Rapid Urinary Tract Infection (UTI) Diagnosis using Laser Scattering and Deep Learning Analysis

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ABSTRACT

Urinary tract infections (UTIs) most occurred due to bacterial infection. As the symptom appears, urine culture is done to have information on the bacteria that causes the infection. The culturing process normally takes 24 to 48 hours to have a result. Therefore, general antimicrobial therapy is done rather than target therapy due to urgency of the patient health. Rapid diagnosis of UTIs can provide accurate information of the infection and able to reduce the unnecessary antimicrobial therapy. In this study, we proposed optical system with deep learning analysis to diagnosis UTI. More specifically, proposed technology reports if the urine is infected with gram positive bacteria or gram-negative bacteria within 30 min. The optical hardware is designed to detect optical property and motility of bacteria using phase delay monitoring. And deep learning analysis is designed to learn phase delay pattern change depending on the concentration and species of bacteria. We have tested with 6 species of bacteria which are *E.coli*, *P. aeruginosa*, *P. mirabilis*, *K. pneumoniae*, *S. aureus*, *C-N-S*. The result shows 91% accuracy for 3 classes (Non-Infection, Infection: Negative, Infection: Positive).

MATERIALS & METHODS

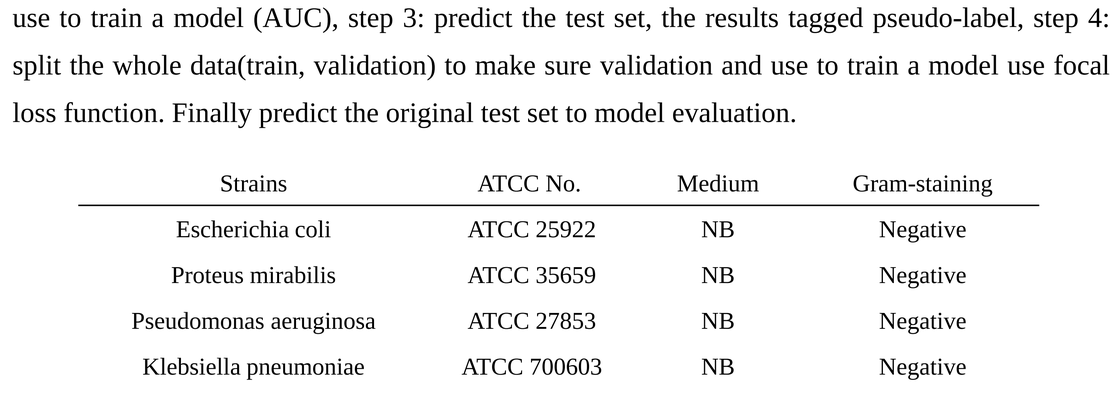

Figure 1. Schematic diagrams of the UTI diagnosis and data processing for deep learning architecture.

Growth and identification of bacteria

Total 6 strains have been distributed from American Type Culture Collection (ATCC). Bacteria using all the experiments were grown both NB-broth and LB-broth, UTI causing strains were performed using the Mac Conkey (BD BBL, USA) medium and Columbia CNA (BD BBL, USA) (with 5% sheep blood) medium and incubated at 37°C for 20 ± 2 h. This suspension was centrifuged at 6000 rpm for 10min, eliminated supernatant. Using to bacterial pellet cells were washed with phosphate buffer saline (1x, PBS) in equal culture media content.

Preparation of urine sample

Data processing for step 1: split training set to train and validation, step 2: train and validation use to train a model (AUC), step 3: predict the test set, the results tagged pseudo-label, step 4: split the whole data(train, validation) to make sure validation and use to train a model use focal loss function. Finally predict the original test set to model evaluation.

Strains	ATCC No.	Medium	Gram-staining
Escherichia coli	ATCC 25922	NB	Negative
Proteus mirabilis	ATCC 35659	NB	Negative
Pseudomonas aeruginosa	ATCC 27853	NB	Negative
Klebsiella pneumoniae	ATCC 700603	NB	Negative
Staphylococcus aureus	ATCC 29213	LB	Positive
Staphylococcus epidermidis	ATCC 12228	LB	Positive

