



Artificial intelligence in healthcare—the road to precision medicine

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Contributions: (I) Conception and design: TQB Tran, S Padmanabhan; (II) Administrative support: All authors; (III) Provision of study materials or patients: All authors; (IV) Collection and assembly of data: All authors; (V) Data analysis and interpretation: All authors; (VI) Manuscript writing: All authors; (VII) Final approval of manuscript: All authors.

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Abstract: Precision medicine aims to integrate an individual's unique features from clinical phenotypes and biological information obtained from imaging to laboratory tests and health records, to arrive at a tailored diagnostic or therapeutic solution. The premise that precision medicine will reduce disease-related health and financial burden is theoretically sound, but its realisation in clinical practice is still nascent. In contrast to conventional medicine, developing precision medicine solutions is highly data-intensive and to accelerate this effort there are initiatives to collect vast amounts of clinical and biomedical data. Over the last decade, artificial intelligence (AI), which includes machine learning (ML), has demonstrated unparalleled success in pattern recognition from big data in a range of domains from shopping recommendation to image classification. It is not surprising that ML is being considered as the critical technology that can transform big data from biobanks and electronic health records (EHRs) into clinically applicable precision medicine tools at the bedside. Distillation of high-dimensional data across clinical, biological, patient-generated and environmental domains using ML and translating garnered insights into clinical practice requires not only extant algorithms but also additional development of newer methods and tools. In this review, we provide a broad overview of the prospects and potential for AI in precision medicine and discuss some of the challenges and evolving solutions that are revolutionising healthcare.

Keywords: Artificial intelligence (AI); machine learning (ML); precision medicine; biobanks; data science

Received: 16 September 2020; Accepted: 26 March 2021; Published: 25 September 2021.

doi: 10.21037/jhmhp-20-132

View this article at: <http://dx.doi.org/10.21037/jhmhp-20-132>

Introduction

The existing paradigm of healthcare is based on the average-patient one-size-fits-all approach to deliver diagnostic, therapeutic and preventive interventions. However, it has become alarmingly clear that, while practical to implement, these broad clinical approaches fail to adequately address the medical needs of a significant portion of the population (1). When it comes to pharmacotherapy, for example, only 40–60% of patients respond to treatment (2,3). The variable drug treatment response rates now widely documented

across medical literature are due to considerable inter-individual variability. A more targeted approach to medicine is thus clearly needed to optimise treatment, which has prompted the emergence of precision medicine. The terms precision medicine and personalised medicine have been used interchangeably, but the preferred current terminology is precision medicine, as there is a consensus that the term personalised medicine could be misinterpreted to imply that treatments and preventions are being developed uniquely for each individual. From an epidemiological, pharmacological and biological perspective, the scale of

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inter-individual and intra-individual variation in drug response as indicated above, it is pragmatic to assume that personalised treatment at an individual level is rather aspirational. Identifying and predicting subgroups with a better or worse response is likely more achievable and has a more realistic potential to revolutionise medicine.

In contrast to the one-size-fits-all model, precision medicine aims to integrate an individual's unique features from clinical phenotypes and biological information obtained from imaging to laboratory tests and health records, to arrive at a tailored diagnostic or therapeutic solution with a higher chance of success (1). It is expected that patients will benefit from early accurate diagnosis, higher treatment efficacy and fewer adverse drug reactions, while broader improvements include greater healthcare savings and economic productivity. Precision medicine thus encompasses both diagnosis and prediction with greater accuracy than current clinical and epidemiological guidelines. The notion of precision medicine emerged from the dramatic successes in the identification of distinct subpopulations within certain cancer categories through advances in genomic sequencing followed by effective targeting of these molecular cancer subtypes by specific drugs. Patients with chronic myeloid leukaemia whose tumours harbour the BCR/ABL translocation ('Philadelphia chromosome') are successfully treated with the drug imatinib that inhibits tyrosine kinase (4); patients with cystic fibrosis can benefit from the drug ivacaftor based on mutations in the *CFTR* gene (5); and the poster child of personalised medicine, trastuzumab, is indicated for patients with metastatic breast cancer overexpressing the human epidermal growth factor receptor-2 (HER-2) (6). These examples, amongst others, demonstrating how unique genetic or molecular perturbations in an individual can lead to tailored therapy, led to strategic initiatives to scale up precision medicine to replicate these successes for other diseases.

