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CAPABILITIES OF ARTIFICIAL INTELLIGENCE IN MODERN RHEUMATOLOGY. LITERATURE REVIEW

Yuliya V. Petrova[1], https://orcid.org/0000-0003-1910-7169

Maiya V. Goremykina[1], https://orcid.org/0000-0002-5433-7771

Raifa L. Ivanova[1], https://orcid.org/0000-0001-9851-2255

Dana K. Kozhakhmetova[1], https://orcid.org/0000-0002-8367-1461

Ainur S. Botabayeva[1], http://orcid.org/0009-0008-9228-7788

Alexandra A. Razvodova[2], http://orcid.org/0009-0004-2016-6400

[1]NCJSC «Semey Medical University», Semey, Republic of Kazakhstan;
[2] LLT "Gippokrat", Kostanay, Republic of Kazakhstan.

Abstract

Relevance: The application of artificial intelligence (AI) in clinical practice opens new opportunities to improve diagnostic and prognostic accuracy in rheumatology, a field characterized by high disease heterogeneity and the complexity of interpreting visual and clinical data

Search strategy: An analysis was conducted on 58 publications selected from 467 relevant sources (2015–2025), identified through PubMed, Google Scholar, and CyberLeninka databases. Included were original studies and review articles focused on the use of machine learning and deep learning methods in rheumatology.

Results: AI is increasingly being implemented to address tasks related to early diagnosis, disease course prediction, and personalized therapy selection in rheumatoid arthritis, spondyloarthritis, systemic lupus erythematosus, and osteoarthritis. Convolutional neural networks, multi-omics approaches, and adaptive prediction models were found to be the most effective, demonstrating high accuracy (with AUC values up to 0.85). Despite this potential, clinical integration remains limited due to small training datasets, the need for external validation, and insufficient model standardization.

Conclusions: AI holds significant practical value in rheumatology. Its integration into healthcare systems requires regulatory frameworks, medical staff training, the development of digital infrastructure, and interdisciplinary collaboration.

Keywords: *artificial intelligence; deep learning; machine learning; neural networks; rheumatology.*

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Резюме

ВОЗМОЖНОСТИ ИСКУССТВЕННОГО ИНТЕЛЛЕКТА В СОВРЕМЕННОЙ РЕВМАТОЛОГИИ. ОБЗОР ЛИТЕРАТУРЫ

Юлия В. Петрова[1], https://orcid.org/0000-0003-1910-7169

Майя В. Горемыкина[1], https://orcid.org/0000-0002-5433-7771

Райфа Л. Иванова[1], https://orcid.org/0000-0001-9851-2255

Дана К. Кожахметова[1], https://orcid.org/0000-0002-8367-1461

Айнур С. Ботабаева[1], http://orcid.org/0009-0008-9228-7788

Александра А. Разводова[2], http://orcid.org/0009-0004-2016-6400

[1] НАО «Медицинский университет Семей», г. Семей, Республика Казахстан;
[2]ТОО "Гиппократ", Костанай, Республика Казахстан.

Актуальность: Применение искусственного интеллекта (ИИ) в клинической практике открывает новые возможности для повышения точности диагностики и прогнозирования в ревматологии, где характерна высокая гетерогенность заболеваний и сложность интерпретации визуальных и клинических данных.

Стратегия поиска: Проведен анализ 58 публикации, отобранных из 467 релевантных источников (2015–2025 гг.), идентифицированных в базах PubMed, GoogleScholar и CyberLeninka. Включены оригинальные исследования и обзорные статьи, посвященные применению методов машинного и глубокого обучения в ревматологии.

Результаты: ИИ активно внедряется для решения задач ранней диагностики, прогнозирования течения и подбора терапии при ревматоидном артрите, спондилоартритах, системной красной волчанке и остеоартрите. Наиболее эффективными оказались сверточные нейронные сети, мультиомные подходы и адаптивные модели прогнозирования, демонстрирующие высокую точность (до AUC до 0,85). Несмотря на значительный потенциал,

клиническое применение затруднено из-за ограниченности обучающих выборок, необходимости внешней валидации и недостаточной стандартизации моделей.

Заключение: ИИ обладает высокой прикладной ценностью в ревматологической практике. Для интеграции в систему здравоохранения необходимы нормативное регулирование, подготовка медицинского персонала, развитие цифровой инфраструктуры и междисциплинарное сотрудничество.

