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REVIEW

Role of artificial intelligence in haematolymphoid diagnostics

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Role of artificial intelligence in haematolymphoid diagnostics

The advent of digital pathology and the deployment of high-throughput molecular techniques are generating an unprecedented mass of data. Thanks to advances in computational sciences, artificial intelligence (AI) approaches represent a promising avenue for extracting relevant information from complex data structures. From diagnostic assistance to powerful research tools, the potential fields of application of machine learning techniques in pathology are vast and constitute the subject of considerable research work. The aim of this article is to provide an overview of the potential applications of AI in the field of haematopathology and to define the role that these emerging technologies could play in our laboratories in the short to medium term.

Keywords: artificial intelligence, haematopathology, lymphoma diagnosis

Introduction

Lymphomas are among the ten most common cancers worldwide,[1] and are characterized by considerable clinical and biological heterogeneity, with variable prognosis and therapeutic response.[2,3] Lymphoma diagnosis requires in-depth histological analysis by expert pathologists, and relies on ancillary tissue staining techniques, now increasingly combined with molecular analyses (fluorescence *in situ* hybridization [FISH], clonality, high-throughput sequencing). However, access to these sophisticated technologies is limited, and the risk of misdiagnosis by nonexpert pathologists remains high, as demonstrated in a French nationwide study (*Lymphopath* Network), which showed that 20% of the diagnoses are inaccurate, with a direct impact on patients' treatment.[4,5] Recent major breakthroughs in deep-learning

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Abbreviations: AI, artificial intelligence; AUCROC, area under the receiver operating characteristic curve; CLL, chronic lymphocytic leukemia/lymphocytic lymphoma; COO, Cell Of Origin; DLBCL, diffuse large B-cell lymphoma; FISH, fluorescence in situ hybridization; FL, follicular lymphoma; H&E, haematoxylin-eosin; IPI, international prognostic index; MIPI-b, biologic-Mantle cell lymphoma international prognostic index; ML, machine learning; NLP, natural language processing; WSI, whole slide image.

techniques have led to wider applications of artificial intelligence (AI) in medicine. In histological pathology, access to whole-slide imaging offers the possibility to apply AI approaches to high-resolution images to extract features in order to develop diagnostic/classification tools and prediction algorithms.

AI encompasses a broad range of techniques and approaches aimed to perform tasks that typically require human intelligence. AI approaches are able to analyse large datasets, extract meaningful insight, and perform complex tasks autonomously or semiautonomously.[6] Recently, several advances have been made in incorporating AI to the diagnostic workflow in pathology for assisting and augmenting the pathologist's capabilities, especially in the field of solid cancers.[7–10] AI-based automated image analysis approaches can be used to extract various morphometric features from digitized haematoxylin-eosin (H&E)-stained slides, and could help to overcome the limitations of subjective visual assessment and capture the complexity of tissue architecture that is sometimes undetectable to the human eye. AI approaches applied to pathology could also synthesize complex phenotypic and molecular data, providing pathologists with precious diagnostic aids, and even predicting prognosis and therapeutic response on the basis of microscopic images alone.[7] In this review we consider these emerging AI technologies as applied to haematopathology, focusing on histology and molecular pathology, both for the production of diagnostic aids and for the development of exploratory approaches aimed at extracting new information useful for classification, patient stratification, and treatment response prediction.

