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DETECTION OF BLOOD CANCER ACUTE MYELOID LEUKEMIA USING AI

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Abstract: Acute Myeloid Leukemia(AML) is a common forms of blood cancer . It can be fatal disease unless and until it is treated correctly with early diagnosis . It is the most critical disease in children and adults .Leukocytes ,produced in the bone marrow , make up around one percent of all blood cells . Due to uncontrolled growth of these white blood cells , leads to the birth of blood cancer . The approach is based on the analysis of the gene activity of cells found in the blood . To detect cancer , requires large amounts of data , we evaluated data on the gene activity of blood cells . Numerous studies have been carried out on this topic and the results are available through databases. Thus there is an enormous data pool . We have collected everything which is currently available .A fast inversion technique i.e. Quasi newton method is used for the interpretation of data is used . We use this method when we have to compute at every iteration . We use this newton method to compute the number of white blood cells present in the bone marrow .

Keywords: Acute Myeloid Leukemia, blood cancer, diagnosis, technique, cells

INTRODUCTION

White blood cells help your body to fight infection . The blood cells are produced in the bone marrow . But in leukemia , however the bone marrow produces abnormal white blood cells . These cells crowd out the healthy blood cells , making it hard for blood to do its work . Acute Myeloid Leukemia is a cancer of myeloid line of blood cells which are characterised by the rapid growth of abnormal white blood cells that build up in the bone marrow . AML progresses rapidly and is typically fatal within weeks or months if left untreated . In acute myeloid leukemia (AML) , there are two many of a specific type of white blood cell called a myeloblast . At the time of diagnosis , patients can have very , very high white blood cell counts . Typically a healthy person has a white blood cell count of about 4,000-11,000. Patients with acute or even chronic leukemia may come in with a white blood cell count up into the 100,000 to 400,000 range.

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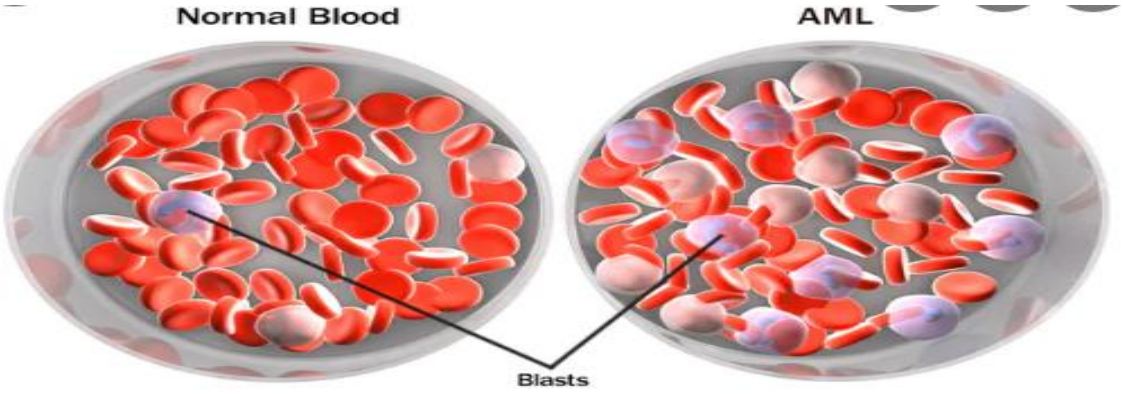

In AML , the blast cells can grow upto more than 20% in the bone marrow . Normally leukocytes make up around only 1-2 % pf blood cells . It is the main criteria which is used for the detection of this type of cancer . The white blood cells are build up by two types of cells – Lymphoid progenitor cells and Myeloid progenitor cells . If the expansion is increased in the Lymphoid progenitor cell , then it give rise to Acute Lymphotic leukemia (ALL). It occurs due to the abnormal expansion of WBC's in the lymphoid progenitor cells . And if there is uncontrolled growth or new plastic change in case of Myeloid progenitor cells , then it give rise to Acute Myeloid leukemia (AML).

