**Compiler name:**

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**Subject Name:**

Diagnosis of leukemia with the help of artificial intelligence in the field of studying dendritic cells

**Programming used:**

with python

**Target library:**

Part by step-by-step method

Introduction:

Leukemia is a type of cancer that affects the blood and bone marrow. It occurs when there is an abnormal growth of blood cells, usually white blood cells, in the bone marrow. The bone marrow produces too many abnormal white blood cells that do not function properly. These abnormal cells destroy healthy blood cells and make the work of blood and bone marrow difficult.

There are several types of leukemia, including acute lymphocytic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML). The type of leukemia depends on the type of blood cell that becomes cancerous and whether it grows quickly or slowly.

Leukemia can affect anyone, but it is more common among people ages 65 to 74, males at birth, and Caucasians. Many people think of leukemia as a childhood cancer, but some types are more common in adults.

Symptoms of leukemia may include fatigue, fever or night sweats, frequent infections, weight loss without effort, swollen lymph nodes, enlarged liver or spleen, easy bleeding or bruising, and small red spots on the skin. However, some people with leukemia may not have noticeable symptoms in the early stages.

The main causes of leukemia are genetic disorders, previous cancer treatment, exposure to certain chemicals, smoking, and a family history of leukemia. However, most people with known risk factors do not develop leukemia, and many people with leukemia do not have any of these risk factors.

Treatment for leukemia depends on the type of leukemia, age and general health, and whether the leukemia has spread to other organs or tissues. Common treatments often include a combination of chemotherapy, radiation, and stem cell transplants.

There are several types of leukemia, including:

Acute lymphocytic leukemia (ALL):

The most common type of leukemia is in children, teenagers and young people up to the age of 39.

Acute myelogenous leukemia (AML):

The most common type of acute leukemia in adults is seen mostly in the elderly (over 65 years old).

Chronic Lymphocytic Leukemia (CLL): It is the most common chronic leukemia in adults, which is mostly seen in people over 65 years of age.

Chronic myelogenous leukemia (CML):

It is more common in the elderly (most common in people over 65), but it can affect adults of any age.

Leukemia can cause a variety of symptoms, including:

Fatigue or weakness

Fever or chills

Frequent or severe infections

Lose weight effortlessly

Swollen lymph nodes, enlarged liver or spleen

Bleed or bruise easily

Frequent nosebleeds

tiny red spots on your skin (spots)

Profuse sweating, especially at night

Bone pain or tenderness

The exact cause of leukemia is not known, but certain factors can increase the risk of developing the disease, including:

Previous cancer treatment

Genetic disorders

Exposure to certain chemicals

smoking

Family history of leukemia

Summary:

The death rate from leukemia is 5.9 per 100,000 men and women per year, based on 2018-2022 deaths by age. The death rate is higher among the elderly. The percentage of deaths from leukemia is the highest among people aged 75 to 84.

Here is a breakdown of death rates by race and ethnicity:

| All races 7.8 |

| Spanish | 5.2

| Non-Hispanic American Indian/Alaska Native | 5.8 |

| Non-Hispanic Islands of Asia/Pacific | 4.3

| Black non-Hispanic | 6.6

| White non-Hispanic | 8.4

By the end of 2024, there will be an estimated 23,670 deaths from leukemia in the United States. Leukemia is the seventh leading cause of cancer death in the United States.

The following causes can cause the death of people with leukemia, including:

The most common cause of death from leukemia is infection, which accounts for about 75% of deaths. Bacterial infections are the most common type of infection, followed by fungal infections. Infections can be systemic or pulmonary, and the most common organisms isolated are Klebsiella pneumoniae, Escherichia coli, and Pseudomonas aeruginosa.

Other causes of death from leukemia include bleeding, often due to thrombocytopenia (low platelet count) or disseminated intravascular coagulation, and organ failure. Cardiovascular mortality is also one of the important causes of death in people with chronic myeloid leukemia.

In addition, patients with leukemia may die from complications related to their treatment, such as graft-versus-host disease (GVHD) in people who have undergone hematopoietic stem cell transplants.

It is worth noting that the causes of death from leukemia can be different depending on the type of leukemia, acute lymphocytic leukemia (ALL) and acute myeloid leukemia (AML) have different causes of death compared to chronic lymphocytic leukemia (CLL) and chronic myeloid. blood cancer (CML).

