Review Article

Current applications of artificial intelligence combined with urine detection in disease diagnosis and treatment

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Abstract: In recent years, the advantages of artificial intelligence (AI) in data processing and model analysis have emerged in the medical field, enabled by computer technology developments and the integration of multiple disciplines. The application of AI in the medical field has gradually deepened and broadened. Among them, the development of clinical medicine intelligent decision-making is the fastest. The advantage of clinical medicine intelligent decision-making is to make the diagnosis faster and more accurate on the basis of certain information. Urine detection technologies, such as urine proteomics, urine metabolomics, and urine RNomics, have developed rapidly with the advancements in omics and medical tests. Advances in urine testing have made it possible to obtain a wealth of information from easily accessible urine. However, it has always been a problem to extract effective information from this information and use it. AI technology provides the possibility to process and use the information in urine. AI, combined with urine detection, not only provides new possibilities for precise and individual diagnosis and disease treatment, but also helps promote non-invasive diagnosis and treatment. This article reviews the research and applications of AI combined with urine detection for disease diagnosis and treatment and discusses its existing problems and future development.

Keywords: Artificial intelligence (AI); urine detection; omics; diagnosis

Submitted Nov 07, 2020. Accepted for publication Feb 22, 2021.
doi: 10.21037/tau-20-1405
View this article at: http://dx.doi.org/10.21037/tau-20-1405

Introduction

Artificial intelligence (AI) was proposed by John McCarthy at the Dartmouth conference held in 1956 in New Hampshire. It refers to a new technology science that researches and develops theories and methods (1). Generally speaking, AI is a kind of computer technology that can simulate human behavior and extend human ability beyond human instructions. In recent years, with the development of data analysis, image recognition, and other technologies, AI application in the medical field is gradually expanding and becoming more in-depth, especially in medical image recognition processing and clinical medical intelligent decision-making. AI provides new opportunities for early detection, accurate diagnosis, and the individualized treatment and management of diseases (2-4).

Urine is a kind of liquid excrement that is excreted from humans and vertebrates through the urinary system and urinary tract as a byproduct of metabolism. Urine contains many substances, such as proteins, electrolytes, sugars, and creatinine, amongst others, which can change under different physiological and pathological conditions (4-6). Therefore, AI combined with urine detection provides the possibility for the diagnosis of diseases. Based on

the different urine components, this paper summarizes the research field and applications of AI combined with urine component detection and analysis in the diagnosis and treatment of urinary system diseases, cardiovascular diseases, digestive tract diseases, and other multisystem diseases, which are also summerized in *Table 1* and *Figure 1*. We also explore its limitations and development prospects. We present the following article following the Narrative review checklist (available at http://dx.doi.org/10.21037/tau-20-1405).

Methods

A systematic literature search was conducted in September 2020 based on computerized databases, including PubMed, EMBASE, the Cochrane Library, and 2 main Chinese databases (WANFANG and CNKI) without language restrictions. Search terms or keywords used included "artificial intelligence", "machine learning", "urine proteomic", "urine metabolomic", "urine RNomics", and "urine cytopathology". Moreover, we performed a search of the reference lists of the included studies or relevant reviews to ensure literature saturation.

