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Rapid detection of urinary tract infection by analyzing the dried spots of biological fluids using convolutional neural networks

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Abstract

To find the cause of infectious diseases such as urinary tract infections, a diagnostic patterning test was used. In this method, the whole blood and serum samples for every person was dried on a glass substrate to create a special pattern due to formation of central and peripheral regions. This event performed during 1 hr at 25°C which is much shorter than the classical and

instrumental methods. This event can be observed by an optical microscope. This study was proposed to classify the UTI patients and healthy people which would be about 600 volunteers. In addition, the images of dried patterns were captured by a camera and the classification analysis was done by convolutional neural network algorithm, executed by graphical user interface. The result of analysis was available after a few minutes, indicating that the accuracies of proposed method were 90.8% (through the analysis of the dried blood spot) and 86.6% (through the evaluation of the dried serum spot) for discriminating the patients from healthy participants. This method could become popular because it has a simple design and does not require skilled personnel toxic standard reagent and expensive equipment. Most importantly, it can identify the contaminated sample as well as the contaminant in a shorter time than other common methods.

Keywords: Urinary tract infection, rapid diagnosis, diagnostic patterning test, convolutional neural network, discrimination analysis

Introduction

Blood or urine culture, relying on the identification of viable microorganisms through culture techniques, is the definitive method for diagnosing urinary tract infections (UTI). However, many pathogens escape detection due to the limitations in the current culture methods. In addition, even in optimal conditions, the results usually take between 12 and 48 hours to arrive ¹. This delay can be critical because early administration of antibiotics is crucial for patient recovery, especially in severe cases ². Instrumental methods such as

gas chromatography, nuclear magnetic resonance, and mass spectrometry were used to identify and determine metabolites in order to diagnose the disease ^{3,4}. The user is reliant on expensive equipment, a time-consuming sample preparation process with chemical substances and solvents, and specific laboratory conditions that hinder the achievement of results ⁵.

To reduce screening time and provide rapid patient treatment, the biosensors have been developed commercially to diagnose UTI and its causative agent ⁶. These sensors either work by interacting with the infectious agent and a specific antibody or by following an enzymatic mechanism ⁷. These methods that can simultaneously analyze multiple microorganisms have high sensitivity and selectivity, but their limitations are caused by the complexity of design and construction, special storage conditions, and price ⁸. In addition, the design of electronic and optical noses has brought a major revolution in the detection of pathogenic bacteria through the analysis of volatile organic compounds emitted from blood and urine samples ⁹. It was possible to measure the infectious agent at low concentrations qualitatively in less than 10 minutes ¹⁰. Achieving an acceptable response requires a large volume of sample, an oven with adjustable temperature, and a significant number of selective chemoresponsive indicators ¹¹.

The diagnostic patterning test is a screening method that examines structural differences in the dried patterns of body fluids (including tears, saliva, sweat, blood, and their secretions) to differentiate between patients

and healthy individuals ¹². The dried spot pattern varies based on the proteins and metabolic profiles present in the biological sample, of course, all samples will have the same drying rate, thickness of the layer formed, and substrate material ¹³. The drying process takes place spontaneously, relying on physical conditions like temperature and pressure, or the addition of chemical or biological reagents. The simplest method is spontaneous drying, which doesn't require external force. To get the best discrimination, it's important to perform this procedure in a constant temperature and humidity ¹⁴⁻¹⁶.

The pattern of the dried spot is composed of two central and peripheral regions. Mineral electrolytes and crystallized proteins are present in the first region, which is followed by an accumulation of dehydrated macromolecules in the next region ¹⁷. The drying process, particularly in the peripheral region, may result in the formation of cracks that are linear, wavy, or curved ¹⁷. The nature of these two regions is examined to determine the difference between the dried patterns. The images of dried spots can be evaluated by transmitted light, reflected light, scanning electron, atomic force, or fluorescence microscopes to find the differences between the patterns by calculating the diameter of the central region, the size of the crystals, the type, number, diameter, angle, or length of the cracks ¹⁸. The comparison can be done with either a portion or the entire drop. To assess the difference between patient and healthy samples, only a part of the drop has been considered by most published studies ^{12,18}. In principle, determining the crystal pattern and

calculating the crack parameters and extracting the differences from a portion of the drop is a process that requires skill and takes a lot of time.

Recently, medical images have been scrutinized using deep learning algorithms, intelligent systems that can automatically and more rapidly recognize subtle differences in images, similar to those of humans¹⁹. These algorithms are capable of running either unsupervised or supervised²⁰. In supervised algorithms, a model is trained using a substantial amount of data points from well-known samples. A validation set is used to evaluate the confidence of the built model. The designed model is ultimately used to identify and categorize an unknown sample. The features extracted from the input data are the basis for pattern recognition and discrimination and the model must be capable of extracting higher-level features to display better performance²⁰. The most widely used deep learning models include multilayer perceptron neural networks, convolutional neural networks, recurrent neural networks, long-term memory neural networks, and generative adversarial networks²¹. The use of convolutional neural networks in medical image analysis has increased in recent years due to their ability to process inputs in two or three dimensions, enabling them to evaluate large amounts of data with high precision, fewer calculations, and less overfitting²².