Medical science has made significant progress in dealing with blood cancer. Immunotherapy has been a game changer in leukemia care and treatment. Bispecific antibodies that bind to both the surface of cancer cells and immune T cells have shown efficacy and safety in clinical trials. CAR T cell therapy, which reprograms a patient's T cells to recognize and attack cancer cells, has been used to treat blood cancers such as leukemia, lymphoma, and myeloma.

Researchers have also developed a potentially "universal" CAR T-cell therapy that could treat almost any blood cancer, including acute myeloid leukemia (AML). This approach uses a newer form of CRISPR gene-editing technology, called base editing, to engineer healthy hematopoietic stem cells and give patients healthy blood and immune systems.

Artificial intelligence (AI) has entered the field of leukemia. Artificial intelligence has been used to support the diagnosis and treatment of leukemia, especially acute myeloid leukemia (AML). For example, AI can analyze high-resolution microscopic images of bone marrow smears to predict the genetic characteristics of AML, enabling more accurate treatment decisions. In addition, artificial intelligence has been used to improve flow cytometry analysis, which is a technique used to analyze the physical and chemical properties of single cells. AI can help identify patients with AML and B-lymphoblastic leukemia (B-ALL) with high accuracy, and can also classify physiological cells.

Artificial intelligence has also been used to analyze the genetic data of patients with AML to determine whether they respond to various drug treatments. This can help identify the most effective treatment options for individual patients. In addition, AI has the potential to improve analysis efficiency and prevent interpretation bias, making it a valuable tool in the fight against leukemia.

In this research, we intend to diagnose leukemia by examining the behaviors and changes in gene expression in dendritic cells (DC) in order to prevent its progression to other cells and tissues of the body. Dendritic cells are considered as an immune checkpoint and checkpoint in the body. which react against any dangerous factor for cells. For this reason, we can react to the diagnosis of leukemia by studying the changes of DC cells in the body.

In this research, it has been tried to use deep learning step by step. In this way, we convert the scanned images into Panda data in Python and analyze them as an image matrix. In this analysis, at the end, we will also have a visualization of gene expression behaviors, giving us a result of 0 or 1. It means malignancy and the further we move away from the infected cell, it decreases to zero. and returns a benign result.

Blood cell:

Blood cells are created from hematopoietic stem cells and are formed in the bone marrow through a highly regulated hematopoietic process. Hematopoietic stem cells are able to transform into red blood cells, white blood cells and platelets.

Blood is a specialized body fluid. It has four main components: plasma, red blood cells, white blood cells and platelets. Blood has various functions, including the following:

1. Transfer of oxygen and nutrients to the lungs and tissues

2. Formation of blood clots to prevent excess blood loss

3. Carrier of cells and antibodies that fight infection

4. Bringing waste materials to the kidneys and liver, which purify and clean the blood

5. Adjust body temperature

An average adult human has more than 5 quarts (6 L) of blood in their body. Blood carries oxygen and nutrients to living cells and removes waste products. It also provides immune cells to fight infections and contains platelets that can form a plug in a damaged blood vessel to prevent blood loss.

Through the circulatory system, the blood adapts to the needs of the body. When you exercise, your heart pumps harder and faster to deliver more blood, and therefore oxygen, to your muscles. During infection, the blood brings more immune cells to the site of infection, where they gather to fight off harmful invaders.

All these functions make blood a precious liquid. Each year in the United States, 30 million units of blood components are given to patients who need them. Blood is considered so precious that it is called "red gold" because the cells and proteins in it can be sold for more than the same weight of gold.

If a blood test tube is left for half an hour, the blood will separate into three layers as the denser components sink to the bottom of the tube and the liquid remains at the top.

The straw-colored liquid that forms the upper layer is called plasma, and it makes up about 60% of blood. The middle white layer is composed of white blood cells (WBC) and platelets, and the lower red layer is composed of red blood cells (RBCs). These two lower cell layers make up about 40% of blood.

Plasma is mainly water, but contains many important substances such as proteins (albumin, coagulation factors, antibodies, enzymes and hormones), sugars (glucose) and lipid particles.

All the cells in the blood come from the bone marrow. They begin life as stem cells and mature into three main cell types – red blood cells, WBCs and platelets. In turn, there are three types of WBC - lymphocytes, monocytes and granulocytes - and three main types of granulocytes (neutrophils, eosinophils and basophils).