Unlike conventional medicine, precision medicine is highly data-intensive and requires health data flow from individual medical records into different research contexts—for instance clinical trials, genomic research, pharmacovigilance, epidemiological studies—and then back into a learning healthcare system for the research outcomes to be integrated into practice (7). Research is an integral component of precision medicine, which requires data collected during the course of clinical care to be applied in the study of real-world clinical outcomes to enhance generalisability of the interventions. The

recognition of the value and potential of precision medicine has led to the development of initiatives to accelerate and support research by collecting vast amounts of clinical and biomedical data. For example, the All of Us (AoU) research program (8) in the United States (formerly known as the Precision Medicine Initiative) aims to gather data from at least one million consenting individuals in the form of electronic health records (EHRs), biomarker and genomic analyses of donated tissue samples, mobile health devices and surveys. Similar initiatives have sprung up in both the public and private sectors across the world: 100,000 Genomes Project and UK Biobank in the UK; BioBank Japan; China Kadoorie Biobank; Biobank Graz in Austria; and FinnGen in Finland (9-12). These repositories of observational data are critical to the delivery of precision medicine despite the known limitations of observational studies to infer causality. This is described below, and some of the justifications for turning to observational data include the relative ease to collect large datasets, the difficulties in setting up randomised controlled trials (RCTs) for rare diseases and the huge sample sizes required for pharmacogenomic studies. Equally important to big data are the artificial intelligence (AI) tools which enable the extraction of clinically meaningful insights from the data (*Figure 1*).

AI and Machine Learning (ML)

The terms AI and ML have been used interchangeably, but it is important to understand the differences between them. AI is a suite of technologies which enables a machine to simulate human behaviour. Two fields of AI which are particularly relevant to healthcare are ML and Natural Language Processing (NLP) (13,14). ML allows a software or algorithm to automatically learn from past data without programming explicitly, while NLP gives machines the ability to read, understand and derive meaning from human languages. We shall focus primarily on ML in this review, as most AI applications in healthcare are based on this subset of AI. The limitations of traditional statistical tools, such as linear and logistic regression which are commonly used for clinical outcome prediction, are well documented—they perform poorly with nonlinear relationships or high-dimensional data and fail to account for unknown interactions between input variables. Furthermore, in the era of big data, they are unnecessarily labour-intensive (15). In contrast to relatively rigid traditional statistical methods, the inherent flexibility of ML along with the scope for