Knowledge and expertise are necessary for utilizing CNN algorithms. Using a graphical user interface (GUI) is a way to overcome this limitation, which allows the user to capture the outputs in the shortest possible time in

the form of numbers or graphs after selecting the inputs and the expected command. This study utilized a CNN-based GUI to analyze the pattern of dried blood and serum spots (DBS and DSS). In optimal conditions, the biological samples are dried spontaneously, and their images are captured using a smartphone camera and entered into the GUI. Once the effective parameters of the CNN model are determined to be the best, statistical characteristics such as sensitivity, specificity, and total accuracy are calculated. The proposed method is evaluated for its ability to discriminate between patients with UTI and healthy individuals and to discover the type of infection.

Results and Discussions

The early screening of UTIs can facilitate the rapid diagnosis and treatment of this disease, which is not possible with current standard methods and developed sensors due to high cost and spending a long time ²³. Identifying diseases can be made easier by investigating the patterns created by the drying of biological samples and analyzing those using deep learning methods ^{24,25}. In this study, the drying pattern of blood and serum samples was verified using a convolutional neural network algorithm that is given to the audience via a graphical interface. The conditions that are best for conducting the experiment and running the algorithm, the patterns generated for each biological sample and the results of the classification analysis are described in detail in the following sections.

Optimization of CNN parameters

The uploaded images were re-sized at $200 \times 200 \times 3$. The CNN model employed five convolutional layers (Con2D) with filters of 16, 32, 64, 128, and 256. After each convolutional layer, a ReLU activation function, a max pooling layer with pool size 2×2 , a batch normalization layer and a dropout layer with a rate of 10% were applied. These layers produce a 3D matrix that is transformed into a vector by passing through a flattened layer and being inputted into the fully connected layer. The fully connected layer was made up of 2 sub-layers, each having 4 nodes. Sequentially, the output of those layers was transferred to the softmax and classification layers. The neural network algorithm was implemented using the Adam optimizer and the training rate, momentum, and epoch values being set to 0.02, 0.02, and 30, respectively.

The conditions of the drying process

Different parameters have the potential to influence the drying process of biological fluid. By adjusting these parameters to their optimal values, it can be easier to detect the subtle differences between DBS and DSS patterns. In this study, we examined the impact of three parameters, size of spot, time of dryin, and temperature. The experiment was conducted on 300 serum and blood samples that were collected separately. The dried spot images were evaluated by the designed CNN model. The total accuracy which was

calculated for the prediction set was used to select the optimal value of each parameter.

The initial step involved pouring different volumes of biological samples, ranging from 1.0 μL to 10.0 μL , onto a glass substrate. The samples were placed in a 25°C drying chamber for 30 minutes. As depicted in Figure 1a, by increasing the volume of spot, the discrimination between the two patient and control groups became desirable. For both DBS and DSS, the highest accuracy was achieved when 6 μL of biological sample was used. The other volumes of spot showed the lower accuracies. At lower volumes, the liquid cannot flow, leading to crystallization and the accumulation of metabolites and proteins in a small area. At higher volumes, the dried spot is so large that it is impossible to view through an optical microscope's eyepiece. Then, the camera only catches a small portion of the peripheral region. Hence, 6.0 μL of sample is utilized for subsequent investigations.

During the next step, the spot was allowed to dry during a period of time between 15 min to 105 min. As illustrated in Figure 1b, the accuracy of classification improved after 60 minutes of drying time. This period allows for the liquid to move and form central and peripheral regions, as well as cracks. Consequently, the distinction between patient and health samples was clearly defined. After this time, there were no significant changes in the patterns of both DBS and DSS.

In the final step, the drying process was studied at different temperatures. To achieve this, the oven's temperature was adjusted to different values of 25 °C, 40 °C, 55 °C, and 70 °C and the sample was kept at a certain temperature for 60 minutes. According to Figure 1c, the increase in oven temperature had a negative impact on classification accuracy due to several reasons: The drying process may be accelerated at higher temperatures, so, there is not enough time crystal formation or dehydrogenation and aggregation of macromolecule. Also, the decomposition of metabolites and proteins can be occurred at these temperature. Therefore, the temperature conditions was adjusted at 25 °C to create the dried spot patterns for further studies.