Types of blood cells:

White blood cells

White blood cells help your body fight infection. They are part of your immune system.

The main types of white blood cells are:

Neutrophils, eosinophils, and basophils (all called granulocytes)

Lymphocytes (there are B lymphocytes and T lymphocytes)

Monocytes

Red blood cells

Your red blood cells carry oxygen from your lungs to all the cells in your body. Inside your red blood cells is a protein called hemoglobin that helps carry oxygen.

Platelets

Platelets help your blood clot. They stick together to stop bleeding in the event of a cut or bruise.

How do blood cells grow normally?

All of your blood cells start as special cells called blood stem cells that are made in the bone marrow (the soft material inside your bones).

Blood stem cells can divide and multiply in the bone marrow and produce many other blood cells. The diagram below shows how blood stem cells can become any of the required blood cells, including white blood cells, red blood cells, and platelets.

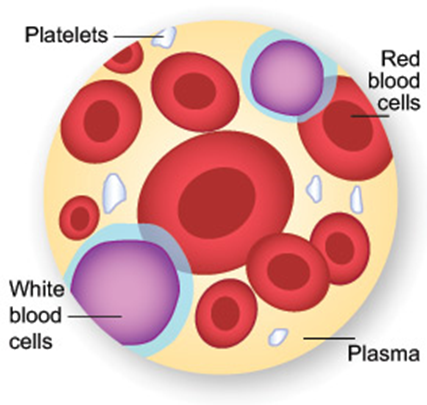
Your bone marrow makes a large number of blood cells every second. If everything is working normally, your body will produce the right number of each type of cell to keep you healthy.

If the following process goes wrong, blood cancer can occur and blood cells may not grow properly or multiply too quickly.

The circulatory system is the way your body's cells get the oxygen and nutrients they need, but the blood is the real carrier of oxygen and nutrients. Blood is made mostly of plasma, which is a yellowish liquid that is 90% water. In addition to water, plasma contains salt, sugar (glucose) and other substances. And most importantly, plasma contains proteins that carry important nutrients to the body's cells and strengthen the body's immune system to fight infection.

An average man has between 10 and 12 pints of blood in his body. An average woman has between 8 and 9 pints. To give you an idea of ​​how much blood that is, 8 pints equals 1 gallon (think a gallon of milk).

Blood is actually a tissue. It is thick because it is made up of different cells, each of which has a different job. In fact, blood is about 80% water and 20% solid.

Figure 1: The tissue of a blood cell 

Blood is made up mostly of plasma, but there are 3 main types of blood cells circulating along with the plasma:]

Platelets help blood clot.

Blood clots stop the flow of blood from the body when a vein or artery breaks. Platelets are also called thrombocytes.

Red blood cells carry oxygen.

Of the 3 types, red blood cells are the most abundant. In fact, a healthy adult has about 35 trillion of them. The body creates these cells at a rate of about 2.4 million per second, and each one has a lifespan of about 120 days. Red blood cells are also called red blood cells.

White blood cells prevent infection.

These cells, which come in different shapes and sizes, are vital to the immune system. When the body is fighting an infection, it increases their number. However, compared to the number of red blood cells in the body, the number of white blood cells is low. Most healthy adults have about 700 times as many red blood cells as white blood cells. White blood cells are also called leukocytes.

Blood groups

There are 4 different blood types: A, B, AB and O. The genes you inherit from your parents (1 from your mother and 1 from your father) determine your blood type.

Blood is always made by cells inside your bones, so your body can usually replace blood lost through small cuts or wounds. But when a lot of blood is lost through large wounds, it must be replaced through blood transfusions (donated blood from other people). In blood transfusion, the blood group of donor and recipient must be compatible. People with type O blood are called universal donors because they can donate blood to anyone, but they can only receive blood from other people with type O blood.

Purpose:

Machine learning algorithms can analyze complex and high-dimensional datasets, automatically select relevant features or biomarkers from large-scale datasets, improve the accuracy and efficiency of cancer classification models. By identifying hidden patterns and relationships in the data, machine learning algorithms can uncover subtle associations between genetic or molecular markers and different types of cancer, leading to improved classification accuracy.

Machine learning is increasingly used in the field of cancer diagnosis and shows promising results in improving the accuracy and speed of diagnosis. By analyzing tissue samples using machine learning algorithms, researchers have achieved accuracy rates as high as 97 percent in detecting certain types of lung cancer.