Prerequisite: AI concepts

AI is the branch of computer science and engineering that consists of developing human-like intelligent computers or machines. Belonging to the field of AI, machine learning (ML) involves the development of algorithms that can automatically learn and predict results from data and improve their performance over time without being explicitly programmed (Figure 1A). ML consists of algorithms discovering patterns (i.e. recurrent motifs) in datasets. There are three main stages in the development of an ML model. The first step consists of selecting and preparing a set of training data that will be used to feed the ML model to learn how to solve the problem for which it is designed. The spectrum of ML ranges from methods entirely guided by humans to those entirely guided by machines. ML can be categorized into three main types: supervised ML, unsupervised ML, and reinforcement ML (Figure 1B). In supervised ML, the algorithm is trained on labelled data (input data are provided to the system with their desired output). During the training step, the algorithm learns how to predict outputs from inputs. Conversely, in unsupervised learning, the training data have no labels leading the algorithm to explore data and find possible patterns on its own. Such an approach requires a vast amount of data to extract relevant features required to sort and classify data without human intervention. Finally, reinforcement learning consists of letting an algorithm learn from its mistakes to reach the most optimal results. In all cases, the training dataset must be carefully chosen and must be representative of original data to avoid any bias that would have a direct impact on the results of future predictions. The second step is to select an algorithm to run on the training dataset. The type of algorithm (regression algorithms, decision tree, random forest, support-vector networks, artificial neural networks, etc.) depends on the type and volume of training data and the type of problem to be solved. The third step involves training the algorithm through an iterative process in which variables are run through the algorithm and the results are compared with those it should have produced. Weights and bias are then adjusted to increase the accuracy of the results. Three datasets are commonly used in different stages of the development of an ML model: training, validation, and test sets. The training dataset is used to fit the parameters. The validation dataset provides an evaluation of the model on unseen data while tuning the model's hyperparameters. Finally, the test dataset is used to provide an unbiased evaluation of the final ML model.

Deep learning is a subset of ML that uses multilayer neural networks to learn intricate representations of data (Figure 1A). Neural networks are algorithms consisting of several layers. The first layer inputs the data, hidden layers draw conclusions from the input data, and the last layer assigns a probability to each conclusion. Each hidden layer refines the results of the previous layer.

Implementation of AI as a diagnostic assistance tool in pathology practice

H&E SLIDE ANALYSIS FOR DIAGNOSIS AND CLASSIFICATION

The diagnosis of cancers relies on the microscopic analysis of histological slides by pathologists. This

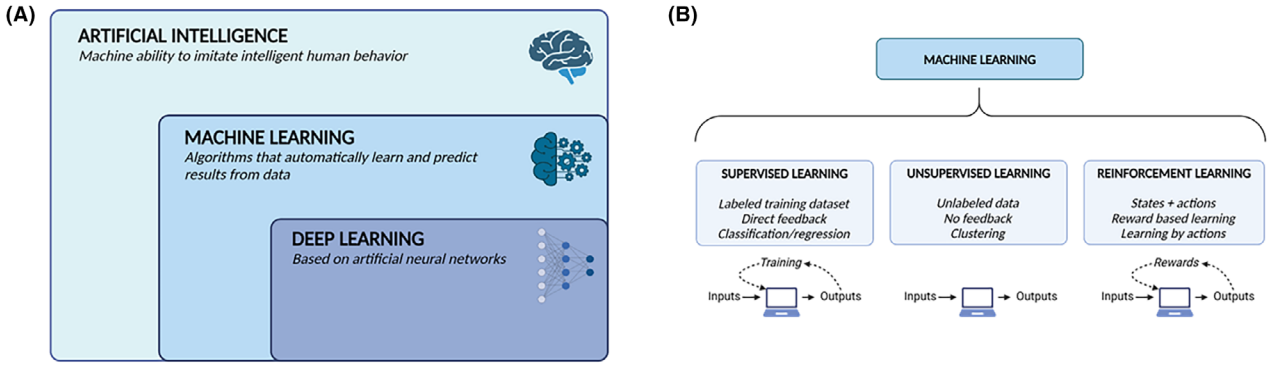

Figure 1. Diagrams illustrating differences between artificial intelligences approaches (**A**) and the three main types of machine-learning methods (**B**). (**A**) Machine learning is a subfield of artificial intelligence. Deep learning is a further subset of machine learning. (**B**) Differences between supervised learning, unsupervised learning, and reinforcement learning. *Created with BioRender.com*.

exercise requires years of training and experience, but remains subjective and not always reproducible. This is particularly the case for lymphoma diagnosis, which can be challenging, especially for nonexpert pathologists due to the rarity of this pathology, which can manifest in around a hundred subtypes, identification of which is crucial for optimal therapeutic management.