AI and medicine

The core technologies of AI include computer vision, machine learning, natural language processing, robotics, and speech recognition (25,26). AI technology applications in the medical field are mainly computer vision and machine learning (27-34). Computer vision aims to replace the visual organ as the input means through the imaging system, then analyzes and processes the image through the computer. Therefore, computer vision is widely used in medical imaging to improve recognition and analysis ability to help predict and diagnose the disease (27-32). AI has been widely used in the image-based diagnosis and has shown strong perandom forestsormance. Kermany *et al.* (31) used the combination of deep learning and optical coherence tomography images to diagnose retinal-related lesions. This technology demonstrated good perandom forestsormance in diagnosing age-related macular degeneration and diabetic macular edema. Also, AI applications based on other data types, such as electronic health records, are developing rapidly. Liang *et al.* (32) developed a natural language processing system based on deep learning, which could effectively extract data from electronic health record and build a diagnostic system based on the data. The results showed that the system could accurately diagnose multiple pediatric diseases. Machine learning is multidisciplinary and interdisciplinary, covering probability theory knowledge, statistics knowledge, approximate theoretical knowledge, and complex algorithm knowledge. It uses the computer to simulate the real-time human learning process and divides existing content into knowledge structures to effectively improve learning efficiency (30-33). With the popularization of computer network technology and the rise of big data, massive medical data holds great value. Machine learning technology can effectively collect and process this data, and improve the level of disease diagnosis or provide the possibility for devising personalized treatment plans. According to different learning methods, AI can be divided into supervised learning, unsupervised learning, and reinforcement learning. Its common algorithms mainly include decision trees, support vector machines, random forests, artificial neural networks, and deep learning, amongst others. Of these algorithms, support vector machines and random forests are widely used in clinical medicine. These algorithms have different characteristics and advantages. Support vector machines can transform the problem of nonlinear separability into a linearly separable problem. A decision tree is a tree-like decision-making model in which each internal node represents a judgment on an attribute, each branch represents the output of a judgment result, and finally, each leaf node represents a classification result. Random forest is a classifier that contains multiple decision trees, randomizes the use of variables (columns) and data (rows), generates many classification trees, and summarizes the classification trees' results. Deep learning is also gradually being utilized in medicine. Through its multilayer structure, the machine can automatically find the features or laws in the data to improve perandom forestsormance to predict and classify the data. According to the different characteristics of the algorithms, they are applied to many aspects. For example, deep learning has obvious advantages in processing the increasing amount of big data in medicine and medical imaging diagnosis. support vector machines and random forests are used to establish AI-assisted diagnosis technologies. Applications of other medical field algorithms are also being continuously developed and evaluated (34-36).

AI and urine detection

AI combined with urine proteomics

Urine produced under normal conditions contains a small

Table 1 Studies using artificial intelligence combined with urine detection

Study	Application	Sample size		Training features	Algorithms/ modes	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC (%)
		Training set	Test set						
Rossing *et al.* (7)	Diagnosed HF	127 HErEF patients; 581 controls	94 HFrEF patients	103 potential HFrEF peptide biomarkers	SVM	NA	93.6	92.9	0.972
Zhang *et al.* (8)	Predicted progression from asymptomatic left ventricular dysfunction to symptomatic HF	57 patients with HF; 38 patients progressed to HF during follow-up; 192 controls	175 patients with asymptomatic diastolic left ventricular dysfunction	96 potential HF peptide biomarkers	SVM	NA	NA	NA	0.7
Von Zur Mühlen *et al.* (9)	Identified specific biomarkers for DVT and PE	17 patients with DVT and DVT+PE; 32 controls	6 patients with DVT and DVT+PE; 41 controls	62 urinary peptides	SVM	NA	100	83	0.90
Zhang *et al.* (10)	Identified biomarkers for lung cancer diagnosis	23 lung cancer; 23 healthy controls	10 lung cancer; 10 healthy controls	5 urinary biomarkers	RF	NA	NA	NA	0.8747–0.9853
Nakajima *et al.* (11)	Distinguished between CRC, benign diseases, and healthy people	201 CRCs; 31 non-CRCs	59 samples	N1, N12-diacetylspermine and other 6 polyamines	Decision tree	NA	NA	NA	0.961
Roux-Dalvai *et al.* (12)	Identified bacterial species causing UTIs quickly	190 samples including inoculated and non-inoculated urine	NA	82 peptides	RF and so on	100	NA	NA	0.98
Eisner *et al.* (13)	Predicted whether a patient needed colonoscopy	355 patients required colonoscopy; 633 normal controls	Data set spilt into several folds	NA	SVM; RF; LASSO	NA	64.00	65.00	0.715
Shao *et al.* (14)	Predicted BCa	87 BCa patients; 65 hernia patients	47 patients	6 putative markers	Decision tree	76.60	71.88	86.67	NA
Kouznetsova *et al.* (15)	Identified early and late BCa	Metabolites obtained from publication (McDunn *et al.* 2015)	205 metabolites of early stage BCa; 42 metabolites of late-stage BCa	All metabolites from the sources	ANN; SGD	72.00 (for early BCa); 65.45 (for late BCa)	NA	NA	NA
Caudarella *et al.* (16)	Predicted the recurrence of calculus in 5 years	80 outpatients	NA	6 parameters from urine of patients	ANN	NA	NA	NA	0.961
Liang *et al.* (17)	Searched for metabolic markers of liver cancer	25 early HCC patients and 12 controls	15 HCC patient and 10 controls	15 kinds of urine metabolites	SVM and so on	NA	96.50	83.00	0.903