Photographs of dried spot patterns

Figure 2 indicates the dried spots of blood and serum samples received from controls (C) and patients (P). For control samples (BC), a central region with a large diameter and a peripheral region with a small diameter band were observed. In the peripheral region, macromolecules are aggregated in compact and regular patterns (Figure 2a). On the other hands, the diameter of the central and peripheral regions decreased in BP1, the dried spot for patient infected with Gram-positive bacteria such as staphylococcus aureus, enterococcus, streptococcus agalactiae, and streptococcus pyogenes. Also, the cracks have formed in the peripheral area, but their order is not as regular as that observed in the control samples. As shown in Figure 2a, a central region was not created in the spot pattern of BP2, the samples

contaminated by Gram-negative bacteria including acinetobacter, klebsiella pneumoniae, pseudomonas and proteus. The cracks in the peripheral region provided a flower-like pattern for these samples. However, the different images were recorded for the samples infected by escherichia coli (BP3), a spider-like pattern was observed due to the distribution of cracks in the peripheral region. As indicated in Figure 2a, the spots of samples contaminated by fungi like candida albicans and candida ssp (as can be seen with BP 4) did not have a regular pattern, the central and peripheral regions was not found in their spots and the atypical cracks were scattered throughout the dried spot.

The patterns derived from the DSS (Figure 2b) demonstrate significant differences between the patient and control samples. For a person without UTI (SC), the pattern has a large and reticulated central region and a narrow peripheral region. As the sample becomes contaminated, the lattice structure of the central region gradually disappeared and a petal liked pattern was formed. As seen, the sample infected by Gram-positive bacteria (SP1) had many narrow petals while the other contained Gram-negative bacteria (SP2) formed a pattern with lower and wider petals. As is evident, the serum samples cannot distinguish between escherichia coli and other Gram-negative bacteria. Similar to DBS, the pattern of DSS infected with fungal agents (SP3) is irregular.

The absence of a central region in the dried spot associated with UTIs can be attributed to the effects of electrolyte imbalance (decreasing zinc and

copper concentrations in serum and calcium, magnesium, sodium, and phosphate levels in blood), changes in blood composition due to increasing the mean concentrations of creatinine and blood urea nitrogen (BUN), cysteine, and phenylacetate and changes in coagulation dynamics²⁶⁻³². These factors collectively affect how blood and serum dry, resulting in a more uniform and less stratified appearance. Also, UTI causes elevated levels of oxidative stress markers (serum malondialdehyde [sMDA] and erythrocytic malondialdehyde [eMDA]) and acute phase proteins (haptoglobin [Hp], serum amyloid A [SAA], fibrinogen [Fb], and IL-6), which could be another reason for the wider peripheral region in bacterially infected samples³³. Fungal proteases contribute to inflammation by interacting with various biological systems, including the kinin system, coagulation, and fibrinolytic pathways³⁴. These proteases cleave fibrinogen into fragments known as fibrinogen cleavage products (FCPs), which play a crucial role in both host defense and inflammation. FCs, in conjunction with $\alpha M\beta 2$ and TLR4 receptors, activate immune cells such as adaptive immune cells (T and B lymphocytes) and innate immune cells (dendritic cells and macrophages), leading to fungal clearance. However, this complex can also trigger an inflammatory response, potentially contributing to autoimmune conditions³⁵. Therefore, the observed irregular structures of DBS and DSS associated with fungal infections can be attributed to complex interactions between coagulation proteins and immune responses.

Discriminant analysis by CNN

The photos of DBS and DSS were captured using a digital camera. Subsequently, they were grouped into distinct and labeled folders and sent to the GUI. The software divided the images of each folder into two sets: Training and Prediction, with a ratio of 80:20. These sets were applied to designing and evaluating models, respectively. By setting the parameters to the optimal value, the CNN model was executed and its outcomes is displayed in Table 1. As indicated, the proposed method can predict the 91.6% of infected samples and 90% of controls after analyzing DBS. In contrast, according to the DSS data, only 265 patients (88.3%) and 255 healthy people (85.0%) were placed in their respective groups. It is apparent that the metabolic and macromolecules profiles in the whole blood sample are more varied and they exist in different types and concentrations. This variety causes that different patterns were created in the central and peripheral areas of dried blood spots resulting in providing an accurate discrimination between patient and healthy groups.

The identification of infectious agents

The performance of the diagnostic patterning test for identification of UTI infectious agents was evaluated. In this step, images of infected samples that were correctly classified by the CNN model were placed in separate folders according to the type of contamination. The new data was subjected to the CNN algorithm. The results of this analysis are given in Table 2. It has been observed that the DBS infected with Gram-positive and Gram-negative bacteria, escherichia coli, and fungi can be identified and detected with a

accuracy of 84.6%, 88.2%, 90.5%, and 66.7%, respectively. It's amazing that the proposed approach identified the spider-like pattern associated with *Escherichia coli* from the flower-like pattern related to other Gram-negative bacteria with high accuracy.

The analysis of DSS pattern indicates that the method can discriminate 91.6% of Gram-positive agents, 85.1% of Gram-negative bacterial samples, and 66.7% of fungal infected sample in the correct groups.

Although, gold standard methods such as bacterial culture, polymerase chain reaction or biosensors are able to detect bacteria and their strains with good sensitivity and selectivity, the proposed method has also shown comparable performance for screening infectious samples. Also, in the present method, the biological sample does not need to be prepared, no toxic reagents and chemicals are used in the analysis process, the response is obtained in a short time and in total, it is a cost-effective assay.