AML is normally a middle –age leukemia means it happens mainly in the age of 15-39 years . It can be found at an early age as well as in later age too but the common group is between 15-39 years . In adults , about 90 % of cases of leukemia are diagnosed with the most common being the acute myelogenous leukemia (AML) , and the chronic lymphocytic leukemia (CLL). Leukemia can also spread to other parts of the body like lungs , heart etc.

SIGNS AND SYMPTOMS

Most signs and symptoms of AML are caused by the replacement of normal blood cells with leukemic cells. A lack of normal white blood cell production makes people more susceptible to infections; while the leukemic cells themselves are derived from white blood cell precursors, they don't have any infection-fighting capacity. The early signs of AML are similar to those of influenza or other common illnesses. Symptoms may include feeling tired , fever, shortness of breadth, easy bruising and bleeding, bleeding under the skin, bone and joint pain, fatique and weakness that doesn't go away, weight loss or loss of appetite and increased risk of infection.

Some people with AML may experience swelling of the gums because of infiltration of leukemic cells into the gum tissue. The very first sign of leukemia is the development of tumor outside the bone marrow, which is common known as chloroma .

CAUSES

Luekemia happens when some blood cells require mutations in their DNA . These causes blood cells to grow and divide quickly and to continue living when normal cells will die . These abnormal cells continue to accumualte and stop the healthy blood cells from growing and functioning normally . Eventually crowding up the normal cells in the blood. Possible risk factors include smoking , previous chemotherapy treatment and exposure to radiation, exposure to certain chemicals such as benzene, Genetic disorders such as Down syndrome . Test that examine the blood and bone marrow diagnose AML .

TECHNOLOGY

Artificial intelligence is a very important aspect in the feild of medicine , especially in the field of diagnostics. Artificial intelligence can detect one of the most common forms of blood cancer -- acute myeloid leukemia (AML) -- with high reliability.

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The main focus is on the "transcriptome," which is a kind of fingerprint of gene activity. The transcriptome holds important information about the condition of cells. therefore wanted to find out what an analysis of the transcriptome can achieve using artificial intelligence .

The current study focused on AML. Without adequate treatment, this form of leukemia leads to death within weeks. AML is associated with the proliferation of pathologically altered bone marrow cells, which can ultimately enter the bloodstream. Ultimately both healthy cells and tumor cells drift in the blood. The input included information about whether a sample came from an AML patient or not. The algorithms then searched the transcriptome for disease-specific patterns. This is a largely automated process. It's called machine learning .

We are using Quasi Newton method which is a type of Convolutional Neural network (CNN). A convolutional neural network is a type of artificial neural network used in image recognition and processing that is specifically designed to process pixel data .

Quasi Newton Method uses an iterative and computational approach which we can use for getting the count of blood cells more accurately and precisely . Segmentation and counting of blood cells are considered as an important step that helps to extract features to diagnose some specific diseases like malaria or leukemia. The manual counting of white blood cells (WBCs) and red blood cells (RBCs) in microscopic images is an extremely tedious, time consuming and inaccurate process . The proposed method uses an iterative structured circle detection algorithm for the segmentation and counting of WBCs.