By learning from vast datasets of digital slides, AI algorithms can automatically identify features and patterns that might be overlooked by the human eye and thus have the potential to greatly improve standardization and diagnostic performance. Automating analysis saves time, improves reproducibility and, in some complex cases, may provide a complement to the pathologist's eye.

In the field of haematopathology, AI models have shown promising results for the detection and classification of lymphomas from whole-slide images (WSIs) with areas under the receiver operating characteristic curve (AUROC) often exceeding 0.90.[5,11–18] However, all these algorithms focus on diagnosing only a few subtypes of the most common lymphomas, such as diffuse large B-cell lymphoma (DLBCL), follicular lymphoma (FL), and chronic lymphocytic leukaemia/lymphocytic lymphoma (CLL), and are far from being able to diagnose the range of lymphoid lesions identified in international classifications. Therefore, the ML approaches currently published do not replicate, to date, the diagnostic approach of the pathologist who, in daily practice, must be able to recognize nearly 100 different subtypes of lymphomas in addition to the reactive lesions, which are also very varied. In haematopathology, the rarity of many subtypes of lymphomas constitutes a major limitation to building exhaustive datasets for training neural networks. To be used in clinical practice, it is therefore essential that the predictions made by AI algorithms be associated with a confidence index to identify any lesions that the algorithm may have failed to classify with a definite degree of certainty. This would enable pathologists not to rely on AI predictions made with a low confidence index. Without replacing the pathologist, automated image analysis should ultimately provide rapid, reproducible, and accurate diagnostic guidance to prevent certain diagnostic errors and guide the prescription of relevant complementary immunohistochemical and molecular techniques for diagnosis.

Beyond lymphoma classification, AI approaches can also standardize grade assignment (follicular lymphoma)[19] and identify progressions (accelerated phases or transformation of CLL)[20] or aggressive subtypes.[15] Indeed, the assignment of these characteristics relies on visual analysis by the pathologist, which is subject to considerable interobserver variability, with potential impact on treatment and prognosis.[4,5,21] Few publications are found on the subject in haematopathology, but recent studies have shown that AI tools could improve the extraction of morphological and architectural features relevant for detecting an accelerated phase or transformation of CLL, which is sometimes difficult to identify.[20,22] These AI approaches could thus eventually constitute a more robust and reproducible tool than the pathologist's eye for grade assignment and detection of aggressive morphological variants. Moreover, beside standardizing assessment of long-standing morphological criteria, AI should also identify new morphological biomarkers related to clinical behaviour.

AUTOMATED ANALYSIS OF IMMUNOHISTOCHEMICAL MARKERS AND FISH IMAGES

The diagnosis of lymphoma relies on the analysis of numerous immunohistochemical markers and, in some cases, on fluorescence *in situ* hybridization (FISH) techniques, which have become indispensable for diagnosing particular lymphoma entities (such as Burkitt lymphoma, high-grade B-cell lymphomas with *MYC* and *BCL2* rearrangements, and some cases of follicular lymphoma, mantle cell lymphoma, and other rare lymphoma entities).[2,3] These analyses are labour-intensive and subject to interpretation. They could therefore be optimized by using automated image analysis approaches, which provide more objective and comprehensive means of quantification. The deployment of automated image analysis tools for immunohistochemistry markers and FISH images has two main objectives: to assist pathologists in their diagnosis and to develop potential new biomarkers.

For example, the Ki67 proliferative index is one of the main prognostic markers in mantle cell lymphoma and is included in the calculation of the MIPI-b (biologic-Mantle cell lymphoma International Prognostic Index) score, which guides therapeutic decisions. However, the method to quantify Ki67 staining and the cutoff values vary from one study to another.[23–26] This disparity is at least in part due to interobserver variability. Automated image analysis and machine-learning approaches could help standardize Ki67 assessment and determine the best threshold for patient stratification.[27] Beyond image analysis, AI can also improve the processing of immunohistochemical data. For example, in DLBCL, ML-based algorithms for immunohistochemical classification into COO (Cell of Origin, i.e. germinal centre or nongerminal centre subtypes) achieved better performance compared to the gold standard Hans algorithm.[28–30]