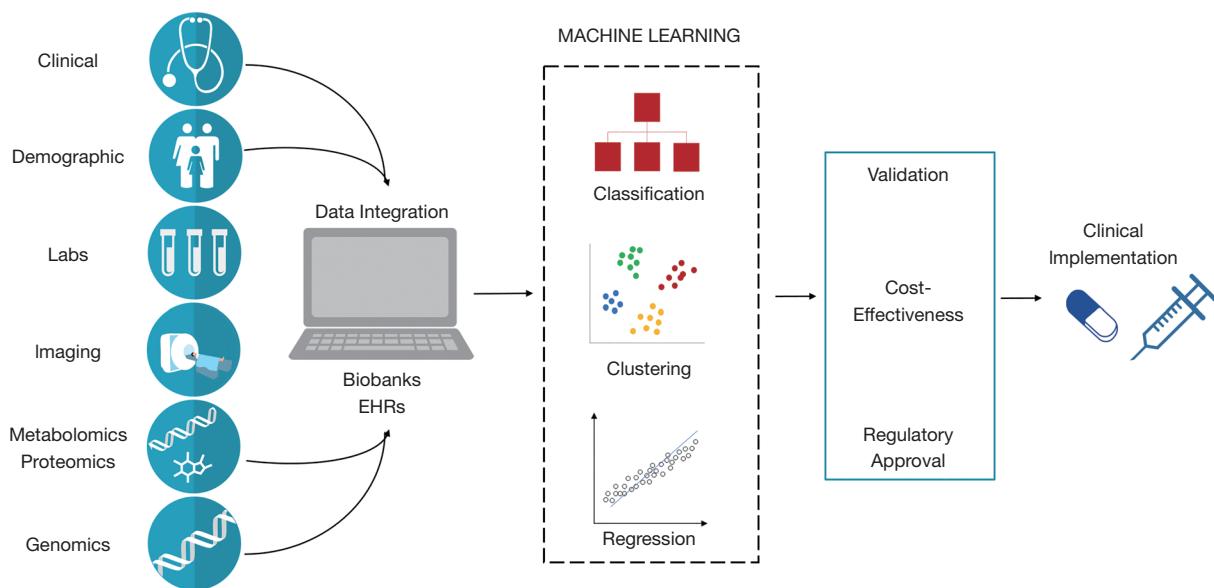


Figure 1 Integration of multiple types of data into biobanks and electronic health records (EHRs), machine learning models and finally clinical implementation.

automation and the ability to learn from input data to progressively improve model performance without requiring explicit programming suggest ML is the right tool to be considered for precision medicine.

Whilst a detailed description of different ML algorithms is beyond the scope of this review, a summary of ML algorithms and their applications in healthcare research is presented in *Table 1* (14). Although this is not an exhaustive list, it reflects the breadth of algorithms and clinical questions that are being explored using ML. ML can be categorized into four learning types: supervised, unsupervised, reinforcement and deep learning (*Figure 2*) (14). Supervised learning algorithms use a dataset labelled by humans to predict a specified or known outcome. Unsupervised learning algorithms, on the other hand, find patterns and associations in unlabelled data without human intervention. Supervised learning algorithms carry out classification and regression tasks, while unsupervised learning algorithms are limited to clustering. Reinforcement learning is a hybrid of supervised and unsupervised learning, which maximises the accuracy of algorithms using trial and error and thus is not applicable in the healthcare setting. Finally, deep learning, which is based on the structure of neural networks of the brain, is an autonomous system with multiple hidden layers of data processing. Deep learning algorithms independently find patterns even in unstructured data, which are then employed to make predictions about

new data (111).

NLP overlaps with ML (deep learning in particular) and has gained traction as a tool for data extraction from EHRs. A significant proportion of medical data contained in EHRs, such as descriptions of clinical features and diagnoses, is unstructured free text and the value of NLP is recognised for parsing clinical notes into practical data inputs including risk assessments (14,112). Furthermore, applying NLP to scientific literature has highlighted its potential for drug repurposing associations (113). In addition to these types of data mining, NLP may also have a future role in facilitating and automating patient engagement through chatbots. Chatbots simulate human conversations (in both written and spoken form) and are already widely used by online customer support services or virtual assistants such as Amazon Alexa. In healthcare, chatbots could serve as a stand-in for a physician as the first port of call to advise on symptoms and give preliminary diagnoses, freeing up some of the time of healthcare workers to focus on tasks which cannot be automated (114).

Prospects for AI in precision medicine

Success in implementing precision medicine in healthcare requires the communication and participation of people across a wide spectrum of disciplines including molecular biology, genetics, pathology, informatics, computer science,

Table 1 Commonly used machine learning models in healthcare with examples of applications

