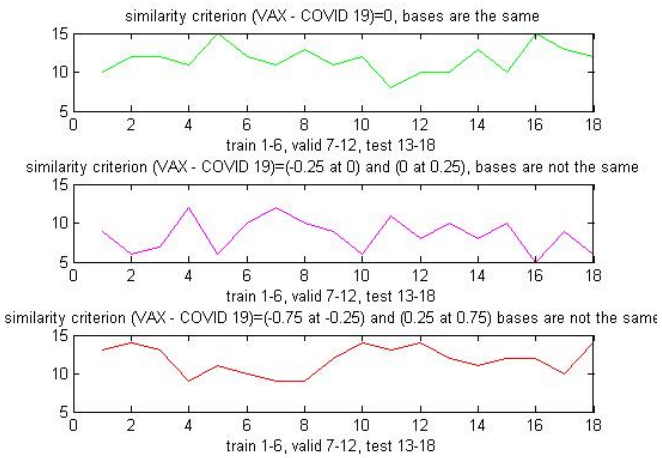


Fig. 10. Training curve after 1000 epoch.

In this case with 1000 Epoch the calculation times were almost one hour, in any case always about five minutes every one hundred Epoch. The next two figures show the similarity criterion if the bases are the same in relation to the "Epochs" performed.



(a)



(b)

Fig. 11. (a) (b) Similarity criterion for the bases, if are the same in relation the result are "0".

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The meaning of this figures three has been highlighted without giving a non-random imprint to the mRNA bases (which in proportion to what is known from COVID-19 it would be enough to decide the value of three bases) this can be done according to the indications of the clinician and the use of a PC that allows you to study 32,000 bases in a reasonable time.

VI. Code Used

All the data used in this article can be obtained by executing the following program lines with Matlab®.

```
clc
clear all
close all
format long
basi = {'A', 'C','U','G'};
basi(ceil(4.*rand(1,1)));
tempC=1;
tempR=1;
for tempR=1:32
COVID19(tempR,1)=ceil(4.*rand(1,1));
for tempC=1:18
vaxCOVID19(tempR,tempC)=ceil(4.*rand(1,1));
virCOVID19(tempR,tempC)=ceil(4.*rand(1,1));
end;
end;
COVID19norm=COVID19(:,:)/4;
vaxCOVID19norm=vaxCOVID19(:,:)/4;
virCOVID19norm=virCOVID19(:,:)/4;
figure
subplot(131);
plot(COVID19norm)
xlabel('COVID19');
hold on
title('COVID19')
axis tight
subplot(132);
plot(vaxCOVID19norm)
xlabel('vaxCOVID19norm');
hold on
title('vaxCOVID19norm')
hold off
axis tight
subplot(133);
plot(virCOVID19norm)
xlabel('virCOVID19norm');
hold on
title('virCOVID19norm')
hold off
axis tight
[IN.PN,minpT,maxpT,OU.TN,mintT,maxtT] =
premnmx(vaxCOVID19norm(1:32,1:6),virCOVID19norm(1:3
2,1:6));
[VN.P,minpV,maxpV,VN.T,mintV,maxtV] =
premnmx(vaxCOVID19norm(1:32,7:12),virCOVID19norm(1:
32,7:12));
epochs=300;
vettMax=zeros(32,1)+1;
vettMin=zeros(32,1);
PR=[vettMin'; vettMax'];
modello=newff(PR',[32 32], {'tansig' 'tansig'},'trainlm');
model=init(modello);
model.trainParam.epochs=epochs;
model.trainParam.show=10;
model.trainParam.goal=0.000001;
model.trainParam.max_fail=epochs;
model.trainParam.min_grad=1.0000e-30;
hold off
figure
model=train(model,IN.PN,OU.TN,[],[],VN);
T = sim(model,vaxCOVID19norm(:,:));
%Post processing
minT=min(min(T));
maxT=max(max(T));
positivT=(T+abs(minT));
positiveNormT=positivT/(abs(minT)+maxT);
for j=1:32
for k=1:18
if (positiveNormT(j,k)>=0 &
positiveNormT(j,k)<=(0.25+0.25/2))
positiveNormT(j,k)=0.25;
end
if (positiveNormT(j,k)>(0.25+0.25/2) &
positiveNormT(j,k)<=(0.5+0.5/2))
positiveNormT(j,k)=0.5;
end
if (positiveNormT(j,k)>(0.5+0.5/2) &
positiveNormT(j,k)<=(0.75+0.75/2))
positiveNormT(j,k)=0.75;
end
if (positiveNormT(j,k)>(0.5+0.75/2) &
positiveNormT(j,k)<=(1))
positiveNormT(j,k)=1;
end
end
end
for k=1:18
U(:,k)=positiveNormT(:,k)-COVID19norm(:,1);
end;
% The zeros of [A] give the similarity, the clinician should
make a genomic metric, now let's consider only the zerosi=0;
index=zeros(32,1);
a=zeros(3,18);
for i=1:18
a(1,i)=length( find( U(:,i)==0 ));
a(2,i)=length( find( U(:,i)>=-0.25 & U(:,i)<0 )) + length( find(
U(:,i)>0 & U(:,i)<=0.25 ));
a(3,i)=length( find( U(:,i)>=-0.75 & U(:,i)<-0.25 )) + length(
find( U(:,i)>0.25 & U(:,i)<=0.75 ));
end;
% similarity criterion (VAX - COVID 19)=0, bases are the
same
figure
subplot(311);
plot(1:18,a(1,:)','g-')
xlabel('train 1-6, valid 7-12, test 13-18');
```

```
title('similarity criterion (VAX - COVID 19)=0, bases are the same')
hold on
subplot(312);
plot(1:18,a(2,:)','m-')
xlabel('train 1-6, valid 7-12, test 13-18');
title('similarity criterion (VAX - COVID 19)=(-0.25 at 0) and (0 at 0.25), bases are not the same')
hold on
subplot(313);
plot(1:18,a(3,:)','r-')
xlabel('train 1-6, valid 7-12, test 13-18');
title('similarity criterion (VAX - COVID 19)=(-0.75 at -0.25) and (0.25 at 0.75) bases are not the same')
```

