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Development of Software and Hardware Complex for Primary Diagnosis of Gastroenterological Diseases on the Basis of Deep Machine Learning

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Annotation: This article discusses the development of a software and hardware complex for primary diagnostics of gastroenterological diseases on the based of deep machine learning. The process of deep machine learning was carried out, the ANN and SVM algorithms were used. The results of deep machine learning were compared, two variants of data sets for training were collected. Based on deep machine learning, it is planned to further develop a software and hardware complex for the primary diagnosis of gastroenterological diseases.

Key words: deep machine learning, algorithm, forecasting, gastroenterological diseases, hardware and software complex, SVM, ANN.

1. Introduction

At present, the development of artificial intelligence in all countries of the world is developing carefully and rapidly. Links in the development of artificial intelligence The President of the Republic of Uzbekistan Sh. Mirziyoyev issued a resolution “On measures to create conditions for the accelerated introduction of artificial intelligence technologies”, this resolution is in accordance with the strategy “Digital Uzbekistan - 2030” [1].

In the field of medicine, digital technologies can be widely used in the diagnosis, treatment of various diseases and different degrees. With the help of digital technologies, the work of doctors can be facilitated, the human factor is reduced, research time is reduced and efficiency is increased.

Within a short time, the doctor can make a decision about the diagnosis. With the help of digital technologies, controversial points can be overcome. Digital technologies use artificial intelligence, neural networks, machine learning and modern programming languages Python [8,9,10].

Artificial intelligence is the science and technology of creating intelligent machines, especially intelligent computer programs. AI is related to the similar task of using computers to understand human intelligence, but is not necessarily limited to biologically plausible methods.

In this process, the analysis of the process of deep machine learning based on the results obtained for the primary diagnosis of gastroenterological diseases is carried out.

The process of deep machine learning was carried out, the ANN and SVM algorithms were used. With the help of gastroenterologists, training materials were collected, that is, the date of the set from patients. Human saliva was chosen for primary diagnosis. The results of deep machine learning were compared. Based on these results, it is planned to develop a software and hardware complex called Saliva for the primary diagnosis of gastroenterological diseases.

Preliminary diagnostics helps to find out the problems, determine the bottlenecks of the enterprise, draw up a program for future changes and should answer the questions: is it possible to solve the identified problems, in what sequence they need to be solved [2,3,4].

In a scientific study, human saliva was taken. With the help of saliva, you can predict about gastroenterological diseases. With illness, the composition of saliva changes dramatically. The composition of saliva is the parameters [20,21,22].

By changing the composition of saliva, you can create a data set for training artificial intelligence algorithms. Table 1 shows the composition of a healthy person [14,15,16].

Table 1. Composition of the Saliva of a Healthy Person

№	*The composition of saliva*	*Qty. (% and g/l)*
1	Water	99.4-99.5%
2	Organic and inorganic components	0.5-0.6%
3	Squirrels	1.4-6.4 g/l
4	Mucin	0.8-6.0 g/l
5	cholesterol	0.02-0.5 g/l
6	Glucose	0.1-0.3 g/l
7	Ammonium	0.01-0.12 g/l
8	Uric acid	0.005-0.03 g/l

2. Algorithms Based On Deep Machine Learning

In the article “Analysis of algorithms for predicting and preliminary diagnosis of gastroenterological diseases” [17,18,19], the initial results were taken, which contain 100 patients. As a continuation of this study, the number of patients was increased to 1000 per data set.

Patient parameters were obtained. Based on the obtained parameters, the data set was trained on the SVM and ANN algorithms.