Clinical study	ML algorithm	Reference
Rapid diagnosis of depression	Boosting algorithm	(16)
Improving warfarin usage for the elderly inpatients	Boosting algorithm	(17)
Predicting sepsis using vital sign data in the emergency department	Boosting algorithm	(18)
Predicting adverse events in patients undergoing major cardiovascular procedures	Boosting algorithm	t(19)
Predicting urinary tract infections in the emergency department	Boosting algorithm	(20)
Classifying lung nodules	Boosting algorithm	(21)
Predicting transition from gestational diabetes mellitus to type 2 diabetes	Decision tree	(22)
Identifying diffusion lesions in acute ischemic stroke	Decision tree	(23)
Diabetic foot amputation risk analysis	Decision tree	(24)
A top-down searching approach for diagnosis	Decision tree	(25)
Performance surveillance of infant incubators	Decision tree	(26)
Improving the prediction of total surgical procedure time	Decision tree	(27)
Predicting graft survival for kidney transplantation	Ensemble methods	(28)
Predicting treatment success in patients with substance use disorder	Ensemble methods	(29,30)
Diagnosing breast cancer	Ensemble methods	(31)
Detecting patients' asthma control level	Ensemble methods	(32)
Early prediction of outcome of cognitive behavioural therapy	Ensemble methods	(33)
Automatic fall detection system for real-life monitoring	Hidden markov	(34)
Detecting QRS complexes in single-lead ECG recordings	Hidden markov	(35)
Real-time circadian phase estimation	Hidden markov	(36)
Multi-channel EEG based automatic epileptic seizure detection	Hidden markov	(37)
Real-time calibration and automatic drug dosing recommendation for chemotherapy treatment plans (Curate.AI)	Hidden markov	(38)
Classifying prognostic phenotypes in heart failure patients	Hierarchical clustering	(39,40)
Detecting disease-specific clusters within aortic arch images	Hierarchical clustering	(41)
Clustering blood results in paediatric inflammatory bowel disease	Hierarchical clustering	(42)
Predicting therapeutic response in IgG4-related disease	Hierarchical clustering	(43)
Detecting thyroid diseases	Hierarchical clustering	(44)
Classifying venomous and non-venomous snake bites	KNN	(45)
Analysing and identifying kidney stone	KNN	(46)
Predicting retinopathy risk	KNN	(47)
Classifying lower back pain	KNN	(48)
Distinguishing physiological from pathological patterns of hypertrophic remodelling	KNN	(49)
Diagnosis of coronary artery disease	LDA	(50)

Table 1 (continued)

Table 1 (continued)

Clinical study	ML algorithm	Reference
Differentiating basal cell carcinoma and healthy skin	LDA	(51)
Early diagnosis of mild cognitive impairment in Alzheimer's disease	LDA	(52)
Predicting and classifying risk level of breast cancer	LDA	(53)
Detecting and classifying dementia subtypes	LDA	(54)
Identifying distinct bronchiectasis phenotypes	LDA	(55)
Monitoring physician prescribing patterns and ensure the appropriateness of treatment	Linear regression	(56)
Predicting conversion time to Alzheimer's disease	Linear regression	(57)
Predicting hypoxemia and Covid-19 disease outcome based on nasopharyngeal viral load	Linear regression	(58)
Predicting maternal vitamin D status during pregnancy and lactation	Linear regression	(59)
Predicting hospitalization and outpatient corticosteroid use in inflammatory bowel disease patients	Linear regression	(60)
Differentiating severe septic patients with acute respiratory distress syndrome from those without	Logistic regression	(61)
Early identification of patients with acute decompensated heart failure	Logistic regression	(62)
Predicting early- and long-term mortality in hospitalized patients at risk of malnutrition	Logistic regression	(63)
Predicting chemotherapy and radiotherapy outcome	Logistic regression	(64)
Predicting autism spectrum disorder diagnosis	Logistic regression	(65)
Microprocessor-based device for real-time prediction of acute cardiovascular events	Naïve Bayes	(66)
Predicting atherosclerosis progression from ultrasound images	Naïve Bayes	(67)
Detecting clinically important colorectal surgical site infection	Naïve Bayes	(68)
Improving detection and diagnosis of bone tumour	Naïve Bayes	(69)
Perceptron multilayer for classifying the risk in paediatric congenital heart surgery	Naïve Bayes	(70)
Detecting diabetic retinopathy	Neural network	(71)
Classifying skin cancer	Neural network	(72)
Estimating optimal dose for intensity-modulated radiation therapy in prostate cancer patients	Neural network	(73)
Identifying autism spectrum disorder from the brain images	Neural network	(74)
Automatic cardiac arrhythmia detection on ECG	Neural network	(75)
Identifying a molecular network predictive of advanced coronary calcium	Neural network	(76,77)
Predicting knee osteoarthritis risk	Neural network	(78)
Predicting adverse drug reactions and identifying the responsible molecular substructures	Neural network	(79)
Predicting lower intestinal bleeding and need for surgical intervention	Neural network	(80)
Automated classification of skin lesions using images	Neural network	(81)
Automated detection of ischemic stroke	Neural network	(73)
Chronic obstructive pulmonary disease staging and acute respiratory disease prediction in smokers	Neural network	(82)

Table 1 (continued)

Table 1 (continued)