Table 1 (*continued*)

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Study	Application	Sample size		Training features	Algorithms/ modes	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC (%)
		Training set	Test set						
Dykstra *et al.* (18)	Predicted the tolerance and response of CRC patients who underwent adjuvant chemotherapy	62 patients with CRC	NA	12 metabolites	LASSO; SVM; RF; decision tree	NA	NA	NA	0.750 (the highest)
Martinez-Vernon *et al.* (19)	Built a diabetes prediction model	72 patients with type II diabetes; 43 healthy controls	NA	Volatile organic compounds in urine	RF; SLR; SVM; ANN	NA	NA	NA	0.825
Sapre *et al.* (20)	Constructed a BCa prediction model	30 patients with active cancer (recurrers); 30 non-recurrers 21 benign controls	NA	6 parameters from urine of patients	ANN	NA	NA	NA	0.961
Connell *et al.* (21)	Found microRNAs related to BCa and constructed a prostate cancer prediction model	358 prostate patients	177 prostate patients	Urine-derived EV-RNA profiles	LASSO	NA	NA	NA	0.770
Sanghvi *et al.* (22)	Developed a model to process whole slide images and predict diagnoses	1,615 voided and instrumented urine cytology cases	790 cases	Hyperchromasia, chromatin coarseness, and nuclear membrane irregularity, N/C	Deep learning	NA	79.50	84.50	0.910
Muralidaran *et al.* (23)	Built an artificial neural networks model to identify urothelial cell carcinoma	59 urothelial cell carcinoma cases; 56 benign cases	NA	Nuclear area, diameter, standard deviation of nuclear area, and so on	ANN	100 (all the benign and malignant cases)	NA	NA	NA
Heckerling *et al.* (24)	Predicted urinary tract infections	212 women presented to an ambulatory clinic with urinary complaints	NA	Urinary frequency, foul urine odor, LE on urine dipstick, and bacteria and epithelial cells on urinalysis	ANN	0.764	0.821	0.744	0.853 (the best)

HErEF, heart failure with reduced ejection fraction; support vector machines, support vector machine; HF, heart failure; DVT, deep vein thrombosis; PE, pulmonary embolism; random forests, random forest; MS, metabolic syndrome; CRC, colorectal cancer; EV-RNA, extracellular-vesicle RNA; LASSO, least absolute shrinkage and selection operator; UCB, urothelial carcinoma of the bladder; BCa, bladder cancer; artificial neural networks, artificial neural network; SGD, stochastic gradient descent; HCC, hepatocellular carcinoma; SLR, sparse logistic regression; N/C, nuclear-cytoplasmic ratio; LE, leukocyte esterase.