Deep learning techniques, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), have gained popularity in cancer prediction. These models have the ability to independently extract relevant features from complex medical data, including images and genomic sequences.

Transfer learning involves applying pre-trained models on large datasets from related domains and adapting them to cancer prediction tasks. By using knowledge from other domains, transfer learning can improve prediction accuracy, especially when the amount of cancer-specific data is limited.

Unsupervised clustering algorithms help identify distinct subtypes by analyzing gene expression patterns or other molecular data.

The purpose of studying deep learning in leukemia diagnosis is to develop accurate and efficient methods for diagnosing and classifying types of leukemia. Deep learning techniques, such as neural networks and convolutional neural networks, can be trained on large datasets of medical images and patient data to learn patterns and features that represent different types of leukemia. This could help doctors and researchers diagnose leukemia more accurately and quickly and develop more effective treatments.

In the context of flow cytometry, deep learning can be used to analyze the physical and chemical properties of individual cells in a heterogeneous population, and identify patterns and features that represent different types of leukemia. This can help improve the accuracy and efficiency of leukemia diagnosis and reduce the need for manual analysis and interpretation of flow cytometry data.

For example, a study published in the journal Scientific Reports used deep learning to analyze flow cytometry data from patients with acute myeloid leukemia (AML) and B-lymphoblastic leukemia (B-ALL). This study showed that the deep learning algorithm is able to accurately classify AML and B-ALL cells with a sensitivity of 94.6 and 98.2%, respectively.

In general, the goal of studying deep learning in leukemia diagnosis is to develop more accurate and efficient methods for diagnosing and classifying different types of leukemia and improving patient outcomes.

The goal of the deep learning study in leukemia diagnosis is to improve the accuracy and efficiency of diagnosing leukemia, a type of cancer that affects the blood and bone marrow. Deep learning, a subset of machine learning, can be used to analyze medical images, e.g., flow cytometry images are used to identify patterns and features that indicate leukemia. This could help doctors diagnose leukemia faster and more accurately, which could lead to better treatment outcomes for patients. In addition, deep learning can help automate the analysis of medical images, which can reduce the workload of doctors and other medical professionals, and can also help identify new biomarkers for the diagnosis of leukemia.

This could help doctors diagnose leukemia faster and more accurately, which could lead to better treatment outcomes for patients. In addition, deep learning can help automate the process of analyzing medical images, which can reduce the workload of doctors and other medical professionals.

CNNs can be used to analyze images of bone marrow cells to identify abnormal cell morphology, which can be a sign of leukemia. RNNs can be used to analyze time series data, such as the results of multiple flow cytometry tests, to identify patterns and trends that are indicative of leukemia.

The aim of this study is to develop a model with the help of deep learning to detect leukemia by dendritic cells. This model uses machine learning algorithms to analyze the interactions between DC cells and leukemia cells, enabling accurate and efficient diagnosis of leukemia.

Why should we study the gene expression of dendritic cells in the diagnosis of leukemia?

The study of gene expression of dendritic cells is important in the diagnosis of leukemia for several reasons:

1. Dendritic cells play an important role in the immune system:

Dendritic cells are a type of immune cells that help identify and respond to pathogens, including cancer cells. They can recognize and process tumor antigens and then present them to T cells, which can help stimulate an immune response against cancer.

2. Dendritic cells are affected in leukemia: In leukemia, the normal function of dendritic cells can be disrupted, leading to impaired immune responses against cancer. By studying the gene expression of dendritic cells in leukemia, researchers can gain insight into how cancer affects the immune system.

3. Gene expression changes can be used as biomarkers:

Changes in gene expression of dendritic cells can be used as biomarkers for the diagnosis of leukemia. By identifying specific gene expression patterns associated with leukemia, researchers can develop new diagnostic tests that can help diagnose the disease earlier and more accurately.

4. Understanding the biology of dendritic cells can lead to new treatments:

By studying the gene expression of dendritic cells in leukemia, researchers can gain insight into the underlying biology of the disease. This could lead to the development of new therapies that target dendritic cells, such as immunotherapies that aim to restore normal dendritic cell function.

Some of the key genes involved in the function of dendritic cells in leukemia are:

CD1a is a gene that plays a role in presenting antigens to T cells

CD80: a gene that plays a role in the activation of T cells

CD86: a gene that plays a role in the activation of T cells

IL-12: A gene involved in the production of cytokines that stimulate the immune response.