Feasibility of the method

To evaluate the method's performance, 30 unknown samples were collected from the laboratory. After preparation, these samples were assessed using a standard clinical method and the proposed assay (DBS and DSS). The results are presented in Table 3. Among the 30 samples received, 18 tested positive and 12 tested negative using the clinical method. Notably, two infected samples were incorrectly identified by the DBS and DSS-based methods. Furthermore, one healthy sample in the DBS test and two healthy samples in

the DSS test were misclassified as having a Urinary Tract Infection (UTI). Based on these data, the accuracy of the proposed method for detecting infected samples (using both DBS and DSS) was 88.8%. For identifying healthy samples, the accuracy was 91.6% with the DBS-based method and 83.3% with the DSS-based method, respectively. These results show good correlation with the data obtained from analysis of the prediction set using CNN. Overall, these findings indicate that the proposed method could serve as a suitable alternative to conventional methods for diagnosing UTIs.

Evaluation of repeatability

To assess repeatability, we tested one contaminated and one healthy samples—whose analysis was confirmed by the standard clinical method—using the proposed method for 10 times. The results for the DBS-based and DSS-based methods are presented in Table 4. As can be seen, the CNN algorithm correctly identified all contaminated and healthy blood spots. However, this method failed to detect one serum spot belonging to both patient and healthy samples. Based on these results, although the accuracy achieved by the method approximately overlaps with that presented in Table 1, the repeatability of the DBS-based method is better than the DSS analysis.

Outlooks

Although this paper proposes a simple and rapid method for diagnosing infectious diseases like UTIs, more precise statistical information would have helped the reader to understand the mechanism and validity of detecting and discriminating patients from healthy participants. This information, which

will be considered in future studies, includes: a comparison of the designed application's results with pre-trained models such as ResNet and MobileNet; the use of explainable methods like Grad-CAM for better interpretation of morphological patterns obtained from dried biological droplets; the impact of augmentation (rotations, flips, intensity shifts) on diagnostic features; increasing the population of the studied groups and the effects of comorbidities, age, and gender on the morphology of the resulting patterns.

Conclusions

In summary, a screening method was devised to diagnose UTI by analyzing the dried patterns of whole blood and serum samples. The dried spot images were evaluated using the optimized CNN model for a more in-depth investigation. The ability of the proposed method was demonstrated to identify differences between UTI patients and control people, as well as to discriminate between the families of infected agents. This method is solely effective in identifying one type of pathogen (*Escherichia coli*) by analyzing dried whole blood samples with high accuracy. Offering the opportunity to conduct the experiment without the assistance of a skilled device and operator, this method holds significant promise for improving the diagnosis of bloodstream infections, especially in the field of UTIs. The alterations in protein and electrolyte levels associated with various pathogens, among other biochemical changes, influence the unique morphological patterns observed in DBS and DSS. These changes reflect the complex interplay of immune responses and metabolic alterations induced by infections,

suggesting that an in-depth analysis of dried spots could unveil critical diagnostic information. While promising, further research is needed to refine and validate this technique. By addressing the limitations associated with environmental factors, individual variability, and subjective interpretation, dried spots analysis could emerge as a valuable tool for early and accurate diagnosis of UTIs and other infectious diseases.

Method

Equipment

The spot drying process was executed on a glass substrate with dimensions of 2 cm x 3 cm and a thickness of 2 mm. The spot was injected onto the substrate using a BRAND Transferpette® S pipette. A Leica CME microscope was used to visually observe the dried pattern. The dried spot was captured in pictures with a Samsung Galaxy A52. The temperature of the drying process was adjusted with the MEMMERT UN 30 oven.

Participants

To conduct this study, we obtained residuals of whole blood and serum samples from 300 patients with UTI and 300 control subjects (who were free from any infectious disease) from the clinical laboratory of Baqiyatallah Al-Azam Hospital prior to disposal. All samples were irreversibly anonymized before use and were not subjected to any further treatment. They were taken from individuals who had fasted for at least 6 hours prior to sampling. The age of the patient and control groups was averaged at 51 and 54, respectively.

People who used tobacco, psychotropic drugs, and alcohol, as well as pregnant and lactating women, were not included in the study. By using a bacterial culture method ³⁶, the infectiousness of the samples belonging to the patient group was confirmed. Table 5 contains more detailed information about the study population.

Practical procedure

A certain volume (in microliters) of blood or serum sample was automatically poured onto a glass substrate and allowed to dry at a specified temperature and period of time. Note that, the substrate was rinsed with water and dried with a soft cloth and then with warm air. The drying process was carried out in an oven with adjustable temperature. A hygrometer embedded into the oven reported the relative humidity range was in the range of 20 to 25% at the time and temperature of measurement. Using an optical microscope, it was examined how the biological spots dried. The dried samples were photographed with a smartphone (Galaxy A52s with the camera features of "64 MP, f/1.8, 26mm (wide), 1/1.7", 0.8 μ m, PDAF, OIS") attached to the microscope eyepiece. The images that were received were saved in distinct folders with the "jpg" format, one for 'Patient' and one for 'Control', and then transported as input to the GUI. The experimental process employed in this study is schematically depicted in Figure 3 and the block diagram is shown in Figure 4.