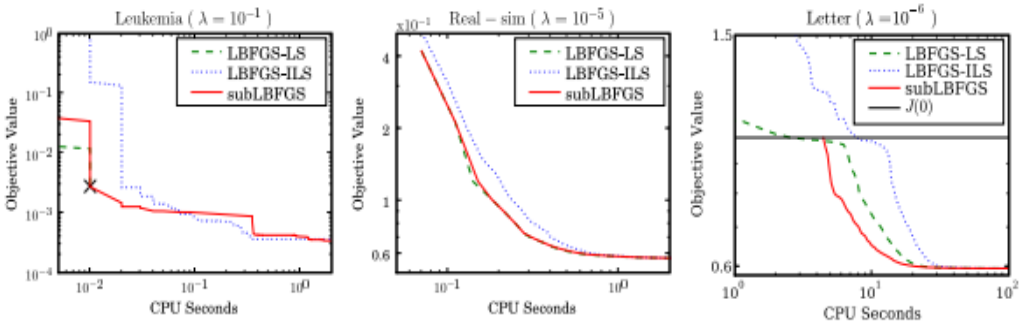
METHODOLOGY

Quasi Newton method is an optimization method that we use in Non-Linear Programming when other methods or approaches are too time consuming or difficult to use . These methods are used to find the global minimum of function f(x) that is twice differentiable .

Recently, Andrew and Gao (2007) introduced a variant of LBFGS, the Orthant-Wise Limitedmemory Quasi-Newton (OWL-QN) algorithm, suitable for optimizing L1-regularized log-linear models:

$$J(w) := \lambda kwk1 + 1\ n\ n \sum i=1 \ln(1+e - ziw\top xi) \mid \{z\}$$

The problems faced by smooth quasi-Newton methods on non-smooth objectives are not only encountered in cleverly constructed toy examples, but also in real-world applications. To show this, we apply LBFGS to L2-regularized risk minimization problems with binary hinge loss , a typical non-smooth optimization problem encountered in machine learning. The figure shows the behaviour of LBFGS with this exact line search (LBFGS – LS) on two data sets, namely Leukemia and Real-sim.



It can be seen that LBFGS-LS converges on Real-sim but diverges on the Leukemia data set. This is because using an exact line search on a nonsmooth objective function increases the chance of landing on nonsmooth points, a situation that standard BFGS (resp., LBFGS) is not designed to deal with. To prevent (L)BFGS' sudden breakdown, a scheme that actively avoids nonsmooth points must be used. One such possibility is to use an inexact line search that obeys the Wolfe conditions .

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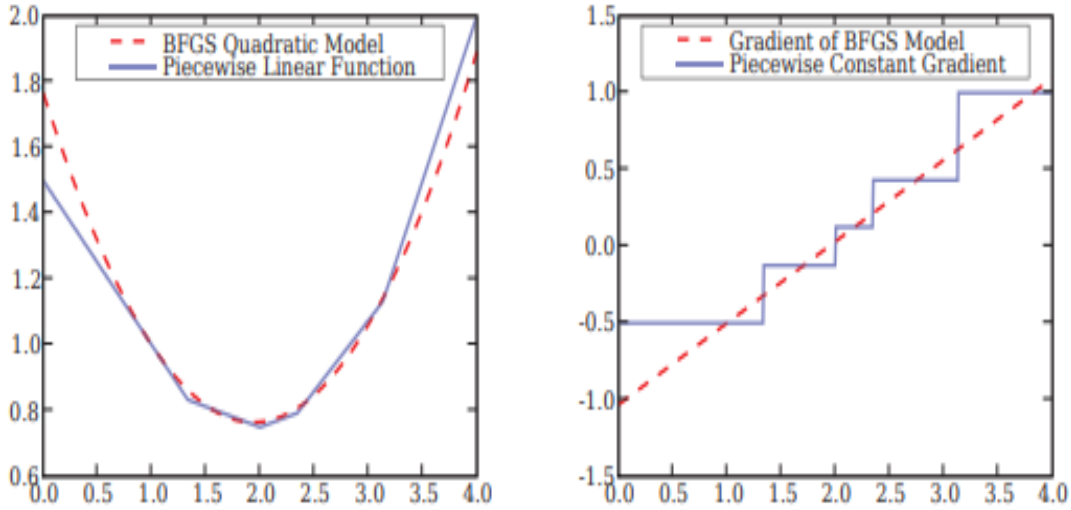
Here we used an efficient inexact line search that uses a caching scheme specifically designed for L2-regularized hinge loss. This implementation of LBFGS (LBFGS-ILS) converges on both data sets shown here but may fail on others. It is also slower, due to the inexactness of its line search. In machine learning, the hinge loss is a loss function used for training classifiers. The hinge loss is used for "maximum-margin" classification, most notably for support vector machines (SVMs).