Clinical study	ML algorithm	Reference
Risk assessment for major complications and death after surgery	Neural network	(83)
Predicting early graft rejection in antibody incompatible kidney transplantation	Neural network	(84)
Reinforcement learning for blood pressure regulation in post-cardiac surgery patients	Proprietary algorithms	(85)
Predicting medical adherence of patients with heart failure	Proprietary algorithms	(86)
Automatic IMRT planning in Philips Radiation Oncology Systems for head and neck cancer treatment	Proprietary algorithms	(87,88)
Automated speech analysis to measure and predict psychosis onset	Proprietary algorithms	(89,90)
The Seattle Heart Failure Model for heart failure survival analysis	Proprietary algorithms	(91)
Predicting future myopia development in school children	Random forest	(92)
Differentiating pituitary metastasis from autoimmune hypophysitis	Random forest	(93)
Predicting early graft rejection in antibody incompatible kidney transplantation.	Random forest	(94)
Predicting hospitalization and outpatient corticosteroid use in inflammatory bowel disease patients	Random forest	(85)
Predicting rheumatoid arthritis mortality	Random forest	(61)
Predicting in-hospital length of stay among cardiac patients	Random forest	(95)
Predicting presence of advanced coronary artery calcium	Random forest	(96)
Predicting risk of suicide attempts over time	Random forest	(78)
Assessing risk of fibrosis and other liver-related outcomes in chronic Hepatitis C patients	Random forest	(97)
Predicting long-term cognitive outcome following breast cancer	Random forest	(98)
Predicting readmission rate in heart failure patients	Random forest	(99)
Automatic detection of seizures in single-channel intra-cranial electroencephalograph recording	SVM	(100)
Detecting structural imaging signature of schizophrenia	SVM	(101)
Differentiating responders and non-responders to depression treatment	SVM	(102)
Discriminating between hypovolemia and euvoolemia using photoplethysmographic signals	SVM	(103)
Predicting medication nonadherence in Crohn's disease maintenance therapy	SVM	(104)
Landmark text mining example of disease-chemical relationships to predict a benefit for using fish oil in Raynaud's syndrome	Text mining	(105)
Information retrieval and document triage in the Pharmacogenomics Database	Text mining	(106)
Rule-based text mining approach for microRNA expression in cancer cells	Text mining	(107)
Phenotype extraction from electronic health records	Text mining	(108)
Patient outcome prediction through similarity analytics	Text mining	(109,110)

KNN, K-nearest neighbours; LDA, linear discriminant analysis; SVM, support vector machine.

statistics and clinical science along with health economists, health insurers and hospital managers. The potential roles of AI span data-integration, making work-flows efficient and error-proof, generating clinically meaningful insights

from big data, and developing new medicines. However, the published evidence across all these domains are predominantly represented by early-phase *in silico* studies with little validation and do not fully cover potential sources