In this method, we first load the data:

# Load the gene expression data

2library(GEOquery)

3gse <- getGEO("GSE12345", destdir = "./")

Then we will extract gene expression data from cellular data:

dendritic\_cells <- gse[[1]][, grep("dendritic cell", colnames(gse[[1]]))]

We will perform the desired analysis for the extracted gene expression data:

library(DESeq2)

10dds <- DESeqDataSetFromMatrix(countData = dendritic\_cells,

11 colData = data.frame(condition = c("leukemia", "healthy")),

12 design = ~ condition)

13dds <- DESeq(dds)

We will identify and extract the different genes in the desired data:

res <- results(dds, contrast = c("condition", "leukemia", "healthy"))

We draw the results:

library(ggplot2)

20ggplot(res, aes(x = log2FoldChange, y = -log10(padj))) +

21 geom\_point() +

22 theme\_classic()

In this code, we used the DESeq2 package to perform differential gene expression analysis on gene expression data from dendritic cells in leukemia patients compared to healthy individuals. Then we plotted the results using ggplot2.

Expected results:

Improved Accuracy:

It is expected that the model with the help of deep learning will achieve higher accuracy in leukemia diagnosis compared to manual analysis.

Increase efficiency:

This model enables rapid analysis of large data sets and reduces the time and effort required to diagnose leukemia.

Standardization:

This model provides a standardized approach for leukemia detection by DCs, reducing variability and improving reproducibility.

Dendritic cells (DCs) play an important role in innate and adaptive immune responses.

DCs acquire and process tumor-associated antigens (TAAs) and present them on MHC molecules to activate T cells, which then target and attack cancer cells. do

To use bioinformatic tools and techniques to identify TAAs, we need to analyze DC infiltration in tumor samples, and evaluate the efficacy of DC-based immunotherapies.

To obtain raw data, we will compare a set of public repositories with experimental measurements. After comparing, we clean them and after cleaning, we have to normalize them according to our data processing.

In order to obtain raw data, we must first analyze public data. There are various methods for data analysis, including pattern recognition, statistical methods, machine learning, and statistical analysis. In this article, we will use artificial intelligence based on machine learning, in such a way that we analyze the gene expression related to the person by machine learning. And we will draw the graph related to the desired gene.

This analysis will help us in the process of tumor recognition (TAAs) by DC cells for diagnosis and appropriate response in cancer.

By interpreting the data analysis that is done with the help of artificial intelligence, it can provide us with the accurate and correct path of biological processes and signaling, which these signals will show the results involved with the cancer tumor. Artificial intelligence With the help of a learning model drawn by machine learning libraries, it provides a suitable signaling pathway from the site of safe engagement with leukemia.

With the help of algorithms and functions in machine learning, a signaling path is created. This path, which is produced from multiple evaluations and troubleshooting, follows a general interpretation of the results. For such troubleshooting, it will work as follows:

D1 => (w + b) / ½

As it is known, each input data has a weight and bias, which our function calculates the set of half of them. For the first time, this may have error detection variables. The function checks these variables and returns determines a specific value.

We do the comparison between the data. We consider a desired data and compare all other data with the specified desired data. This will help us to eliminate repetition and data noise. This work we will do it with the help of artificial intelligence functions. In this way, we will make a function to compare the data, and it will return a value of 0 or one for us. If it returns a value of 1 for us, it will show us that Our data is free of repetition and noise.

In this function, in fact, we distinguish the closest data that is similar to leukemia. That is, the data we want to compare with the same cancer data is already defined. This data contains all the differences between the cancer data in one frame. be

This distinction can include the type of data, form, behavior and the type of data placement together. The size and form of data can be an index criterion among the characteristics related to this data.

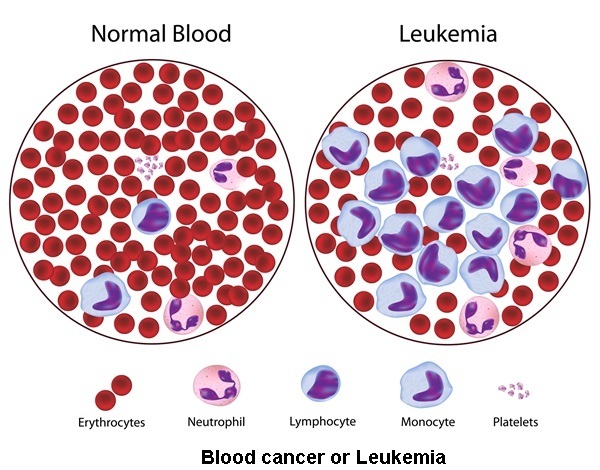


Figure 2: A cell infected with leukemia (right) and a healthy cell (left)

In this infected cell on the right side of the picture, as we can see, as the cell becomes more infected, the amount of immune cells (lymphocytes) increases. To protect the body against tumor or blood cancer by secreting B and T lymphocytes. This is a criterion. It can be used to detect blood cancer.