In machine learning one often encounters L2-regularized risk minimization problems (30) with various hinge losses (31, 42, 55). Since the Hessian of those objective functions at differentiable points equals λI (where λ is the regularization constant), one might be tempted to argue that for such problems, BFGS' approximation Bt to the inverse Hessian should be simply set to λ −1I. This would reduce the quasi-Newton direction pt = −Btgt , gt ∈ ∂J(wt) to simply a scaled subgradient direction. To check if doing so is beneficial, we compared the performance of our subLBFGS method with two implementations of subgradient descent: a vanilla gradient descent method (denoted GD) that uses a random subgradient for its parameter update, and an improved subgradient descent method (denoted subGD) whose parameter is updated in the direction produced by our direction-finding routine (Algorithm 2) with Bt = I.



THE NEED TO ESTIMATE HESSIAN FUNCTION

To ensure positivity of BFGS' estimate Bt of the inverse Hessian, we must have (∀t) s ⊤ t yt > 0. Extending this condition to nonsmooth functions, we require

(wt+1 − wt) ⊤(gt+1 −gt) > 0, where gt+1 ∈ ∂J(wt+1) and gt ∈ ∂J(wt)

If J is strongly convex,5 and wt+1 6= wt , then (25) holds for any choice of gt+1 and gt . 6 For general convex functions, gt+1 need to be chosen (Line 12 of Algorithm 1) to satisfy (25). The existence of such a subgradient is guaranteed by the convexity of the objective function. To see this, we first use the fact that ηtpt = wt+1 − wt and ηt > 0 to rewrite as

p ⊤ t gt+1 > p ⊤ t gt , where gt+1 ∈ ∂J(wt+1) and gt ∈ ∂J(wt).

Using the stopping criterion suggested by Andrew and Gao (2007), we ran experiments until the averaged relative change in objective function value over the previous 5 iterations fell below 10−5.

For our first set of experiments, we applied subLBFGS with exact line search (Algorithm 3) to the task of L2-regularized binary hinge loss minimization. Our control methods are the bundle method solver BMRM (Teo et al., 2010) and the optimized cutting plane

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algorithm OCAS (Franc and Sonnenburg, 2008),13 both of which were shown to perform competitively on this task. SVMStruct (Tsochantaridis et al., 2005) is another well-known bundle method solver that is widely used in the machine learning community. For L2-regularized optimization problems BMRM is identical to SVMStruct, hence we omit comparisons with SVMStruct.

	L_1-reg. logistic loss			L_2-reg. binary loss	
Data Set	λ_{L_1}	k_{L_1}	$k_{L_1 r}$	λ_{L_2}	k_{L_2}
Covertype	10^{-5}	1	2	10^{-6}	0
CCAT	10^{-6}	284	406	10^{-6}	0
Astro-physics	10^{-5}	1702	1902	10^{-4}	0
MNIST-binary	10^{-4}	55	77	10^{-6}	0
Adult9	10^{-4}	2	6	10^{-5}	1
Real-sim	10^{-6}	1017	1274	10^{-5}	1

Regularization parameter λ and overall number k of direction-finding iterations in our experiment respectively.

RESULT

We proposed subBFGS , an extension of the BFGS quasi-Newton method , for handling non-smooth convex optimization problems. We also proved its global convergence in objective function value.

We applied our algorithm to a variety of machine learning problems employing the L2-regularized binary hinge loss and its multiclass and multilabel generalizations, as well as L1-regularized risk minimization with logistic loss. Using this approach we are able to find an accurate and could easily get the estimation of white blood cells .

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