Ключевые слова: *искусственный интеллект, глубокое обучение, машинное обучение, нейронные сети, ревматология.*

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Түйіндеме

ҚАЗІРГІ РЕВМАТОЛОГИЯДАҒЫ ЖАСАНДЫ ИНТЕЛЛЕКТІНІҢ МҮМКІНДІКТЕРІ. ӘДЕБИЕТТІК ШОЛУ

Юлия В. Петрова[1], https://orcid.org/0000-0003-1910-7169

Майя В. Горемыкина[1], https://orcid.org/0000-0002-5433-7771

Райфа Л. Иванова[1], https://orcid.org/0000-0001-9851-2255

Дана К. Кожахметова[1], https://orcid.org/0000-0002-8367-1461

Айнур С. Ботабаева[1], http://orcid.org/0009-0008-9228-7788

Александра А. Разводова[2], http://orcid.org/0009-0004-2016-6400

[1] «Семей медицина университеті» КеАҚ, Семей қ., Қазақстан Республикасы.
[2] "Гиппократ" ЖШС, Қостанай, Қазақстан Республикасы

Өзектілігі: Клиникалық тәжірибеде жасанды интеллектіні (ЖИ) қолдану ревматология саласында диагноз қою мен болжау дәлдігін арттыру үшін жаңа мүмкіндіктер ашады. Бұл салада аурулардың гетерогенділігі және визуалды әрі клиникалық деректерді түсіндірудегі күрделілік жоғары.

Іздеу стратегиясы: PubMed, Google Scholar және CyberLeninka дерекқорларынан анықталған 467 дереккөздің ішінен іріктелген 58 ғылыми жарияланымға талдау жүргізілді (2015–2025 жж.). Ревматологияда машиналық және терең оқыту әдістерін қолдануға арналған түпнұсқалық зерттеулер мен шолу мақалалары қарастырылды.

Нәтижелер: ЖИ ерте диагностикалау, ауру барысын болжау және жекелендірілген емді таңдау міндеттерін шешу үшін кеңінен енгізілуде. Бұл ретте ревматоидты артрит, спондилоартрит, жүйелі қызыл жегі және остеоартрит сияқты аурулар қарастырылған. Ең тиімді әдістер ретінде — өте дәл нейрондық желілер, мультиомдық тәсілдер және бейімделген болжамдық модельдер танылды. Олар жоғары дәлдікпен (AUC 0.85-ке дейін) ерекшеленді. Дегенмен, оқыту деректерінің шектеулілігі, сыртқы валидация қажеттілігі және модельдерді стандарттаудың жеткіліксіздігі клиникалық қолдануға кедергі келтіруде.

Қорытынды: Жасанды интеллект ревматологиялық тәжірибеде жоғары қолданбалы құндылыққа ие. Денсаулық сақтау жүйесіне интеграциялау үшін нормативтік реттеу, медициналық персоналды даярлау, цифрлық инфрақұрылымды дамыту және пәнаралық ынтымақтастық қажет.

Түйінді сөздер*: жасанды интеллект, терең оқыту, машинамен оқыту, нейрондық желілер, ревматология.*

Дәйексөз үшін:

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Introduction:

The rapid advancement of artificial intelligence (AI) has ushered in a new era in clinical medicine, where precision and standardization of diagnostic decision-making are becoming equally essential. In the field of rheumatology - marked by heterogeneity in clinical presentation and disease trajectory - AI has the potential to enhance consistency and reproducibility in diagnostic algorithms and therapeutic planning [41].

In particular, AI technologies are increasingly being applied to address variability in the interpretation of clinical, laboratory, and imaging data in diseases such as rheumatoid arthritis (RA), ankylosing spondylitis (AS), psoriatic arthritis (PsA), systemic lupus erythematosus (SLE), and osteoarthritis (OA). Neural networks have demonstrated the ability to identify signs of joint inflammation in radiographs and even to generate synthetic computed tomography (CT) images, enabling standardized and non-invasive disease assessment [22, 40].

Beyond diagnosis, AI contributes to patient stratification, treatment optimization, and outcome prediction. The ability to forecast disease progression and the likelihood of flares is especially critical in chronic inflammatory conditions,

where timely therapeutic interventions can significantly alter patient trajectories [39].

Despite these advancements, several barriers remain. Integrating heterogeneous data—ranging from clinical records and imaging to molecular and behavioral data—demands robust, high-quality training datasets. Moreover, the development of explainable and generalizable models remains a methodological challenge. Nevertheless, promising studies demonstrate the feasibility of AI applications in predicting RA exacerbations and identifying metabolomic profiles associated with gout flares, indicating the maturity of this research domain [27, 55, 56].

The potential of AI in healthcare is of particular relevance to Kazakhstan. While foundational steps such as electronic health records (EHRs) implementation and telemedicine platforms are being developed in major cities like Astana and Almaty, the broader adoption of AI in rheumatologic care remains limited [1, 34]. Key obstacles include underdeveloped digital infrastructure in rural areas, gaps in healthcare workforce training, and data privacy concerns [34].