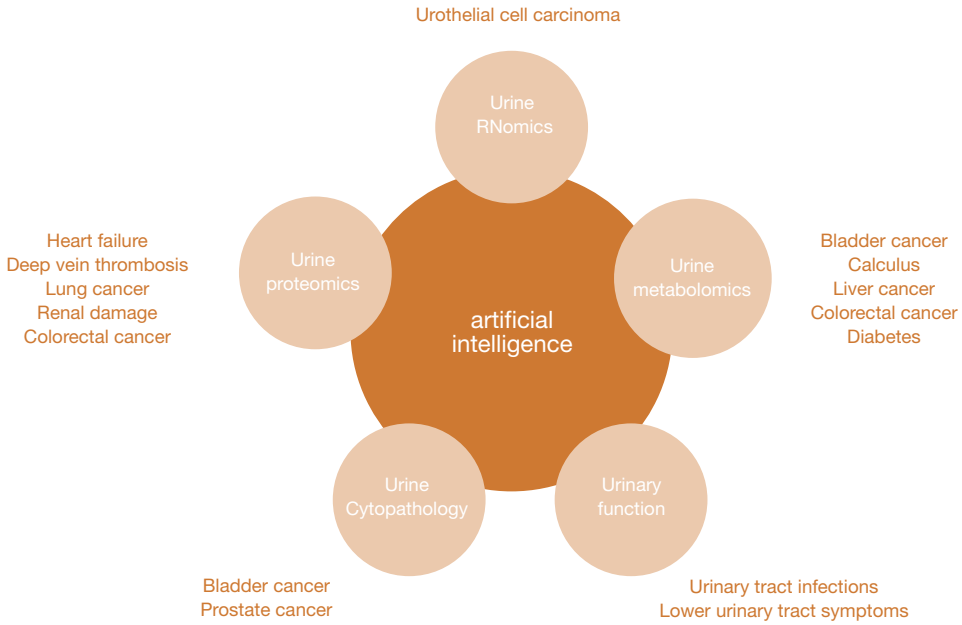

Figure 1 The applications of artificial intelligence combined with urine detection.

number of polypeptides and proteins. When the body undergoes physiological and pathological changes, the types and content of polypeptides and proteins in the urine may change. Therefore, it is possible to recognize the changes of related proteins in urine through AI and carry out disease diagnosis (37-40). In 2016, Rossing *et al.* (7) of the University of Copenhagen in Denmark obtained urine proteins by capillary electrophoresis combined with mass spectrometry. Based on this, a machine learning algorithm for heart failure with decreased ejection fraction was established. After testing, the area under the receiver operating characteristic (ROC) curve (AUC), sensitivity, and specificity of the model were 0.972, 93.6 %, and 92.9 %, respectively.

Similarly, Zhang *et al.* (8) constructed a machine learning model based on 96 potential heart failure-specific peptide biomarkers to predict sudden heart failure, and the results showed that the AUC of the model was 0.7. These results suggest that the technique may help understand the pathogenesis and diagnosis of heart failure with reduced ejection fraction. Von Zur Mühlen *et al.* (9) from the Department of Cardiology of Freiburg University, Germany, used a support vector machines model and urine proteins obtained from capillary electrophoresis coupled to mass spectrometry to construct a prediction model of deep vein thrombosis in a 2015 study. The model's sensitivity and specificity were 100% and 83%, respectively, in an independent cohort of 6 cases and 41 controls. This technique may help find the specific proteins and peptide markers of lower extremity venous thrombosis and assist clinicians in predicting the occurrence of lower extremity venous thrombosis earlier and more accurately in future clinical practice. Zhang *et al.* (10) of the State Key Laboratory of proteomics, China National Center for protein science, combined proteomics technology with a random forests model. They built a lung cancer prediction model by using the random forests algorithm to search for possible lung cancer-specific diagnostic markers in urine, and the feature selection algorithm was used to screen out sensitive urinary protein markers. After testing, the model could correctly classify most lung cancer cases in the training group (n=46) and the test set (n = 14–47), and the AUC ranged from 0.8747 to 0.9853. Nakajima *et al.* (11) of Tokyo Medical University used polyamine biomarkers in the urine combined with machine learning to distinguish between colorectal cancer, benign diseases, and healthy people. They utilized liquid chromatography-mass spectrometry (LC-MS) to profile 7 kinds of polyamines. Based on machine learning algorithms such as decision trees, the classifier achieved an effective prediction of colorectal cancer, and the study found that N1, N12-diacetylspermine had the best AUC (0.794) among these polyamine species.

Moreover, polyamine combination showed a higher AUC of 0.961. Similarly, combining LC-MS with machine learning techniques, Roux-Dalvai *et al.* (12) used data-independent acquisition and machine learning algorithms to define a peptide signature of bacterial species causing urinary tract infection and then investigated the unknown urine samples by targeted proteomics. This technology effectively shortened the detection time of pathogens and had 100% accuracy when looking at data above the clinical threshold of 1×10^5 CFU/mL (CFU: colony forming units). The studies described above show that AI provides possibilities for non-invasive and precise diagnosis of diseases based on urine proteomics information.