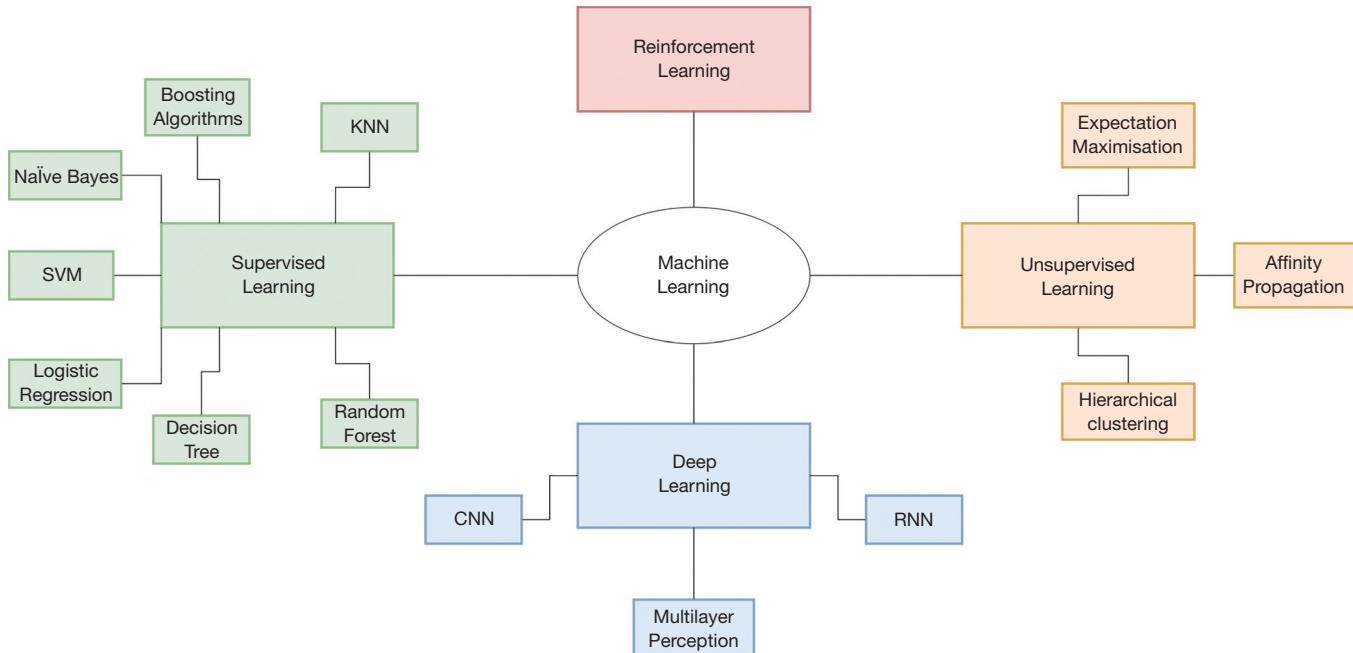


Figure 2 Subtypes of machine learning, with representative examples of models. CNN, convolutional neural network; KNN, K-nearest neighbours; RNN, recurrent neural network; SVM, support vector machine.

of bias specific to AI systems (115). In relation to precision medicine, ML approaches mainly feature in three areas with tangible successes evident in the first two (116): (I) prediction of pharmaceutical properties of molecular compounds and targets for drug discovery (117); (II) faster diagnosis using pattern recognition and segmentation techniques on medical images (from, e.g., retinal scans, pathology slides and body surfaces, bones and internal organs) (71,72,118); and (III) the development of predictive models using deep learning techniques on multimodal data sources such as genomic and clinical data (119). The paucity of use cases of AI in precision medicine may partly be related to studies not conforming to RCT level rigour that is crucial for regulatory approval and clinical adoption.

Technical challenges of ML in precision medicine

Despite technical advancements in informatics, computer science and mathematics, the development and application of ML models remains a challenging process. When building ML models, data is split into training and testing sets. The training set teaches the model, while the model's performance is evaluated by how well it describes the testing set. Researchers typically split the data at random. However,

data in real life are rarely random and show trends over time, for instance differences data collection processes, measurement methods or changes in guidelines. These variations can have an impact on prediction accuracies.

Overfitting and underfitting

Overfitting is a major issue for all ML models. Overfitting arises when an algorithm learns to make rules which fit both random noise and meaningful signals in training data accurately and specifically, but fail with testing data (120). The resulting algorithm can thus perfectly predict the training data but only at the price of its performance on new data. Because of the availability of an enormous variety of clinical variables recorded in EHRs and biobanks, it can be tempting to develop a highly specific model with a multitude of predictive features for a given disease. Such a model is likely to show excellent performance in its training dataset but fail in validation, limiting applicability in the real world, resulting in little more than wasted healthcare resources. This is the opposite of underfitting, which occurs when a model is too simple (informed by too few features or regularized too much) making it inflexible in learning from the dataset (121). Overfitting and underfitting can

be overcome by making modifications to the training set or by optimising the parameters of the model. For these reasons, training of a good model often requires large datasets, competent informatics skills, domain knowledge and an adequate means of validation (121). When a model is developed by an ML expert with little knowledge of the clinical context of variables within an EHR, feature selection may be misguided leading to erroneous predictions and poor model performance. Thus, collaboration between medical and informatics experts is essential to extract value from big data.