Finally, FISH techniques can be used to identify chromosomal rearrangements or gene fusions and to detect chromosome number anomalies or gene amplifications. With the emergence of digital pathology, the digitization of FISH slides has increased the comfort and speed of interpretation. This has also facilitated the use of automated FISH image capture and analysis systems.[31] Besides saving time and enabling analysis of a large number of nuclei, these tools standardize counting methods and positivity thresholds. They also enable the development of methods to compensate for truncated nuclei in tissue sections and to detect aneuploidies and alternative fusion partners.[31]

STANDARDIZATION AND ASSISTANCE FOR THE INTERPRETATION OF GENOMIC DATA

Lymphoma classification is essential to guide therapeutic management and is increasingly based on genomic data obtained through molecular sequencing methods. High-throughput sequencing generates a large number of variants, which interpretation represents a critical step. Indeed, the classification of variants in pathogenic/probably pathogenic/of uncertain significance/probably benign/or benign classes conditions its inclusion in the final diagnosis. This variant classification is based on a combination of factors and is partly carried out manually by pathologists or biologists with potential interobserver variability, particularly regarding the class of variants of uncertain significance and their consideration or not for molecular profile interpretation. Factors taken into account for interpretation have varying weights and are integrated in bioinformatics algorithms that are highly hand-engineered. They include epidemiological data (databases), clinical criteria, co-occurrence of variants, predictive bioinformatics, and functional data.[32,33] However, unlike solid cancers, molecular data serving almost exclusively for classification purposes and not as therapeutic target, no practice guidelines exist for interpreting clinical relevance of genomic variants found in the context of lymphomas. This lack of consensus and the paucity of reference samples make the interpretation challenging and particularly prone to interobserver variability. AI approaches could thus help standardize the interpretation of variants and offer the possibility of deeper data analysis to improve the molecular diagnosis of lymphomas. Clinical genomics not only exploits classical genomic data from targeted, whole-exome or whole-genome sequencing, but also RNA-sequencing, methylation analyses, copy number variation analyses, and others as sources of information.

Deep-learning-based methods have recently been developed to improve variant calling and somatic mutation detection with better accuracy compared to conventional bioinformatics tools.[34,35] Besides the optimization of basic bioinformatics tasks, ML tools can also be used to help classify lymphomas by analysing genomic data. For example, gene expression data were used in several studies to train ML algorithms to recognize and distinguish different lymphoma entities/subtypes.[36–38] For example, Bobée *et al.* trained a random forest algorithm to discriminate the seven most frequent B-cell non-Hodgkin lymphoma entities from gene expression data.[36] While not replacing histological diagnosis, which

remains essential, this screening test could be used as a complementary diagnostic tool, helping the pathologist to make an accurate diagnosis. However, the main limitations to the use of AI approaches for the molecular diagnosis of lymphoma is the paucity of available data due to the rarity of certain lymphoma entities, on the one hand, and to the fact that high-throughput sequencing is not yet widely adopted as the standard of care in clinical pathology laboratories. Thus, most studies focus on DLBCL, which remains the lymphoma entity offering the largest databases, including, in particular, molecular data. For example, ML can be used to categorize DLBCL patients into distinct molecular subtypes based on gene expression patterns.[39–41] More recently, Zhang *et al.* identified nonmutually exclusive genetic signatures in DLBCL through an AI-driven bioinformatics system.[42] In conclusion, although AI approaches offer significant potential to improve the molecular diagnosis of lymphomas by enhancing variant interpretation and facilitating subtype classification, their current application is limited by the scarcity of comprehensive databases and the still constrained access to high-throughput sequencing techniques in laboratories. Further research and expansion of genomic databases will be crucial to overcome these challenges and take full advantage of the benefits of AI in lymphoma molecular diagnostics.