AI combined with urine metabolomics

Metabolomics is a research method that conducts a quantitative analysis of all metabolites in organisms' bodies and seeks to determine the relative relationship between metabolites and physiological and pathological changes (41,42). Urine, as the excreta produced by human metabolism, contains much metabolomics information. However, due to the variety of metabolites, a mass of data, and the remaining uncertainties regarding research on diseases' pathophysiological changes, using urinary metabolites for disease diagnosis and treatment in the past mostly remained theoretical. The development of AI technology makes it possible to process urinary metabonomics data, which contains much noise. Eisner *et al.* (13) used machine learning algorithms to establish a predictive model, which aimed to predict whether a patient needed a colonoscopy based on urine's metabolic profile. The study used the urine metabolic profiles, colonoscopy results, and medical histories of 988 patients (633 normal and 355 who required colonoscopy) to build a predictive model through machine learning algorithms such as support vector machines. The predictor judged whether a new patient needed a colonoscopy by analyzing their urine profile and medical history. The results showed that the predictive model had a sensitivity of 64% and a specificity of 65%, and the experimenter could balance and adjust the two. Shao *et al.* (14) analyzed the metabolites in patients' urine with bladder cancer and hernia by ultra-high perandom forestsormance liquid chromatography-mass spectrometry. They then established the prediction model of bladder cancer based on the urine metabolism spectrum and 6 candidate urine markers. The algorithm's diagnostic accuracy, sensitivity, and specificity were 76.60%, 71.88%, and 86.67%, respectively.

Similarly, Kouznetsova *et al.* (15) combined urine metabolites and machine learning algorithms to identify early and late bladder cancer. The best performing model was able to predict metabolite class of different stage with an accuracy of 82.54% and the area under precision-recall curve of 0.84 on the training set. Caudarella *et al.* (16) utilized an artificial neural network to process 6 parameters, including serum Na and K, Na, P, Oxalate, and the AP (CaP) index (ion-activity products, AP; calcium phosphate, CaP) from the urine of patients with urinary calculi and the recurrence of calculus in 5 years. They found that these parameters had a significant nonlinear relationship with the recurrence of calculus. The results suggested that this model could partly predict the recurrence of calculus. Liang *et al.* (17) analyzed the urine metabolism spectrum using liquid chromatography-quadrupole time of flight-mass spectrometry and then searched for liver metabolic markers cancer through a machine learning algorithm. They found that 15 kinds of urine metabolites were helpful for the diagnosis of liver cancer. Among them, the sensitivity and specificity of palmitic acid, alpha-N-Phenylacetyl-L-glutamine, phytosphingosine, indoleacetyl glutamine, and glycocholic acid for liver cancer diagnosis were 96.5% and 83.0%, respectively. Such techniques can be used not only to diagnose diseases but also to predict prognosis. Dykstra *et al.* (18) established a machine learning algorithm by combining urine metabonomics with AI to predict the tolerance and response of colorectal cancer patients after adjuvant chemotherapy. In this study, 4 different machine learning algorithms, including the least absolute shrinkage and selection operator algorithm, support vector machines, decision tree, and random forests, were used to construct prediction models to predict the 5-year survival rate, tumor recurrence, chemotherapy dose reduction, and treatment cycle extension of colorectal cancer patients after adjuvant chemotherapy. For 5-year survival, the AUC of the optimal prediction model was 0.612, the AUC of the optimal prediction model of cancer recurrence was 0.650, chemotherapy dose reduction was 0.542, and treatment cycle extension was 0.750. Martinez-Vernon *et al.* (19) used field asymmetric ion mobility spectrometry to analyze and determine the volatile organic compounds in the urine. These data used a variety of machine learning algorithms to build a diabetes prediction model, including random forests, sparse logistic regression, support vector machines and so on. Among them, the best AUC of the model based on sparse logistic regression was 0.825 [95% confidence interval (CI): 0.747–0.9], which could effectively identify

diabetes. These findings suggest that urine metabolomics is a promising additional tool for clinicians to use in disease diagnosis and prognosis assessments.