VI. Conclusion

This application was developed with Matllab® that is an excellent calculator/simulator and has a serious and professional toolbox also on neural networks.

After having pre-treated the inputs, proceed anyway with the outputs and using the toolbox functions on the NN you should have the error turn down in the training phase; or rather the NN is said to have learned without generalizing and over learning; this is possible if in the validation phase never seen viral genomes are used (genomes pre-treated can be used if they do not have others) in training.

If the network has learned what do we have?

The answer is represented in Fig. 6; that is, a system that, upon the presentation of the output from the bases "involved" in the neural learning of the various bases and their chains, which can be considered in percentage as elements of a mix of the different vaccines seen in the training phase. They may not be many, but everything focuses on base chains known to vaccine workers. And if the viral genomes presented in the training phase have been presented sequentially and it will also be in the test phase with the output we would have the (positive) filament of the vaccine.

We hope this summary was useful especially in the construction phase of any rules filters for post and pre-treatment of data. In the end there is a spreadsheet that can be used in the main functions as a cliché to try with us hand. Even if to be precise it is us ideas to create time series where there are none and thus to be able to use statistical functions perhaps useful for the representation of knowledge. The development of the calculation sheet (which could be two alternative ways but if the procedures are correct could give an important and winning synergy) requires fantasy and imagination.

The only numerical datum from which we started is that the genomic size of coronaviruses varies from about 26 to 32 kilobases, the largest for an mRNA virus. I will consider 32 kilobases [11].

In the following listing there are commands that should simulate a neural network where the possession of twenty viruses is assumed and the first thirty vaccines and that of the COVID-19 that can be obtained following the similarity test with the various vaccines in possession that are marked by the neural response to COVID-19. The spreadsheet uses Matlab® commands and is set up with 32 bases taken and aligned at 10 to 10; having a serious PC and software you could run the simulation at 32 kbases taken at 1000 to 1000 with an important neural network in size. The simulations would still be useful to understand if a mix/cocktail of vaccines at hand can be useful to weaken the COVID-19.

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