Also, in the infected cell, the amount of monocyte also increases, as is clear from the figure. This dendritic cell, which is also called, is made in the bone marrow. will be reproduced there.

With the amount of contamination of each cell in the body, the blood platelets corresponding to that cell also decrease. With each platelet decrease, we will see blood cancer in the body.

These three criteria (lymphocytes, platelets, and monocytes) will tell us an important indicator to detect cell contamination. It has already penetrated into the body and after entering the cell through our blood, we notice it.

1. monocyte

data\_cancer: 2) lymphocyte

3) platelets

This means that any blood cancer can involve three basic parts of the body's defense. Our main discussion is on monocyte, which is the dendritic cell. Our pattern should be related to the increase of this cell. A preliminary result of the number of this Consider cells.

We must have all the states and times of the value of this cell. Any change in the trend of these values ​​can give us a serious warning.

1) after

Monocyte:

2) before

We will compare before and after. In this way:

m\_cell\_before<=>after

Any change in this process can be a warning about the development of cancer in a cell.

By training artificial intelligence algorithms, we can provide a suitable model for data analysis. These data, which are created from medical images such as MRI, mammography and ultrasound images, can help doctors in this field.

In addition to cellular stimulation, any cancer patient can also be involved genetically. This created pattern can also provide the ability to analyze data related to a person's genetics.

**Artificial intelligence help to diagnose cancer:**

Different techniques are used to diagnose leukemia. Some of the techniques are:

High resolution microscopic images of bone marrow smear:

This method involves analyzing high-resolution images of bone marrow smears to predict the genetic characteristics of the disease.

Convolutional Neural Networks (CNN):

CNN is a type of artificial intelligence technique widely used for image recognition. It can be used to classify images of blood cells and diagnose leukemia.

Computational intelligence techniques:

These techniques can be used to help doctors quickly identify and classify acute lymphoblastic leukemia (ALL).

Blood cell image classification methods:

These methods include classifying images of blood cells to diagnose leukemia.

Genetic testing:

Genetic testing is used to identify genetic abnormalities in patients with leukemia. However, this method is expensive and time consuming.

Artificial intelligence techniques such as CNN and computational intelligence techniques are increasingly used to diagnose leukemia. These techniques can help analyze large data sets and provide personalized treatment recommendations.

Imaging with the help of artificial intelligence can play many advantages for the diagnosis and treatment of cancer in the human body.

Any pattern created by an artificial intelligence algorithm can reduce all the false noisy data, both positive and negative. We will not need all the data in the study, but we need the data that the relevant cell is infected

First: We select the infected data. Later: We compare all other data with that infected cell. And we do the work according to the determined criteria.

with the changes made on platelets, monocytes and lymphocytes, which are all related to the bone marrow. It promises the possibility of the cell being involved with cancer. The artificial intelligence algorithm can enter and measure the changes of these three in this field. The criterion helps in the diagnosis of leukemia. Of course, for the early diagnosis of the affected person, one should consider the initial symptoms and evaluate these criteria as little as possible with each symptom. The results are evaluated with the results before the calculation and with The decrease and increase of any measure will issue an early warning.

in such a way that:

before\_tottal\_monocyte <=> after\_tottal\_monocyte

It compares the initial value of the monocyte with the changes made on the dendritic cell. Any change in this comparison can be a warning for the cell to be infected.

before\_tottal\_lymphocyte <=> after\_tottal\_lymphocyte

It compares the initial value of the lymphocyte with the changes made on the dendritic cell. Any kind of change in this comparison can be a warning for the cell to be infected.

before\_tottal\_platelets <=> after\_tottal\_platelets

It compares the initial value of the platelet with the changes made on the dendritic cell. Any kind of change in this comparison can be a warning for cell contamination.