Interpretability and explainability

As ML (especially deep learning) models grow more sophisticated and powerful with multiple hidden layers of data transformation and analysis between the input and output data, their decision-making process becomes more challenging for a human to conceptualise. While interpretability implies some sense of understanding how the technology works, explainability implies that a wider range of users can understand why or how a conclusion was reached. The complex architecture of deep learning models, for example, makes them more difficult to understand and interpret than their supervised and unsupervised counterparts (111). Lack of interpretability presents one of the greatest barriers to the acceptance of ML into clinical practice. For instance, if a clinical expert and an ML algorithm are presented with the same patient data but arrive at different diagnoses, it may not be possible to interrogate the algorithm to find where and why the decision-making processes diverge. The translation of these so-called “black-box models” into clinical practice thus requires institutions and researchers to place a significant amount of blind trust in the development process of the algorithms, as well as in the soundness of the data on which the models were trained, tested and validated. This is particularly problematic in clinical practice given the potentially devastating and long-lasting consequences of a faulty model to patients’ wellbeing (122).

Each model is unique and often requires a combination of mathematical equations, verbal descriptions and visual representations, such as Bayesian networks, to communicate and justify their inner workings (123). The development of interpretable models will not only improve trust in their logic but will also allow the users of the model to identify faulty or infeasible outputs. Furthermore, the ability to interpret and question a model’s behaviour may

reveal patterns and associations in data which would not be recognised by humans, providing valuable scientific insight. The importance of this is reflected in the considerable amount of research being carried out in the field of explainable AI (XAI) (124).

Observational data and causality

While it is clear that ML can be used to discover previously unknown associations in observational data, it is often forgotten that observational data cannot be used to directly infer causality. Establishing causality requires not only sufficient information about the environment of measured variables, but also the removal of various biases that undermine observational studies (125). RCTs meet both of these conditions and are thus considered the gold standard for deducing causality (126). Observational data, on the other hand, rarely contain enough contextual information to allow for robust causal data analysis. This is particularly problematic if correlations are mistaken for causation when developing health intervention models, which have a direct impact on clinical care (126). As most of the big data resources that are available for ML are cross-sectional observational data, rather than controlled clinical trials, solutions are needed to overcome these limitations. One strategy to infer causality from observational data is to model counterfactual predictions. Counterfactuals allow us to ask “What would have happened, had a different intervention been applied?”, rather than being limited to “What happened?” or “What will happen?” and this is a line of research that shows promise (123).

Algorithmic bias

Algorithmic unfairness poses another major obstacle to the translation of ML to clinical practice. Because ML models adaptively improve their performances by “learning” information directly from the data, the success of the model is acutely sensitive to data quality. Under-representation of minority subgroups in the dataset may create a blind spot in the model and introduce a discriminatory bias toward that group of patients (127). The problem is almost always an unintended property of the dataset and not the conscious choice of the researchers, but there is a risk of the model being implemented into practice with the algorithmic bias remaining undetected. For instance, multiple patients from African or unspecified ancestry had their benign genetic variants misclassified as pathogenic (128). The cause for

genetic misdiagnoses and potential health disparities was identified as the failure to account for genetic diversity in non-European populations at the time of testing. The misclassification was resolved with the inclusion of genetic data for African ethnic patients in the training groups (128). For this reason, algorithms should always be designed after careful consideration of all relevant variations in patient demographics and pathologic states in real-world settings. This is to ensure the training data truly represents the population of the intended deployment community.

Validation and generalisability

Other than technical limitations, there are other issues that obstruct the realisation of ML's potential in real-world practices. Medicine is an ever-changing field, where clinical and operational practices in clinical settings constantly evolve. The introduction of an ML algorithm may lead to a paradigm shift in normal practice. Subsequently, the input data will also change and no longer resemble the data that was used to train the model (129). To maintain performance over time, models should be constantly monitored for deteriorating performance and may need to be subjected to periodical recalibration or retraining. Dataset shift may occur due to the technical differences between institutions as well as variations in local clinical practices (130). Thus, it can be challenging to implement an ML model in a different setting to where it was originally trained. This issue can be mitigated by conducting site-specific training to adapt the existing model to a new study population. For instance, a deep learning model for diagnosing diabetic retinopathy from medical images failed to perform as expected when implemented across clinics in Thailand, partly due to the fact that the model was trained with images collected from clinics with different lighting conditions (131).