AI-based exploratory approaches

PREDICTING MOLECULAR ALTERATIONS/SIGNATURES FROM H&E SLIDES

Analysis of the tumour genome is becoming more and more important for diagnostic, prognostic, and predictive purposes. However, molecular analyses are expensive, time-consuming, and require a well-trained staff and significant investments in infrastructure. As H&E morphology reflects the genetic and epigenetic makeup of the tumour cells, analysis of the morphology could be used to predict the underlying genetic defects in a tumour.[43–46] As H&E slides are readily available, this could save time and costs. In solid tumours, deep-learning based on histopathology images has been used to predict the presence of mutations in multiple tumour types. For example, in nonsmall cell lung cancer, a subset of frequently occurring mutations could be predicted, based on H&E slides with an AUROC of 0.73–0.86.[46] In gastrointestinal carcinoma, multiple deep-learning models have been used to predict the presence of microsatellite instability with an AUROC of up to 0.96 in a large international cohort.[47–49] Such a model could be useful in daily practice as an automated screening tool to sort patients for confirmatory testing, potentially reducing the number of patients tested, resulting in substantial savings in terms of labour and testing costs. In addition to specific tumour types, deep-learning approaches have also been used with success across tumour types to predict molecular alterations, although the detection rate of mutations varies between the tumour subtypes and genes investigated.[45,50]

Associations between morphology and underlying genetic alterations are also well-established in lymphomas and these form the basis of the 'entity-based approach' in the classification system in which morphology, immunophenotype, clinical presentation, and molecular alterations are combined to come to a specific diagnosis. For example, a morphology which is consistent with mantle cell lymphoma or hairy cell leukaemia is strongly associated with the presence of a *CCND1* rearrangement or *BRAF* mutation, respectively. With the advent of AI, there is a potential to find more subtle associations between morphology and genetic alterations in lymphoma with a high accuracy in comparison with assessment by a pathologist. To date, a small number of studies have been published on this topic, limited to large B-cell lymphoma. Three studies in DLBCL used machine learning on H&E morphology to predict the presence of a *MYC* rearrangement, resulting in an AUROC of 0.68–0.83.[51–53] In another study on 57 large B-cell lymphomas, the presence of 'double or triple hit' rearrangements (i.e. the presence of both an *MYC* and a *BCL2* and/or *BCL6* rearrangement) based on H&E slides could be predicted with a sensitivity of 100% and a specificity of 87%; however, this was a single-centre study on a small number of selected of samples.[54] Taken together, these H&E morphology-based deep-learning models offer promising potential for predicting genetic alterations in tumours, including lymphomas. These AI-driven approaches could significantly reduce costs and rationalize molecular diagnostics by serving as automated screening tools that complement traditional pathology. However, their widespread clinical application is currently limited by the need for further validation in larger, more diversified cohorts.

PREDICTING PROGNOSIS AND RESPONSE TO THERAPY

To predict prognosis and response to therapy based on characteristics of the tumour and its

microenvironment, multiple types of information can be used as input for AI analysis, including H&E morphology, immunophenotype, and gene expression profiles.

In a recently published study, H&E slides were used to predict the response to R-CHOP immunochemotherapy in DLBCL.[55] Based on histopathology only, an AUROC of 0.74 was found. Interestingly, morphological features that are known to have prognostic relevance, such as centroblastic or anaplastic morphology, were predictive of response to therapy.[55] These morphological features have been part of earlier classifications, but were abandoned due to high intra- and interobserver variability, which could be addressed by automatic AI-based quantification or analysis approaches.

AI analysis of gene expression profiles has been used to identify relevant data both across lymphoma entities and within specific types of lymphoma. Using AI to analyse results from gene expression profiling in 184 patients with follicular lymphoma allowed prediction of overall survival based on the expression of 43 genes.[56] In DLBCL, analysis of gene expression data with AI has been used to predict the clinical course,[57,58] response to bortezomib,[59] and to determine the cell-of-origin classification.[60,61] Compared to classic supervised and unsupervised clustering approaches in gene expression data analyses, AI models, especially deep learning, excel at processing complex and high-dimensional datasets. Moreover, by uncovering subtle patterns and relationships that might not be apparent with classic methods, AI can provide deeper biological insights and improve prediction accuracy in both research and clinical applications.