AI combined with urine RNomics

RNAs are key molecules that regulate protein synthesis and cell functions in the body. Urine generally contains a small amount of microRNAs, which regulate gene expression by binding to mRNA molecules and affect their stability or translation. Therefore, microRNAs are often specifically expressed during tumor occurrence. These abnormal microRNAs can act as molecular biomarkers to assist in tumor diagnosis, predict prognosis, and evaluate treatment responses, and can be detected and analyzed using AI (43,44). Sapre *et al.* (20) selected 12 microRNAs that may be related to the occurrence of bladder cancer through previous research and constructed a bladder cancer prediction model based on a machine learning algorithm. The study confirmed that the prediction model of bladder cancer was constructed by miR16, miR200c, miR205, miR21, and miR34a with 88 % sensitivity and 48% specificity. The AUC of the best predictor to distinguish patients with bladder cancer from non-recurrers was 0.85, especially for stage T1 bladder cancer with an AUC of 0.92. The results suggest that this model can reduce the cystoscopy rate in the validation queue by 30 %. Connell *et al.* (21) constructed a prostate cancer prediction model based on urine-derived extracellular vesicle RNA. Through verification, the AUC of the model in diagnosing clinically significant middle and high-risk prostate cancer was 0.77. It also had a better predictive ability for the prognosis of prostate cancer patients who underwent active monitoring, providing a new direction for the non-invasive diagnosis of prostate cancer. The above results suggest that AI technology has high accuracy in diagnosing bladder cancer, prostate cancer, and other diseases based on the type and content of RNA in the urine.

AI combined with urine cytopathology

Under both physiological and pathological conditions, a variety of cells can be observed in urine, and most of them are of great significance to the diagnosis of urinary system diseases. White blood cells and pus cells in urine often indicate urinary system infection. Urine red blood cell morphology can be used to distinguish glomerular diseases from other diseases. The urinary tract's epithelial cells come from the entire urinary system, from the kidney to the urethra. When urinary tract tumors occur, they can provide pathological evidence for diagnosis (45,46). Qin *et al.* (47) used support vector machines to efficiently recognize urine cell images, combined with hue saturation intensity color parameters, spatial parameters, and grid search cross-validation optimization selection parameters. Sanghvi *et al.* (22) developed a deep learning computational pipeline with multiple tiers of convolutional neural network models to process whole slide images and predict diagnosis. The algorithm's sensitivity was 79.5%, and the specificity was 84.5% for high-grade urothelial carcinoma. Similarly, Muralidaran *et al.* (23) built an artificial neural networks model to identify urothelial cell carcinoma based on the visual and morphometric data from urine cytology. This model diagnosed all the cases correctly in the test set, except a low-grade case, which was diagnosed as high grade.

AI combined with urinary function

Lower urinary tract symptoms (LUTS) are common symptoms of urinary system diseases and mainly include symptoms that impact urinary storage and micturition period (48). The former refers to frequent urination, urinary urgency, increased nocturia, while the latter mainly refers to dysuria, thin urine line, slow urine flow and so on. LUTS are of great significance in diagnosing benign prostatic hyperplasia, urinary tract infection, neurogenic bladder, and other diseases. Moreover, Gacci *et al.* (49) found that older men with moderate to severe LUTS had an increased risk of cardiovascular events. Thus, LUTS are also significant for the diagnosis of some non-urinary diseases. However, the diagnosis of LUTS mainly depends on the patient's description, urination log, and other methods at present, which have shortcomings of subjectivity and inaccurate record keeping, which makes it difficult to judge symptoms diagnose diseases. Heckerling *et al.* (24) combined artificial neural networks and genetic algorithms to evaluate urine and predict urinary tract infections. Firstly, they used genetic algorithms to select the 5 best urine variables that could be used to build predictive models, including urinary frequency, foul urine odor, leukocyte esterase on urine dipstick, and bacteria epithelial cells on urinalysis. Then they used artificial neural networks to construct a predictive model. The ROC area of the model for identifying urinary tract infection and non-infection was 0.853, and when the network output threshold was 0.25, the sensitivity was 0.821, the specificity was 0.744, and the accuracy was 0.764. Yuan *et al.* (50) established a machine learning algorithm based on the data collected by a portable urination recorder, such as daily urination volume, times, night urination volume, and

night urination times, to objectively evaluate the degree of patients' LUTS and provide evidence for accurate diagnosis and individualized treatment of the disease.

Discussion

The application of AI in the medical field has a bright prospect. Taking China as an example, an average of 57 million cases are misdiagnosed each year in clinical care, and the total misdiagnosis rate is as high as 27.6% (51). Both disease diagnosis and medical imaging analysis depend on the personal experience and subjective judgment of clinicians and imaging physicians. Therefore, in areas with poor medical conditions and weak medical systems, the chance of misdiagnosis and missed diagnosis is even higher. AI-assisted diagnosis technology can undoubtedly help to reduce misdiagnosis and missed diagnosis. Also, the development of big medical data has brought many possibilities for basic medicine and clinical diagnosis and treatment; however, the huge amount of data and redundant medical data are accumulating over time. AI technology can efficiently and accurately process this data and improve itself in the continuous accumulation and processing of data. It is unrealistic and inefficient to rely on humans to deal with this data. The above advantages are also well reflected in AI combined with urine detection. Urine-related data has the characteristics of large volume, easy collection, and rich information. The effective use of the data obtained from urine can help us understand many diseases' pathological mechanisms and assist clinicians in diagnosis and treatment. It is noteworthy that urine collection is non-invasive and simple, providing new diagnostic methods and ideas for many diseases that rely on invasive procedures for diagnosis.