Convolutional neural network

There are multiple layers in a convolutional neural network (CNN) such as input, convolution, activation, pooling, flattening, fully connected, and output³⁷. The input can consist of an image or a set of images that are split into small kernels within the convolution layer. The kernels are processed by a set of weights that identify the features of the input images³⁷. In the end, these features are gathered in a group known as feature maps and transferred as output to the next layer. The model learns the features and complexities of the input data by applying a nonlinearity activation function after each convolution layer. Otherwise, the neural network only processes linear functions³⁸. The Rectified Linear Unit (ReLU) is the most prevalent activation function utilized in CNN, preserving positive values and returning negative values to zero³⁹. After this layer, reducing the spatial size of the input data (width and height) can be done with assistance from the pooling layer, which results in a decrease in the number of variables³⁸. By doing this, the problem of large and time-consuming calculations is solved and data processing becomes easier to handle. The maximum and average functions are utilized in this process³⁸. The first function is commonly employed in the middle of the network design, while the second function is utilized at the end. The pooling layer is typically 2x2³⁸. To minimize overfitting, a dropout layer is implemented that randomly excludes some connections from the next layer. Typical networks have a dropout rate between 0.1 and 0.5⁴⁰. The feature maps obtained after the convolution and pooling layers are flattened into a one-dimensional vector so that they can be passed to a fully connected layer

for classification or regression ³⁸. It must be noted that the data undergoes batch normalization throughout the network before entering each convolution or fully connected layer ⁴¹.

Graphical User Interface

The collected images were analyzed and classified using the CNN method through the use of a graphical user interface. Figure 5 illustrates that this application is made up of five parts. Through the 'Input images' box in part A, the program is given the images collected in separate folders (regarding each category). In the first step, the nature of the data is known so that the user selects the option "Evaluation with known data" in the "type" box. The input data is divided into two training sets for building the CNN model and the prediction set for evaluating the designed model. The user has the ability to choose the data division ratio in the 'numTrainfiles' box. The 'Convert image size' box allows for the size of the input images to be changed based on the importance of classification analysis and extraction of more relevant information. In this study, the Images was re-sized at different size such as 300×300 , 250×250 , 200×200 , 150×150 and 100×100 . The optimum size was used for further procedures. The 'Filter to learn' box specifies the number of convolution layers and filters used in each layer needed for the CNN architecture. Also, the optimization of Epoch value, activation function, and dropout rate takes place in part B. In section C, the optimizer, momentum, and learning rate are adjusted to fit the general parameters of the neural network algorithm. Then, the algorithm's execution command is

given in the next section (d). In addition, the built model can be saved and classification data can be received in other formats, such as Excel. In section e, you can see the outcomes of the analysis and classification parameters like total accuracy, sensitivity, and specificity for both training and prediction sets. After validating, the model that was designed is used to identify the type of unknown samples. In order to accomplish this, the user must upload the relevant images from the 'Input images' box and then choose the 'Evaluate with built model' option from the 'Type' box. After running the program, the class of the analyzed sample appears in the “Unknown set” box embedded in section e.

Compliance with ethical standards

All procedures involving human samples were conducted in accordance with the Declaration of Helsinki and the National Guidelines of the Iranian Committee for Ethics in Biomedical Research (<https://ethics.research.ac.ir>). The Residual whole blood and serum samples from patients and control individuals were obtained from the clinical laboratory of Baqiyatallah Al-Azam Hospital prior to their disposal. According to national regulations, the use of anonymized leftover biological samples does not require obtaining informed consent, provided that approval from the relevant ethics committee has been secured. All samples were irreversibly anonymized before use and were not subjected to any further treatment. This study was approved by the Research Ethics Committee of Baqiyatallah University of Medical Sciences (Approval ID: IR.BMSU.BAQ.REC.1402.036).

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Author contributions

H. B conceived the idea, designed, discussed the concepts and experiments, writing-review, and editing. R. H, A. P, H. Kh, G.B. P and H. S discussed the concepts and experiments. M.M. B, F. NMGH, A. Sh and M. A performed the experimental work, analyzed the data and writing-original draft preparation. All authors discussed and commented on the manuscript.

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This research received no external funding.

Data availability

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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Legends of Figures and Tables:

Figure 1. The effect of different conditions on drying process: (a) spot size, (b) drying time period and (c) temperature.

Figure 2. The dried spot pattern for (a) whole blood and (b) serum. In this Figure, BC and SC are the patterns of control sample, BP1 and SP1 are related to sample infected by Gram-positive bacteria, BP2 and SP2 are defined as sample with Gram-negative bacteria, BP3 is the spot contaminated by Escherichia coli and BP4 and SP3 are the samples with fungal infections. The photos were captured at optimal conditions.