EXPLORATORY INTEGRATIVE APPROACHES

Tumours can be studied on many different levels and the tools used are generating an ever-growing amount of data. Prognostic or predictive information can be present in clinical data, radiology, microscopic morphology, data from gene expression analysis, and (epi)genetic data and AI has the potential to allow an integrative analysis of data from different sources. As data from these different 'magnifications' do not stand alone but are strongly related (i.e. a certain genetic alteration could change protein expression levels to generate aggressive microscopical features and an aggressive clinical presentation), studies into integrative analysis of data from different sources could teach us which types of data are most informative. At present, these multimodal approaches are still used infrequently, but this is increasing. For studies combining morphology and genetic data, almost two-thirds of the studies were published in the past 2 years according to a recent systematic review.[62] No multimodal studies using primary morphological and genetic data in lymphoma were identified in that review.

There have been integrative studies in lymphoma that used machine learning to analyse large datasets containing different types of data. In high-grade B-cell lymphoma, Kong *et al.* used machine learning to generate a prognostic model based on data from morphology, immunophenotype, and clinical features.[63] They identified several independent risk factors for high-grade B-cell lymphoma and showed that first-line treatment with R-CHOP had dismal efficacy in this aggressive lymphoma subtype.[63] Another study used data from national lymphoma registries to predict outcome in DLBCL and showed a better performance than the international prognostic index (IPI) score.[64]

Despite the encouraging performance of existing computational pathology approaches, the performance of task-specific ML models depends on the availability of many annotated training datasets, which is a limiting factor for the development of AI in pathology. Recently, self-supervised learning has shown promising results in exploiting unlabelled data to pretrained foundation models in the medical domain.[65–68] Foundation models, the latest generation of AI approaches, are very large task-agnostic AI models trained using massive unannotated datasets. Foundation models learn general-purpose feature representations and can then be adapted to more specific downstream tasks using a modest amount of task-specific annotated data. Foundation models are robust and generalizable across different datasets and patient populations. This is crucial in pathology, where variability in staining techniques, image quality, and patient demographics can affect the accuracy of traditional models. Generative AI is another advanced AI approach that can be used in digital pathology to create synthetic data, enhance image quality, and even simulate disease progression. While these technologies hold great promise in digital pathology, their integration into clinical practice is hampered by limitations related to data availability, computational demands, interpretability, and regulatory and ethical concerns.

Finally, using text mining or natural language processing (NLP) algorithms, ML approaches can also be used to explore, extract, and structure the information contained in complex reports, allowing the use of unstructured data for data analysis.[69] In the

medical domain, unstructured text data (i.e. free-text reports without a specific format) represent a rich source of information. NLP encompasses a wide range of AI techniques that addresses the interpretation and comprehension of texts to obtain structured information. In the last decade, several advances in the field of pathology have resulted from the application of NLP to pathology reports. For example, NLP can process patients' clinical information useful for diagnosis and assist the pathologist in generating an accurate diagnostic report. NLP approaches could also be used for data analysis and visualization to increase interoperability between information systems.[70]

Figure 2 illustrates the potential implementations of AI approaches in haematopathology as diagnostic assistance tools and exploratory approaches.