Despite more and more research and AI achievements in medicine, there is still a long way to go before AI products are widely used in medical practice. Firstly, the lack of evaluation standards for AI in terms of effectiveness, clinical applicability, and safety is still a big problem for most countries. Taking the urinary proteome as an example, the type and content of protein in urine are closely related to gender, age, race, and laboratory platform level and are affected by the test's storage temperature and whether protease inhibitors are added. Therefore, the internal scientificity and external applicability of disease evaluation models based on AI still need to be further verified. In 2016, the Food and Drug Administration issued the first guideline for evaluating AI systems, which provides preliminary specifications and standards for AI products' clinical application (52,53). The guidelines and specifications are still in their infancy and need to be further established and improved.

Furthermore, as medicine-related AI products are for human application, this will raise many ethical issues, including medical safety and responsibility attribution. Misdiagnosis and missed diagnosis by doctors can cause damage and risks to patients. When AI products cause medical accidents, how will responsibility be divided? Will regional differences in the application of AI products lead to medical inequality? When the conclusion of AI is inconsistent with that of doctors, will it increase patients' distrust of doctors and hospitals and worsen the doctor-patient relationship? These problems need to be solved in different cultural and social environments (54-58).

At present, the development of most AI products relies on a large amount of medical data. Through the collection and analysis of more and more extensive data, AI's perandom forestsormance will further improve. These medical data involve patients' basic information, such as name, gender, and age, and often involve privacy-sensitive information, such as past medical history, history of present illness, and family history. If the server or cloud storing this information is invaded, it will lead to patient information leakage and privacy breaches. Therefore, there is an unavoidable problem in applying AI in the medical field, that is, the contradiction between the efficiency of AI products and the privacy information of patients. If we want to improve AI's efficiency, we will inevitably need more patient information, including sensitive and private information. If we want to fully respect and protect patients' privacy, limiting the collection of their data will limit the effectiveness of AI products. Achieving a balance between the two is an ideal goal for the development of medical-related AI. However, this is a big challenge and is affected by disease types, national laws and regulations, and social cognition (59-61).

Conclusions

In summary, AI is conducive to making full use of the increasing amount of big data in medicine. In this article, we have demonstrated the use of AI in processing and analyzing urine detection data, such as urine proteins, urine metabolites, and urine RNA, which not only contributes to the early and accurate diagnosis of diseases but also provides new ideas for the non-invasive and simplified diagnosis of diseases. Currently, AI is still in the early stages of development, and urine-related AI is mostly used

in the auxiliary diagnosis of urinary system diseases. The accuracy and specificity of AI for diagnosis need to be further improved. However, with the rapid developments in computer technology and medicine, AI combined with urine detection is expected to become another important means of disease diagnosis and treatment and is also expected to be more widely used in the early diagnosis, treatment, and follow-up monitoring of various diseases.

Acknowledgments

Funding: This work was supported by the Sichuan Science and Technology Program (2018TJPT0018), Chengdu Science and Technology Program (2019-YFYF-00087-SN), and the 1-3-5 project for disciplines of excellence-Clinical Research Incubation Project, West China Hospital of Sichuan University (2019HXFH015).

Footnote

Reporting Checklist: The authors have completed the Narrative Review reporting checklist. Available at http://dx.doi.org/10.21037/tau-20-1405

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at http://dx.doi.org/10.21037/tau-20-1405). FQ and JY have the patent Portable Urine Recorder issued. The other authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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Cite this article as: Tan J, Qin F, Yuan J. Current applications of artificial intelligence combined with urine detection in disease diagnosis and treatment. Transl Androl Urol 2021;10(4):1769-1779. doi: 10.21037/tau-20-1405