However, Kazakhstan's unique geographic, demographic, and epidemiological context offers opportunities for AI-driven solutions. The integration of AI may bridge gaps in rheumatologic care delivery across the country, particularly in underserved regions. Government initiatives in digital health, combined with partnerships with international research centers and targeted education in medical informatics, could accelerate the adoption of AI in clinical practice.

This review aims to provide a critical synthesis of current and emerging applications of AI in rheumatology, with an emphasis on their potential implementation in Kazakhstan's healthcare system.

Search Strategy

A comprehensive literature search was conducted to identify peer-reviewed publications related to the application of AI in rheumatology. The search was performed using internationally recognized databases of evidence-based medicine and electronic scientific libraries, including PubMed, Google Scholar, and CyberLeninka. *Inclusion criteria* were as follows: original research articles, systematic reviews and narrative reviews; publications in English and Russian; full-text availability with structured abstracts; publication years ranging from 2015 to 2025. *Exclusion criteria* included: book chapters, dissertations, and conference abstracts; publications lacking original data or relevance to AI applications in rheumatology; articles without abstracts or full-text access; unpublished manuscripts.

The search strategy incorporated the following keywords: "artificial intelligence", "machine learning", "deep learning", "neural networks", and "rheumatology".

The initial search identified 467 articles. After screening titles, abstracts, and full texts according to the predefined eligibility criteria, 58 publications were selected for detailed analysis.

Results and Discussion:

Types, concepts and methods of artificial intelligence

AI is an interdisciplinary domain within computer science focused on the development of algorithms capable of simulating human cognitive functions, including learning, pattern recognition, prediction, and decision-making. Among the core subfields of AI is machine learning (ML), which enables systems to detect patterns in data without relying on explicitly defined rules. This adaptive capability allows ML models to solve complex problems by learning from input data [58].

In contrast to traditional statistical approaches that emphasize hypothesis testing and causal inference, ML methods prioritize predictive accuracy. However, this often comes at the expense of model interpretability—a critical concern in clinical settings where transparency and accountability are essential.

Deep learning (DL), a subdomain of ML, utilizes multilayered artificial neural networks. The rise in computational capacity and the growing availability of large-scale datasets have led to the widespread use of DL, particularly in medical image analysis, genomics, and drug discovery [28]. A hierarchical structure of AI technologies is illustrated in **Figure 1.**

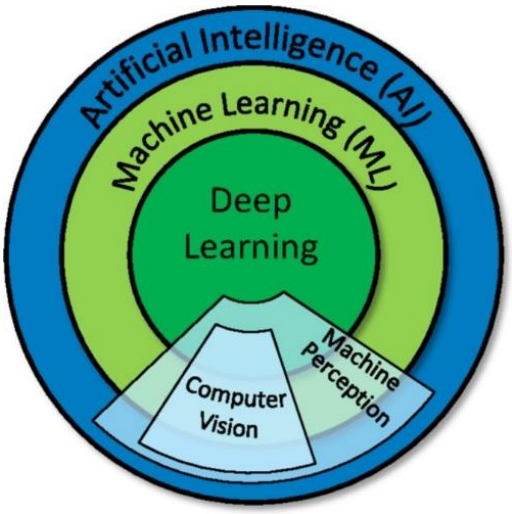

Figure 1. Hierarchy of Artificial Intelligence Technologies

ML methods are conventionally divided into three primary categories, each tailored to specific problem types:

1. Supervised Learning

Supervised learning involves training algorithms on labeled datasets, where both input features and corresponding target outputs are known. Applications include disease classification from medical images, analysis of EHRs, and prediction of disease recurrence risk. Common supervised algorithms include random forests, support vector machines (SVM), convolutional neural networks (CNNs), and natural language processing (NLP) models [58].

2. Unsupervised Learning

This approach is employed when labeled data are unavailable. The objective is to uncover underlying structures, clusters, or patterns in the dataset using techniques such as clustering or dimensionality reduction. Examples in medicine include patient subgrouping based on disease risk or phenotypic characteristics, and identification of novel disease subtypes.

3. Reinforcement Learning

In this paradigm, the model learns optimal strategies through interactions with its environment, receiving feedback in the form of rewards or penalties. Reinforcement learning is actively applied in robotic surgery and in optimizing adaptive therapeutic strategies, including dynamic treatment planning [21].

A comparative summary of widely used supervised ML algorithms is provided in Table 1.

Table 1.

Comparative Characteristics of Major Machine Learning Algorithms.