Table 1. Characteristic of bacteria

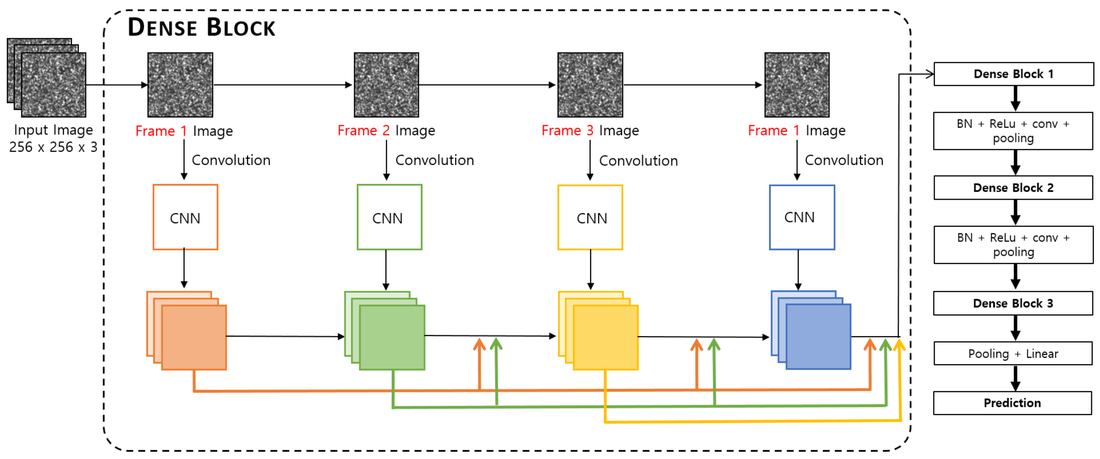

Figure 2. Proposed Time Aligned Dense-Net architecture

Deep learning architecture

Individual speckle image frames are encoded using a CNN and then fed to an encoder where each layer represents a time-step. Inspired by, each layer is connected to all its preceding layers. At time step T, the encoder outputs $K \times T$ feature maps as representation of the sample speckle images where K is the number of output feature maps dedicated to layer t.

RESULTS

(a)

True \ Prediction	Non-Infection	Infection: Negative	Infection: Positive
Non-Infection	91	5	4
Infection: Negative	6	93	1
Infection: Positive	11		89

(b)

0 minutes		Output sample label (number of image)			Accuracy (%)
		Non-Infection	Infection: Negative	Infection: Positive	
Input sample label	Non-Infection	13,082	700	618	90.8
	Infection: Negative	558	8970	72	93.4
	Infection: Positive	512	0	4288	89.3
Average acc (%)					91.5

Figure 3. Infection and gram classification percentage performance of the Time aligned Dense-Net architecture. Performance of classification deep learning architecture was illustrated for (a) confusion matrix, (b) detailed performance of the speckle analysis through Time aligned Dense-Net architecture.

(a)

True \ Prediction		Non-Infection						Infection					
								Negative				Positive	
		E. coli	*K. pneumoniae*	*P. aeruginosa*	*P. mirabilis*	*S. aureus*	*C-N-S*	*E. coli*	*K. pneumoniae*	*P. aeruginosa*	*P. mirabilis*	*S. aureus*	*C-N-S*
Non-Infection	*E. coli*	76	12		1		1	5	4		1		
	K. pneumoniae	5	82	2	2	1		1	4	2	1		
	P. aeruginosa	15	2	75	3			1	1	3			
	P. mirabilis		1	1	61	27					9	1	
	S. aureus			1	20	66						13	
	C-N-S			1	4	5	77				1		12
Infection: Negative	*E. Coli*	8		4	1			84	3				
	K. pneumoniae		6	1	1			2	88	1	1		
	P. aeruginosa			2				13		89			
	P. Mirabilis							1	12	7	78	2	
Infection: Positive	*S. aureus*					13						65	22
	C-N-S					3	5					8	84

Figure 4. Architecture performance breakdown by class. (a) confusion matrix for 12 classes: Non-infection and infection grouping-level, indicated by colored boxes.

CONCLUSION

We demonstrated a rapid classification method of Urinary Tract Infection(UTI) in artificial urine medium based on laser speckles image trained deep learning (DL) technique defined as 'Time aligned Dense-Net'. The proposed DL technique encapsulates a wide range of statistical variations for the model to be sensitive to speckle decorrealations. Specifically, we aim to evaluate intensity variation of speckle image from culturing medium by developing a structure based on convolutional neural network (CNN). Our DL framework achieves classification of maximum accuracy 91% for Non-Infection, Infection: Negative and Infection: Positive. In summary, we envision that time analysis neural network combined with deep learning will be a useful tool in UTI. We believe that more detailed understanding of speckle image pattern promise for rapid and low-cost bacteria identification.

ACKNOWLEDGEMENT

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