The purpose of the algorithm involved in SVM:

In other words, “The goal is to maximize the minimum distance.” for the distance is given:

$$d_{H(\varphi(x_0))} = \frac{|w^T(\varphi(x_0)) + b|}{||w||_2}$$

$$w^* = arg_w \max[min_n d_H(\varphi(x_n))]$$

So, now that the goal is clear. By making predictions for the training data, which was binary, classified into positive and negative groups, if a point is replaced from the positive group in the hyperplane equation, we will get a value greater than 0 (zero), mathematically,

$w^{T} (\varphi (x)) + b > 0$

And predictions from the negative group in the hyperplane equation would give a negative value as

$w^{T}(\Phi(x)) + b < 0.$

But here the signs were about the training data, that is, how we train our model. This is for a positive class, give a positive sign, and for a negative class, give a negative sign.

But when testing this model on the test data, if we correctly predict a positive class (positive sign or sign greater than zero) as positive, then two positives results in a positive and therefore greater than zero result. The same applies if we correctly predict the negative group, since two negatives will again result in a positive result.

But if the model error classifies the positive group as negative, then one plus and one minus constitute a minus, hence less than zero overall.

To summarize the above concept:

The product of the predicted and the actual label will be greater than 0 (zero) if the prediction is correct, otherwise less than zero.

$$y_n[w^T\varphi(x)+b] = \begin{cases} \geq 0\ i\,f\ correct \\ < 0\ i\,f\ incorrect \end{cases}$$

For ideally separable datasets, the optimal hyperplane classifies all points correctly, additionally substituting the optimal values into the weight equation.

arg max is an abbreviation for max arguments, which are basically points in the area of the function where the function maximizes the values.

Also, taking the independent weight term outward gives:

$$w^* arg_w max \frac{1}{||w||_2}[min_n y_n|w^T(\varphi(x)+b)|]$$

The inner term $(\min_n y_n | w^T\Phi (x) + b |)$ basically represents the minimum distance from the point to the decision boundary and the nearest point to the decision boundary H.

Rescaling the distance to the nearest point as 1, i.e. $(\min_n y_n | w^T\Phi (x) + b |) = 1$. Here the vectors remain in the same direction, and the hyperplane equation does not change. It's like zooming in on an image; objects expand or contract, but the directions stay the same and the image stays the same.

Distance rescaling is done by replacing:

$$w \rightarrow cw, \qquad b \rightarrow cb$$

$$(cw)^T\varphi(x_n) + (cb) = c(w^T\varphi(x_n) + b) = 0$$

The equation now becomes (describing that each point is at least 1/| | w || 2 away from the hyperplane) as

$$w^* = arg_w max \frac{1}{||w||_2}, s.t. min_n y_n[w^T\varphi(x_n) + b] = 1$$

This maximization problem is equivalent to the following minimization problem, which is multiplied by a constant, since they do not affect the results.

An artificial neural network algorithm is a mathematical model, software or hardware implementation for organizing the construction of neural networks as a living organism. An artificial neural network is not programmed, but trained. Learning takes place in finding the coefficients of connections between neurons. The ability to learn is one of the advantages over algorithms.

The artificial neural network algorithm is also used in forecasting. This happens after training, that is, the neural network is able to predict the future value of the sequence based on several previous values and those that exist at the moment.

Forecasting will be when the previous change in the actual degree overrides the future. For example, predicting a disease of a different type.

There are two types of learning process:

- ✓ Learning with a teacher
- ✓ Blended learning

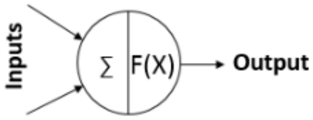


Fig1. Simple neuron

Activation of the input signal with the F(X) function. The activation function is sigmoid, ReLu, tanh, etc. This example uses a sigmoid activation function at layer nodes.

$$F(X) = \frac{1}{1 + e^{-x}}$$

Figure 1 shows a simple neuron. Now the task will be solved through the function. The value of the hidden layer is 1= (1*0.1) +(1*0.1) +(1*0.1) =0.3.

$$Y_{in} = \sum X_i * W1_{ij}$$

3. Development Of Software And Hardware Complex

Devices for the primary diagnosis of diseases of the gastrointestinal tract is called "Saliva". The device consists of sensor, ADC, microcontroller, UART, Regulator and Bluetooth. When developing the Saliva device, special attention was paid to its low cost and ease of carrying.