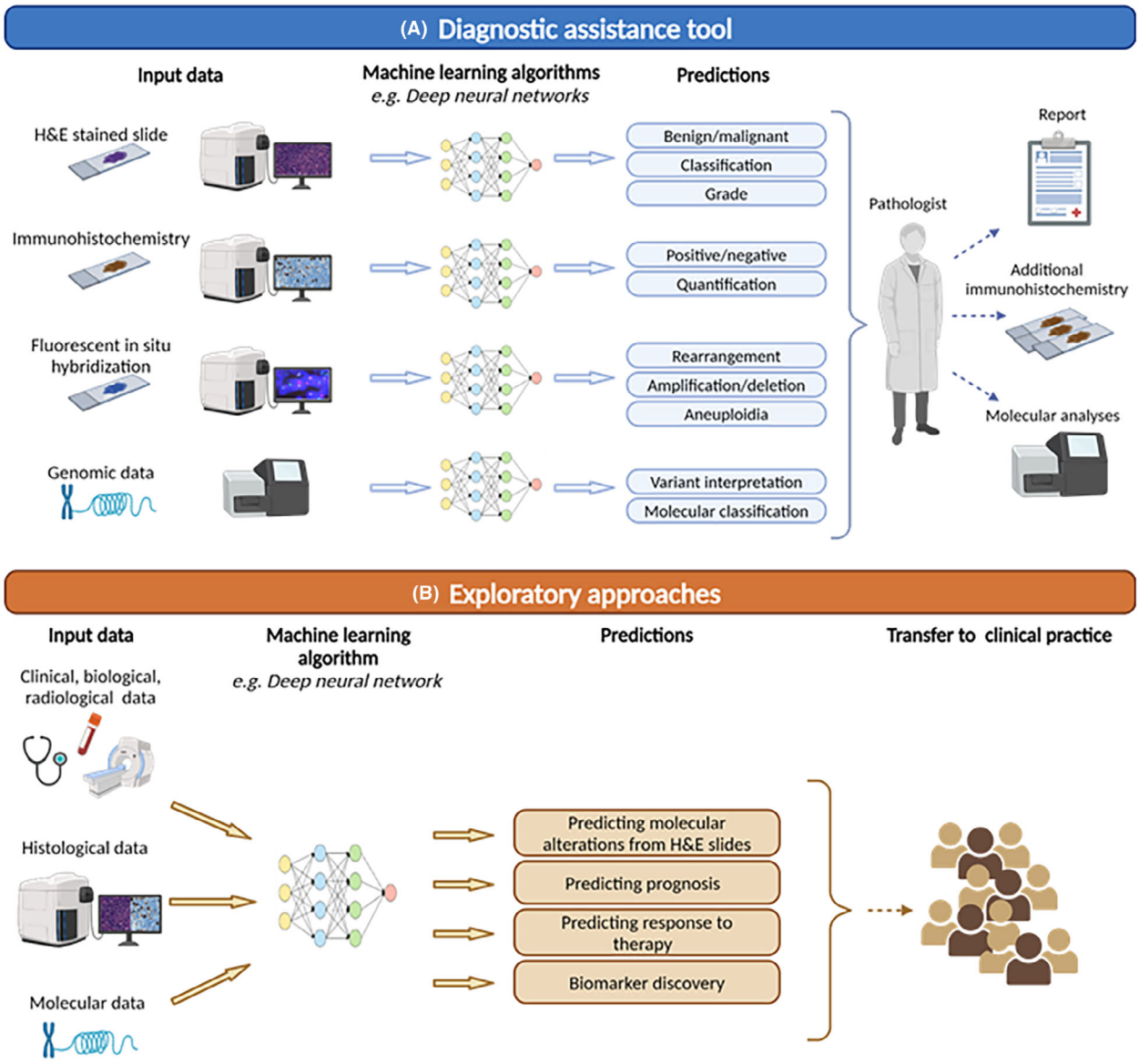

Figure 2. Workflows of artificial intelligence implementations in haematopathology as diagnostic assistance tools (**A**) and in exploratory approaches (**B**). (**A**) Depending on the input data, machine-learning algorithms can be designed for diagnosis and classification purposes, automated analysis/quantification of immunohistochemical and FISH images, standardization, and assistance for the interpretation of genomic data. (**B**) Exploratory approaches include multimodal data integration to predict molecular alterations, prognosis, and response to therapy, as well as to discover new biomarkers. *Created with BioRender.com.*

Current limitations and challenges of AI in pathology

Although the use of AI in haematopathology has a large potential to improve the diagnostic process and interpretation of research data, its application is currently still limited. To implement AI tools in diagnostic practice requires a thoroughly validated application that is preferably directly available within the image management system and easy to use. It is also most easily implemented if the workflow is already strongly digitized, which is presently not the case for many laboratories. It is expected that many new algorithms for digital pathology will complete the implementation phase in the coming years, but at present this number is still limited to ~50 applications with CE certification in Europe and six applications in the field of pathology with FDA approval in the United States. These applications mostly focus on solid tumours, and dedicated applications for haematopathology are currently lacking.[71]