Figure 3. The experimental procedure for the proposed method: (a) collecting whole blood and serum samples for both patients and controls volunteers, (b) injecting the samples on a glass substrate, (c) transferring the samples to an oven and allowing them to dried, (d) observing the dried pattern using an optical microscope with a smartphone mounted on its eyepiece, (e) saving the images in folders related to each studied groups.

Figure 4. The block diagram of the experimental procedure for the proposed method.

Figure 5. The structure of CNN based graphical user interface.

Table 1. Classification results obtained by CNN analysis. The data obtained at optimal conditions.

Table 2. Discrimination of infected agent families using CNN models. The data obtained at optimal conditions.

Table 3. Demographic data of the studied population

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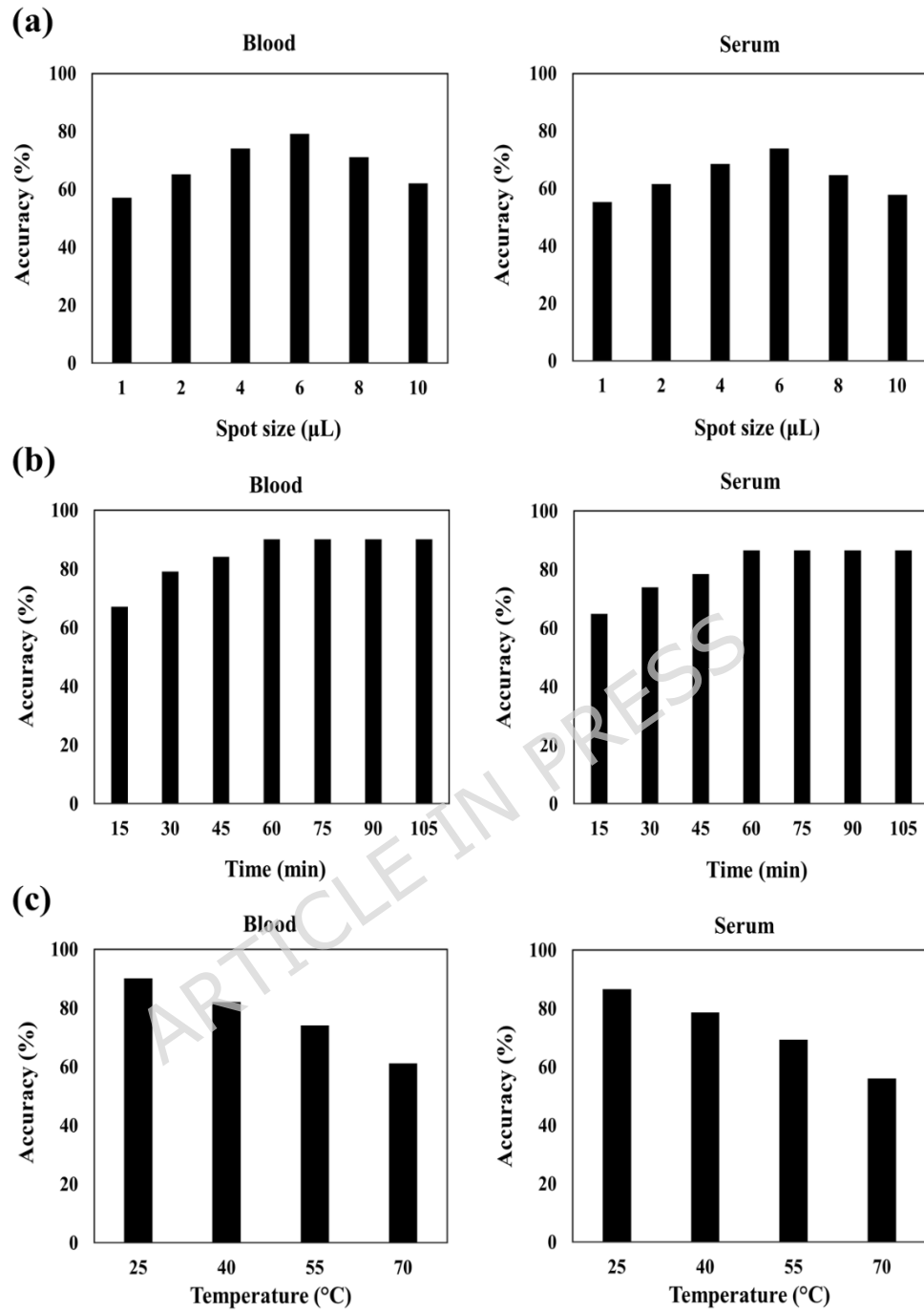