The architecture of the "Saliva" system consists of functional blocks and each performs certain tasks, Figure - 2 The "Saliva" system consists of 5 main modules, and they make up the hardware-software complex.

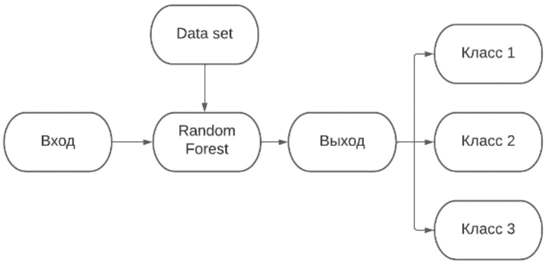


Fig 2. Functional module of the "Saliva" device

Sensors. According to the selected data set parameters, a set of protein, glucose, mucin, cholesterol, ammonium, and uric acid sensors was assembled.

ADS1298. An analog-to-digital converter (ADC) is a low-power, multi-channel 24-bit delta-sigma ADC device developed by Texas Instruments. In the ADS1298 chip, all channels are discredited simultaneously. The gain parameters of the ADS1298 can be controlled by the PGA. This chip allows you to measure the patient's saliva according to the selected parameters, it can use the RLD scheme. The data transmission of the chip can reach the speed of 500-32 kbps (the value of the transmitted discrete frequency is 103 seconds). The connection between the "Saliva" device and the computer is established via the UART interface [22,23,24].

Below are the specifications of ADS1298 A/D Converter:

- ✓ 8 low-noise PGA and 8 high-precision ARC';
- ✓ Channel power: 0.75 mW/channel.
- ✓ Noise level: 4 mVpp (bandwidth 150 Hz, G = 6).

- ✓ Bias current: 200 pA.
- ✓ Data rate: 250 SPS - 32 kSPS.
- ✓ Common mode rejection: -115 dB.
- ✓ Programmable gain: 1, 2, 3, 4, 6, 8 or 12
- ✓ ADC AAMI EC11, EC13, IEC60601-1, IEC60601-2-27 and IEC60601-2-

It complies with the requirements of standard 51.

- ➢ Provides single polarity and bipolarity:
- ✓ AVDD = 2.7V - 5.25V
- ✓ DVDD = 1.65V - 3.6V
- ➢ Built-in RLD amplifier, trigger detection, WST

terminal, speed detection, test signals.

- ➢ Built-in breathing impedance measurement.
- ➢ Ability to measure speed digitally.
- ➢ Built-in oscillator.
- ➢ SPI interface.

Atmega328 microcontroller. The microcontroller receives the primary processed saliva sample signals coming from the ADS1298 microcircuits in the power supply of the Saliva device and performs secondary processing and transmits them to the Bluetooth module via the SPI interface. The microcontroller also controls the ADS1298 module, a 12-channel device for a discrete and analog-to-digital saliva sample signal converter and other peripheral devices. Communication between the Atmega328 and peripherals was implemented using the SPI module. Block diagram of the Atmega328 microcontroller.

The Atmega328 microcontroller is connected to two SPI interfaces that support high-speed communication with ADS1298 and NS-05 devices. The ADS1298 module provides a serial communication timing system. Synchronization in all communication processes should be at least minimal. The low power and high efficiency Atmega328 8-bit microcontroller has the following features.

Fig 3. Atmega328 microcontroller.

Below are the specifications of the Atmega328 microcontroller:

- ✓ Working with perfect short commands.
- ✓ AVR with 40 contacts.
- ✓ 32 kB flash memory.
- ✓ 1 KB of permanent memory.

- 2 KB of RAM.
- The number of input and output contacts is 23.
- Timer: 2 8-bit and 1 16-bit.
- 10-bit 6-channel analog-to-digital converter.
- 6-channel wide pulse modulator.
- Separate oscillator.
- Supports SPI master-slave and I^{2}C mode.
- External oscillator 20 MHz.
- Universal synchronous-asynchronous receiver and transmitter.