By sending the genetic profile of each person and his medical history to the model created by artificial intelligence, we can treat it according to the degree of cancer after diagnosis. It treats it. In other words, it performs a type of error detection and evaluation on it.

This action can act by stimulating the dendritic cells and creating properties related to B cells and the secretion of vitamin T in the body of an intercellular barrier to shoot the cancer cell and destroy it.

The AI ​​model was able to map suspected cancer areas without human supervision, which could help less experienced radiologists diagnose cancer more accurately.

By analyzing genetic data and MRI imaging, artificial intelligence can even find out what factors lead to cancer in a person's body. It can also detect the type of cancer by interpreting the image data.

Artificial intelligence (AI) has been increasingly integrated into the diagnosis of leukemia and enables advanced methods to provide timely and efficient treatment. Artificial intelligence is one of the solutions it has provided so far in this field. to the analysis of miRNA samples. This technique can diagnose leukemia.

The analysis of miRNA data usually includes tasks such as miRNA target prediction, miRNA expression profiling, and miRNA-based disease diagnosis. Artificial intelligence techniques such as machine learning and deep learning can be applied to these tasks to improve their accuracy and efficiency.

miRNAs are short RNA molecules with a length of 19 to 23. which are used as the main regulators of a wide range of biological processes through controlling the expression of various genes.

For example, machine learning algorithms such as support vector machines (SVM) and random forests can be used to predict miRNA targets by learning patterns in the data. Deep learning techniques such as Convolutional Neural Networks (CNN) and Recurrent Neural Networks (RNNs) can be used to analyze miRNA expression profiles and identify patterns associated with specific diseases.

It should also be pointed out that this is only one example of an artificial intelligence solution to detect blood cancer, while there are different ways to detect it in this field, which is briefly discussed below.

1. Machine learning:

It is a machine vision. In this method, each machine vision is equipped with artificial intelligence patterns and through the observation of cancer cells and bone marrow, it deals with the reactions and behaviors of the cells, and it can treat and diagnose cancer by creating a pattern.

2. Natural language processing:

In this method, artificial intelligence with the help of model (NLP) actually pays attention to the conversations between the patient and the doctor. And according to these conversations between the doctor and the patient, it analyzes them. This analysis is based on the behavior and reaction of the cells (platelets), lymphocytes and monocytes). In the end, he will provide a result of the decrease or increase of the three desired characteristics for the specialist doctor and according to this result, the treating doctor will make the final decision.

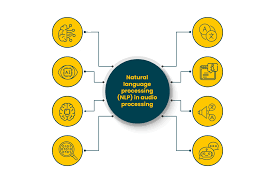


Figure3: An example of a pattern

NLP

**Working method:**

Dendritic cells play an important role in the immune system, and their analysis can provide valuable insights into the presence and progression of leukemia.

Here we aim to detect leukemia by dendritic cells using deep learning patterns.

Deep learning can process large data or a set of data at the same time. Each model can work on a variety of data. To diagnose cancer with the help of dendritic cells, because the gene expression in dendritic cells must also be used. and to analyze the cellular behaviors in the infected patient, so we must consider a suitable model to be able to analyze the desired data.

In a deep learning model, after taking the input images from image scans, we convert them from real dimensions to 227x227 dimensions for better management and processing. This makes the data that we analyzed at a high speed also increase the speed of our diagnosis. However fast our model can be in diagnosis, it can analyze massive data. And also, it can recognize the appropriate characteristics and behaviors of each cell.

Each dendritic cell has a series of individual genomic expressions, which has many effects in determining the reactive behavior of cells. Deep learning is a neural network that can firstly examine the genes in a cell. Neural network models analyze the amount of substance T secretion based on the color images of the genomes of these monocytes that they evaluate. The more this substance secretion is, it can be a serious warning in a person's body. As we said, it is an immune and inspection cell in the body that secretes T substance with other changes expected.

As a result, we need a strong processor with high speed that can analyze the data of CT scanned images and provide us with the desired result in less time.

Well, now the genes in an adult dendritic cell should be able to be calculated and extracted by our created model.

With the help of RNA-seq microarray method, we will analyze the gene expression of dendritic cells. This data set is in gene expression profit and its task is to identify the most relevant genes involved in the immune response.

We will do this pattern step by step on the extracted image data.

First step:

Data preprocessing:

We load a set of data.

# Load the gene cell photo image

cell\_image = Image.open('2.png')

This data is a scanned city photo.