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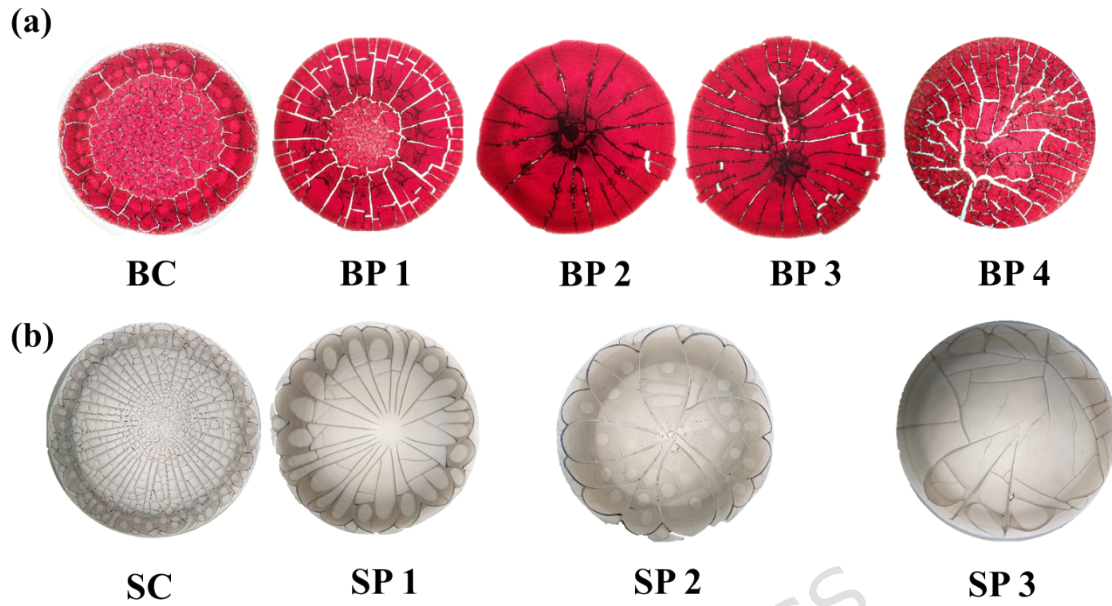


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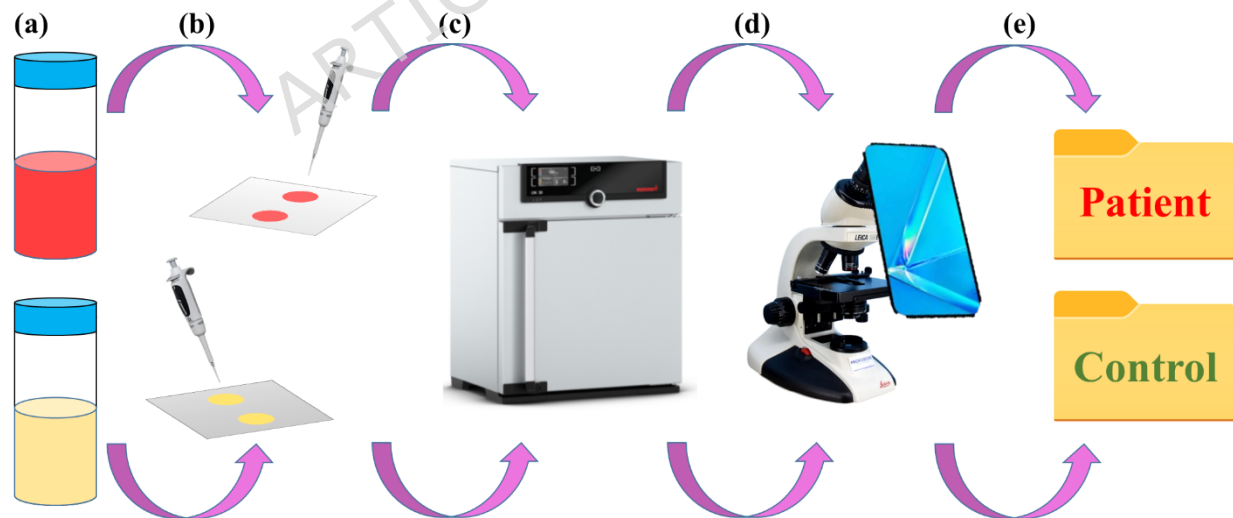