Bluetooth HC-05. Bluetooth HC-05, one of the main power supply modules of the “Saliva” device, provides the process of wireless data exchange between the computer and the “Saliva” device via the UART interface. The frequency range of the HC-05 module and the data transmission channel correspond to ISM, i.e. 2.4 GHz. This intermediate frequency is a range of radio frequencies defined by the radio regulations of the International Telecommunication Union.

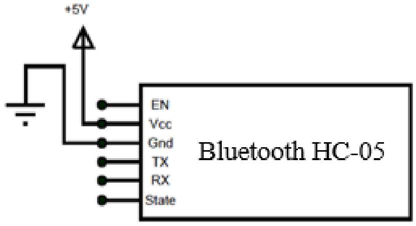


Fig 4. Block diagram of Bluetooth module HC-05

The total size of information of 8 channels coming from the ADS1298 is 224x8 = 224x23=227, i.e. 227x50/8 = 838 860 800 or 838 860 800/1024 = 819 200 Kbps or 800 Mb.

If this value is expressed in the 16th number system, it will be equal to 800/216=0.0122 MB. The total bandwidth of the Bluetooth NS05 device selected for the design of the ECG device is 2.1 Mbps, which is about 10 times more than the digital data (0.0122 Mbps) generated by the ADC device, which is in line with the current demand.

Bluetooth HC-05 has two different states (modes): command state and transmit/receive state. 38400kbps in command mode and 9600kbps in data transmission/reception mode.

Below are the technical specifications of the NS05 Bluetooth device.

- Bluetooth chip: HC-05 (BC417143).
- Radio frequency range: 2.4-2.48 GHz.
- Transmission power: 0.25 - 2.5 mW.
- Signal sensitivity: -80 dBm (0.1% BER).
- Supply voltage: 3.3-5V.
- Required current: 50 mA.
- Impact radius: up to 10 meters.
- Interface: serial port (UART).
- Mode: master, slave, master/slave mode.

- ✓ Working temperature: -25…75 °C.
- ✓ Dimensions: 27 x 13 x 2.2 mm.
- ✓ Standardized based on IEEE 802.15.1.
- ✓ FHSS – radio signal transmission method, modulation type is used.
- ✓ The default baud rate is 38400, but 9600, 19200, 38400, 57600,
- ✓ Supports 115200, 230400, 460800 baud.

Universal asynchronous transceiver (UART). A very simple protocol that uses only two wires between transmitter and receiver to transmit and receive in both directions. Both ends are also grounded.

Communication in a UART can be simplex (data is transmitted in one direction only), half duplex (each side transmits, but only in turn), or full duplex (both sides can transmit at the same time). Data in the UART is transmitted in the form of frames.

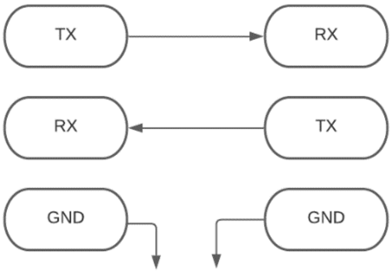


Fig 5. Data in the UART is transmitted in the form of frames.

One of the big advantages of UART is its asynchrony - the transmitter and receiver do not share a common clock signal. Although this greatly simplifies the protocol, this property imposes certain requirements on the transmitter and receiver.

Since they do not share a common clock signal, both ends must transmit at the same predetermined rate in order to have the same bit timing. The most common UART baud rates in use today are 4800, 9600, 19.2 kbps, 57.6 kbps, and 115.2 kbps. In addition to the same baud rate, both sides of the UART connection must also use the same frame structure and parameters. The best way to get an idea of the protocol is to look at the UART frame.

LM2596 regulator. The LM2596 series regulators are monolithic.