We will perform quality control on our data.

# Convert the image to a numpy array

cell\_image\_data = np.array(cell\_image)

# Get the dimensions of the image

height, width, channels = cell\_image\_data.shape

That is, we will convert our data into csv data type. Then we will make a matrix.

We will standardize our quality control data using RMA (Robust Multiple Array Averaging) techniques.

Then we will remove or filter the genes that have low vision ability in the immune system.

# Reshape the image array to a 2D array with pixel values

gene\_expression\_data = cell\_image\_data.reshape(height \* width, channels)

# Create a pandas DataFrame with the pixel values

gene\_expression\_df = pd.DataFrame(gene\_expression\_data)

# Add a column for the gene expression values

# NOTE: Replace with actual gene expression values

rng = np.random.default\_rng()

gene\_expression\_df['Gene\_Expression'] = rng.normal(loc=0, scale=1, size=len(gene\_expression\_df))

# Add a column for the cell type

# NOTE: Replace with actual cell type values

gene\_expression\_df['Cell\_Type'] = rng.binomial(n=1, p=0.5, size=len(gene\_expression\_df))

# Print the first few rows of the DataFrame

print(gene\_expression\_df.head())

Second step:

We selected our own desired features to reduce the dimensionality of the data, to use to identify the most informative genes.

In this regard, we have used the techniques of mutual information, that is, placing a data scale with each other.

rng = np.random.default\_rng()

gene\_expression\_df['Gene\_Expression'] = rng.normal(loc=0, scale=1, size=len(gene\_expression\_df))

# Add a column for the cell type

# NOTE: Replace with actual cell type values

gene\_expression\_df['Cell\_Type'] = rng.binomial(n=1, p=0.5, size=len(gene\_expression\_df))

# Print the first few rows of the DataFrame

print(gene\_expression\_df.head())

Third step:

We will use clustering in ML functions for data visualization. We did this pattern with the help of k-means function. After the clustering is done, we will start visualization with the help of PCA (Principal Component Analysis) technique.

This visualization will help to separate the infected cells from the healthy ones and will save time.

# Visualize the distribution of gene expression values

plt.violinplot(gene\_expression\_df['Gene\_Expression'])

plt.title('Gene Expression Distribution')

plt.xlabel('Gene Expression')

plt.ylabel('Frequency')

plt.show()

# Visualize the relationship between gene expression and cell type

plt.scatter(gene\_expression\_df['Gene\_Expression'], gene\_expression\_df['Cell\_Type'])

plt.title('Gene Expression vs Cell Type')

plt.xlabel('Gene Expression')

plt.ylabel('Cell Type')

plt.show()

Cancer diagnosis code with the help of gene expression using deep learning:

import pandas as pd

import numpy as np

from PIL import Image

import matplotlib.pyplot as plt

# Load the gene cell photo image

cell\_image = Image.open('2.png')

# Convert the image to a numpy array

cell\_image\_data = np.array(cell\_image)

# Get the dimensions of the image

height, width, channels = cell\_image\_data.shape

# Reshape the image array to a 2D array with pixel values

gene\_expression\_data = cell\_image\_data.reshape(height \* width, channels)

# Create a pandas DataFrame with the pixel values

gene\_expression\_df = pd.DataFrame(gene\_expression\_data)

# Add a column for the gene expression values

# NOTE: Replace with actual gene expression values

rng = np.random.default\_rng()

gene\_expression\_df['Gene\_Expression'] = rng.normal(loc=0, scale=1, size=len(gene\_expression\_df))

# Add a column for the cell type

# NOTE: Replace with actual cell type values

gene\_expression\_df['Cell\_Type'] = rng.binomial(n=1, p=0.5, size=len(gene\_expression\_df))

# Print the first few rows of the DataFrame

print(gene\_expression\_df.head())

# Visualize the distribution of gene expression values

plt.violinplot(gene\_expression\_df['Gene\_Expression'])

plt.title('Gene Expression Distribution')

plt.xlabel('Gene Expression')

plt.ylabel('Frequency')

plt.show()

# Visualize the relationship between gene expression and cell type

plt.scatter(gene\_expression\_df['Gene\_Expression'], gene\_expression\_df['Cell\_Type'])

plt.title('Gene Expression vs Cell Type')

plt.xlabel('Gene Expression')

plt.ylabel('Cell Type')

plt.show()