For all these reasons, the generalisability and real-world performance of the model need to be externally validated against adequately sized datasets from institutions other than where it was originally trained. However, there is a critical scarcity of public healthcare repositories at the present time. Multitudes of usage policies, security, and privacy concerns further add to the complexity of data collaboration (132). A 2019 systematic review for the diagnostic use of ML in medical imaging found that external validation was performed only on 6% of 516 published studies (133).

Finally, ML models, although not being a major concern at present, are susceptible to adversarial attack and manipulation (134). We must always be mindful that

machine learning models do not truly learn and understand their tasks – at least not in the same way that a human does. The models are simply a chain of mathematical algorithms, designed to mathematically map the input data to the targets. As such, ML models are brittle and can be easily fooled by explicitly designed inputs (134). For example, by adding the noise from a picture of a malignant mole to that of a benign mole, a study managed to trick the ML model into classifying the benign mole as malignant (135).

These findings highlight an alarming trend that AI studies are neither carried out nor reported with the same rigour as other medical research. To improve the quality of scientific AI investigations and to accelerate the clinical adoption of AI-based solutions, AI extensions have been added to both the SPIRIT (Standard Protocol Items: Recommendations for Interventional Trials) and CONSORT (Consolidated Standards of Reporting Trials) guidelines (SPIRIT-AI and CONSORT-AI, respectively) (136).

Conclusions

The realisation of precision medicine requires effective distillation of high-dimensional data across clinical, biological, patient-generated and environmental domains. AI, especially ML, is a critical enabler in this respect. The low-hanging fruit of ML in medicine are already successfully deployed in automating routine clinical processes to reduce the burden on clinical staff, for instance by prioritizing triage order in the emergency department or automating medical image evaluation. Whilst most of ML is currently based on analysis of observational data, which limits causal inference, the convergence of computational power, data, algorithms and greater traction with healthcare researchers has created the right inflection point for an exponential growth in rigorous discovery and implementation studies in precision medicine, as reflected in the number of publications in the area over the last five years. The hype hitherto associated with the precision medicine and ML narrative has waned with the growing realisation that ML is not a quick fix obviating the need for clinical and scientific expertise and scrutiny. However, to ensure that these applications are clinically useful and operationally feasible, a number of well-recognised methodological challenges still need to be overcome along with development of a rigorous framework for evidence generation demonstrating patient safety and benefit fulfilling all regulatory requirements.

Acknowledgments

Funding: SP and CdT acknowledge support from Health Data Research UK which receives its funding from HDR UK Ltd (HDR-5012) funded by the UK Medical Research Council, Engineering and Physical Sciences Research Council, Economic and Social Research Council, Department of Health and Social Care (England), Chief Scientist Office of the Scottish Government Health and Social Care Directorates, Health and Social Care Research and Development Division (Welsh Government), Public Health Agency (Northern Ireland), British Heart Foundation (BHF) and the Wellcome Trust.

Footnote

Provenance and Peer Review: This article was commissioned by the editorial office, *Journal of Hospital Management and Health Policy* for the series “AI in Healthcare - Opportunities and Challenges”. The article has undergone external peer review.

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at <http://dx.doi.org/10.21037/jhmhp-20-132>). The series “AI in Healthcare - Opportunities and Challenges” was commissioned by the editorial office without any funding or sponsorship. Sandosh Padmanabhan served as the unpaid Guest Editor of the series. Clea du Toit and Sandosh Padmanabhan acknowledge support from Health Data Research UK which receives its funding from HDR UK Ltd (HDR-5012) funded by the UK Medical Research Council, Engineering and Physical Sciences Research Council, Economic and Social Research Council, Department of Health and Social Care (England), Chief Scientist Office of the Scottish Government Health and Social Care Directorates, Health and Social Care Research and Development Division (Welsh Government), Public Health Agency (Northern Ireland), British Heart Foundation (BHF) and the Wellcome Trust. The authors have no other 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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doi: 10.21037/jhmhp-20-132

Cite this article as: Tran TQB, du Toit C, Padmanabhan S. Artificial intelligence in healthcare—the road to precision medicine. *J Hosp Manag Health Policy* 2021;5:29.