ICs providing all active functions for a buck switching regulator capable of 3-A load control with excellent line and load regulation. These devices are available in 3.3V, 5V, 12V fixed output and adjustable output voltage.

Requiring a minimum of external components, these controls are easy to use and include internal frequency compensation and a fixed frequency oscillator. The LM2596 series operates at a switching frequency of 150 kHz, which allows the use of smaller filter components than what is required for low frequency switching regulators. Available in a standard 5-pin TO-220 package with several different lead bending options and a 5-pin TO-263 surface mount package.

5. Results

An example of the data of the set is indicated in table No. 2. The parameters and the name of the composition of human saliva are indicated.

An analysis of the ANN and SVM algorithms was made, the number of patients was 100 and 1000. The corresponding results were obtained [9,10,11].

Table 2. Data Set Parameters

Data set parameters	*The name of the composition of saliva*
Parameter_1	Protein
Parameter_2	Mucin
Parameter_3	cholesterol
Parameter_4	Glucose
Parameter_5	Ammonium
Parameter_6	Uric acid

The first time the training process was carried out on the number of 100 patients in the data set. (Figure 6,7)

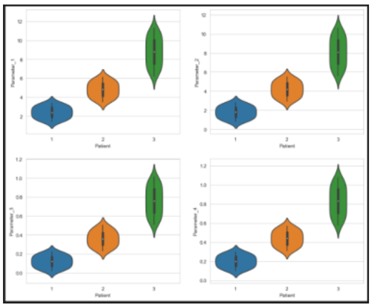


Fig 6. Determining the importance of parameters and predicting the likelihood of a patient's illness. (ANN)

In this algorithm, the result appeared on three colors. Accordingly, the result of training can be determined by colors:

- ✓ Blue - the probability of illness is higher
- ✓ Orange - the probability of illness is lower
- ✓ Green is healthy

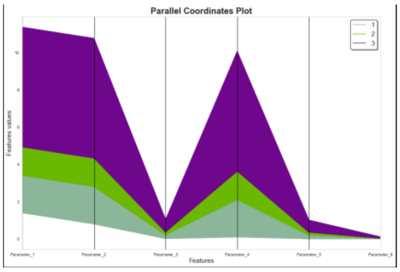
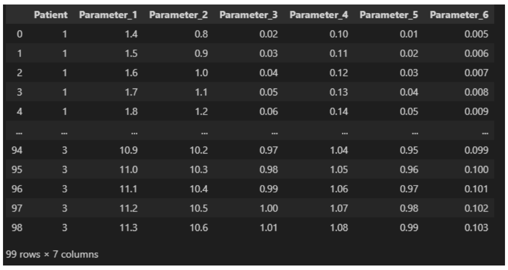


Fig 7. Determining the importance of parameters and predicting the likelihood of a patient's illness. (SVM)

In this algorithm, the result appeared on three colors. Accordingly, the result of training can be determined by colors:

- ✓ Violet - the probability of illness is higher

- ✓ Green - the probability of illness is lower
- ✓ Pistachio – healthy



	Patient	Parameter_1	Parameter_2	Parameter_3	Parameter_4	Parameter_5	Parameter_6
0	1	1.4	0.8	0.02	0.10	0.01	0.005
1	1	1.5	0.9	0.03	0.11	0.02	0.006
2	1	1.6	1.0	0.04	0.12	0.03	0.007
3	1	1.7	1.1	0.05	0.13	0.04	0.008
4	1	1.8	1.2	0.06	0.14	0.05	0.009
...	...	...	...	...	...	...	...
94	3	10.9	10.2	0.97	1.04	0.95	0.099
95	3	11.0	10.3	0.98	1.05	0.96	0.100
96	3	11.1	10.4	0.99	1.06	0.97	0.101
97	3	11.2	10.5	1.00	1.07	0.98	0.102
98	3	11.3	10.6	1.01	1.08	0.99	0.103

99 rows × 7 columns

Fig 8. Data set of 100 patients

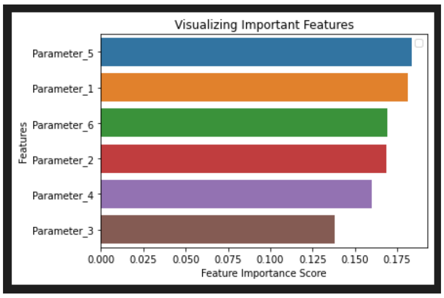


Fig 9. Importance of parameters from the data set (100)

The second time the training process was carried out on the number of 1000 patients in the data set.