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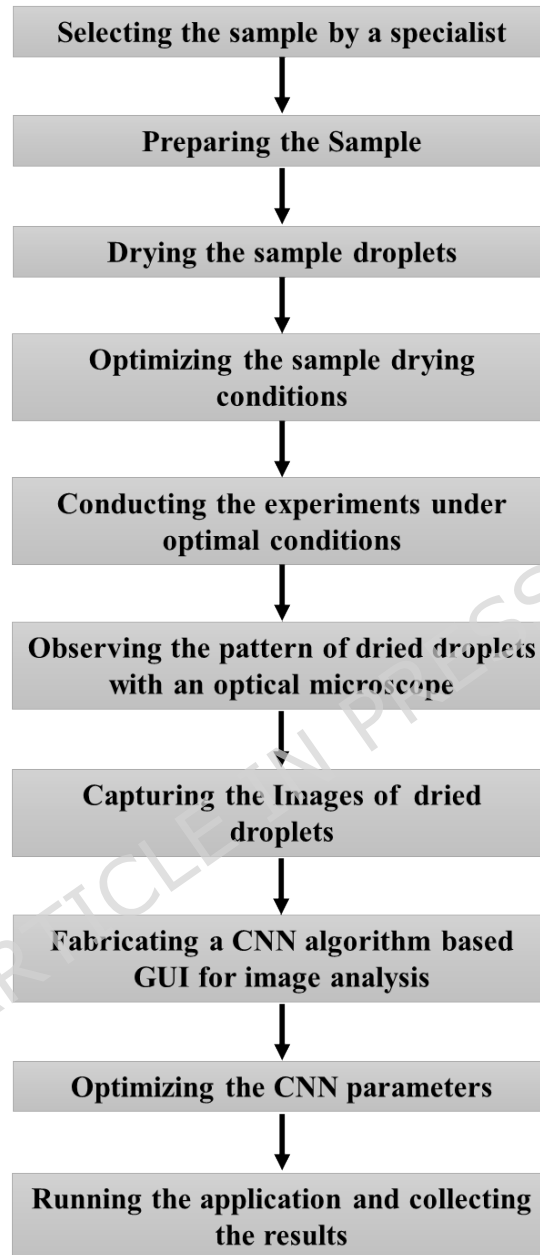


Figure 4. The block diagram of the experimental procedure for the proposed method.

Help

(a) **Input Images**

Type:

numTrainFiles:

Convert image size to: X

(b) **CNN Architecture**

Filter to learn:

MaxEpochs:

Act Func:

Dropout rate:

(c) **NN function**

Optimizer:

Momentum:

InitialLearnRate:

Plots:

(d) **RUN**

Save model

Export results to WS

Export results to Excel

(e) **Results**

Training set:

Prediction set:

Unknown set:

Figure 5. The structure of CNN based graphical user interface

Table 1. Classification results obtained by CNN analysis. The data obtained at optimal conditions.

Sample	Set	Voluntaries	Sensitivity (%)	Specificity (%)	Accuracy (%)	Error rate (%)
Blood	Training	UTI patients	90.8	88.8	89.8	10.2
		Controls	88.8	90.8		
	Prediction	UTI patients	91.6	90.0	90.8	9.2
		Controls	90.0	91.6		
Serum	Training	UTI patients	87.5	85.4	86.4	13.6
		Controls	85.4	87.5		
	Prediction	UTI patients	88.3	85.0	86.6	13.4
		Controls	85.0	88.3		

Table 2. Discrimination of infected agent families using CNN models. The data obtained at optimal conditions.

Type of sample	Class of UTI agents	Accuracy (%)	
		Training set	Prediction set
		84.3	84.6

Bloods	Gram positive bacteria		
	Gram negative bacteria (without E.Coli)	88.4	88.2
	E.Coli	86.9	90.5
	Fungus	85.7	66.7
Serum	Gram positive bacteria	89.5	91.6
	Gram negative bacteria	83.4	86.1
	Fungus	78.5	66.7

Table 3. The evaluation of assay performance for detection of unknown samples.

Number of sample	Result of Test			Number of sample	Result of Test		
	Clinical	DBS	DSS		Clinical	DBS	DSS
1	-	-	-	16	-	-	-
2	-	-	-	17	-	-	-
3	+	+	+	18	+	+	+
4	+	+	+	19	-	-	-
5	+	+	+	20	-	-	-
6	-	-	-	21	+	+	+
7	-	+	+	22	+	+	+
8	+	+	+	23	-	-	-
9	+	+	+	24	+	-	-
10	+	+	+	25	+	+	+
11	-	-	-	26	+	+	+
12	+	-	-	27	-	-	+
13	+	+	+	28	+	+	+
14	+	+	+	29	-	-	-

15	+	+	+		30	+	+	+
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Table 4. The repeatability of proposed method

Patients			Controls		
Number of sample	Result of Test		Number of sample	Result of Test	
	DBS	DSS		DBS	DSS
1	+	+	1	+	+
2	+	+	2	+	-
3	+	+	3	+	+
4	+	+	4	+	+
5	+	-	5	+	+
6	+	+	6	+	+
7	+	+	7	+	+
8	+	+	8	+	+
9	+	+	9	+	+
10	+	+	10	+	+

Table 5. Demographic data of the studied population

Variable	UTI Patients	Control voluntaries
Number	300	300
Sex		
Male	143	161
Female	157	139
Age		
(Mean±SD)	54.02±22.13	51.74±17.98

Bacteria type

Acinetobacter	16
Escherichia coli	95
Klebsiella pneumoniae	54
Pseudomonas	36
Proteus	9
Streptococcus pyogenes	21
Streptococcus agalactiae	18

Enterococci	7
Staphylococcus aureus	24

Fungus type

Candida albicans	8
Candida ssp	12