For predicting genetic alterations based on H&E morphology in lymphoma, studies have proven the concept that this is possible but the sensitivity and specificity are still too low for use in diagnostic purposes. In the future, it might be a first step to use H&E slides to predict either the absence (high sensitivity) or the presence (high specificity) of a genetic lesion with a high level of certainty. In solid tumours, CE approved algorithms are available that predict the presence of microsatellite instability in colorectal carcinoma and different types of genetic lesions in prostate carcinoma.[72]

For researchers, AI has become a readily accessible tool to analyse complex datasets. However, although user-friendly tools exist, it is often necessary to develop tailored solutions that requires researchers to have or develop basic programming skills.[6]

Another drawback of many current AI tools is the lack of explainability. Although explainability methods are used increasingly, many AI algorithms are still black boxes that are particularly problematic in medicine.[73]

Finally, the deployment of AI in clinical settings raises significant ethical concerns and requires the establishment of robust regulatory frameworks to ensure patient safety and data privacy. The use of AI in clinical decision-making raises questions about the balance between machine autonomy and human supervision. It is essential to determine the extent to which clinicians should rely on AI rather than use it as a support tool.

Conclusion

Currently still in the development stage, AI approaches have a vast range of applications in haematopathology. They enable the management of big data and bring a new dimension to morphological analysis through the automated analysis of histological slides. By allowing the exhaustive extraction of information at various levels of complexity regarding both the tumour and its microenvironment, these computational tools generate a significant amount of information that, in the short- or medium-term, should be integrated into our practices to optimize diagnosis and patient stratification. Eventually, AI-generated results are expected to become part of the criteria that define lymphoma entities. In this respect, it is important to take into account the fact that the use AI tools is costly and not available everywhere.

Applying AI to the diagnosis of rare lymphoma subtypes represents a major challenge, particularly due to data scarcity. Federated learning (AI models training on data from multiple institutions without the data leaving its original location) and collaborative efforts among research institutions and pathology labs should enable the access to larger combined datasets of rare lymphomas. Furthermore, advanced AI techniques, such as generative AI and foundation models, also offer a promising solution to overcome the challenges posed by data scarcity by improving diagnostic accuracy even with limited data.

One of the advantages of AI applied to digital pathology is that it allows simultaneous examination of histopathological images and patient metadata, such as epidemiologic and molecular data, as well as clinical evolution and therapeutic response. Without replacing microscopic analysis, these combined molecular and computational approaches could eventually provide valuable assistance to pathologists, who are often faced with difficult diagnoses. However, the pathologist will always be necessary to validate the performance of the algorithms and control the results they produce. Integrating AI into real-time diagnostic workflows in pathology labs must be carefully managed to ensure it complements the expertise of pathologists and improves patient outcomes. Pre-implementation considerations include validation and regulatory approval, as well as infrastructure readiness with the need of necessary IT infrastructure, including high-performance computing systems and secure data storage. Initially, AI could be introduced through pilot programs in select pathology labs,

focusing on specific diagnostic tasks. Moreover, in high-volume labs, AI could be used first to automate routine diagnostic tasks, enabling pathologists to focus on complex cases. The success of AI in haematopathology, and digital pathology in general, will require the active participation of pathologists, and in our sense the most promising applications of AI will be those that enhance pathologist expertise rather than replace it. Moreover, the AI scope of applications and regulatory framework remain to be defined before its deployment in the clinical environment.

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CS, MVDB, JNK, and CL wrote the article together.

Conflict of interest

CS, MVDB, and CL declare no relevant conflict of interest. JNK declares consulting services for Owkin, France; DoMore Diagnostics, Norway; Panakeia, UK; AstraZeneca, UK; Scailyte, Switzerland; Mindpeak, Germany; and MultiplexDx, Slovakia. Furthermore, he holds shares in StratifAI GmbH, and Synagen GmbH Germany, has received a research grant by GSK, and has received honoraria by AstraZeneca, Bayer, Eisai, Janssen, MSD, BMS, Roche, Pfizer, and Fresenius.

Data availability statement

Data sharing not applicable to this article as no datasets were generated or analysed during the current study.

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