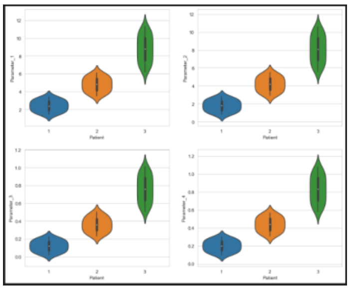


Fig 10. Determining the importance of parameters and predicting the likelihood of a patient's illness. (ANN)

In this algorithm, the result appeared on three colors. Accordingly, the result of training can be determined by colors:

- ✓ Blue - the probability of illness is higher
- ✓ Orange - the probability of illness is lower
- ✓ Green is healthy

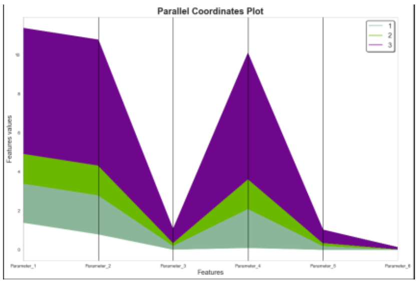


Fig 11. Determining the importance of parameters and predicting the likelihood of a patient's illness. (SVM)

In this algorithm, the result appeared on three colors. Accordingly, the result of training can be determined by colors:

- ✓ Violet - the probability of illness is higher
- ✓ Green - the probability of illness is lower
- ✓ Pistachio – healthy

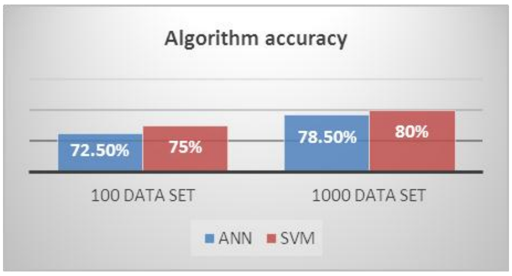


Fig 12. Algorithm accuracy between 100 and 1000 data sets

After deep machine learning of data sets, a comparison was made between the accuracy of ANN and SVM algorithms. Figure 12 showed the accuracy of the algorithms between 100 and 1000 date sets.

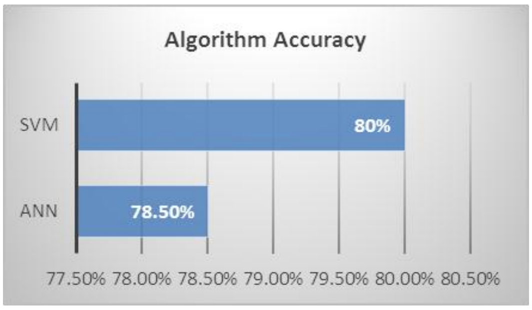


Fig 13. Algorithm accuracy between SVM and ANN

Figure 8 shows the overall accuracy of the algorithms after deep machine learning datasets. The overall accuracy of the algorithms allows scientific research to select a specific algorithm for the primary diagnosis of gastroenterological diseases.

6. Acknowledgment

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7. Conclusion

As a result of the analysis and scientific research, an analysis of algorithms based on ANN and SVM deep machine learning was made. The data set was collected from 100 to 1000 patients. The accuracy of the algorithms between data sets of 100 and 1000 patients was 78.5% and 80%. Further scientific research will be carried out with other algorithms based on deep machine learning.

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