Algorithm	Description	Common use cases	References
Logistic Regression	Model for binary classification, establishes a relationship between input variables and the probability of one of two outcomes occurring. A threshold value is used to define the class.	Flare prediction, clinical decision rules, screening	[25], [29]
Lasso Regression	Regularized linear regression, prevents overtraining due to a penalty (L1-norm) in the loss function, effective for a large number of features	Regression/feature selection, risk modeling	[2]
Support Vector Machine (SVM)	A classifier that constructs an optimal hyperplane for class separation; robust to outliers and applicable to high dimensional problems.	Diagnosis from gene expression or metabolomic data	[24], [27], [29]
Decision Tree	Hierarchical model representing decisions in the form of a tree; easy to interpret but prone to overfitting.	Diagnostic algorithms that sequentially evaluate symptoms and lab results	[25]
Random Forest (RF)	An ensemble method that combines multiple decision trees; improves model accuracy and robustness by reducing overfitting.	Risk prediction, patient stratification, outcome modeling	[2], [5], [18] [23], [24]
Naive Bayes	Classifier assuming feature independence; works quickly and efficiently on large amounts of data.	Disease prediction	[44]
Convolutional Neural Networks (CNN)	A multilayer structure that mimics the operation of neurons; well suited for processing images, text, and other complex data.	Prognosis prediction, disease classification, X-ray/MRI interpretation	[3], [4], [20] [22], [35], [48]

Among ML methods, CNNs have emerged as particularly powerful tools. These architectures have demonstrated high accuracy in diagnosing diseases from radiological images such as X-rays, CT-images, and magnetic resonance imaging (MRI) - in some cases outperforming human experts in specific diagnostic tasks [15, 28]. CNNs are also used in genomics for identifying pathogenic mutations and developing personalized treatment strategies. Nevertheless, these models require large training datasets and substantial computational resources, which can limit their scalability and adoption in routine clinical practice.

A fundamental understanding of AI and ML concepts is increasingly important for healthcare professionals, particularly when evaluating and applying AI-driven tools in clinical workflows. To promote transparency, reproducibility, and safety, various methodological guidelines have been developed - such as CONSORT-AI, SPIRIT-AI, and others - which assist researchers in designing AI studies and aid clinicians in critically appraising AI model performance [26, 31, 33, 45].

In this review, we examined the role of AI - specifically neural network models - in the diagnosis, prognosis, and clinical monitoring of major rheumatologic diseases.

Rheumatoid arthritis

Diagnosis and assessment of disease activity

Modern ML and computer vision (CV) techniques are increasingly applied for early diagnosis of RA, including the preclinical phase. CV algorithms have shown efficacy in analyzing radiographic, ultrasonographic (US), and MRI data to detect early inflammatory changes such as erosions, bone marrow edema, and synovitis.

Stoel B.C. et al. (2019) demonstrated the utility of CNNs in the automated analysis of hand MRI for early RA detection. These models accurately and reproducibly identified bone marrow edema and tenosynovitis, outperforming traditional visual assessment by radiologists. The study highlighted the potential for full automation and emphasized the necessity of interpretable models and high-quality annotated datasets for clinical implementation [48].

Several studies have confirmed the high sensitivity and specificity of AI models for detecting erosions and joint space narrowing on radiographs in RA [13, 20, 35, 43]. However, current models remain insufficiently validated for routine clinical use due to limited dataset diversity, absence of external validation, and inconsistent reporting standards [4].

In the MEDUSA project, an ML-based method was developed to automatically grade synovitis on US images. While the algorithm demonstrated good concordance with expert evaluations, interrater agreement (k-coefficients) between algorithm and experts was lower than that between experts themselves, suggesting potential for improvement [32].

Predicting response to therapy

Another promising application of AI in rheumatology is the prediction of therapeutic response, particularly to biologic and targeted synthetic disease-modifying antirheumatic drugs (DMARDs), which could enable personalized treatment strategies.

Bouget V. et al. (2022) used AI models to predict treatment response to methotrexate and tumor necrosis factor - α (TNF-α) inhibitors using data from the ESPOIR, T-Reach, and Leiden cohorts. The models achieved AUC values ranging from 0.78 to 0.84, indicating high predictive accuracy [5, 6]. AUC, or area under the receiver operating characteristic curve, quantifies model performance: 1.0 reflects perfect discrimination, while 0.5 indicates random classification.

Tao W. et al. (2021) demonstrated that integrating transcriptomic, proteomic, and clinical data significantly improved prediction of response to biologic therapies such as adalimumab and etanercept (AUC = 0.79 in the BiOCURA cohort) [49]. Similarly, Casaburi et al. (2022) applied RNA sequencing and ML methods to synovial tissue to predict early response to conventional DMARDs [9].

In a recent study, *Sonomoto K. et al.* (2024) developed a model to predict clinical remission based on the Clinical Disease Activity Index (CDAI) during TNF- α inhibitor therapy using data from the Japanese FIRST registry (AUC = 0.70) [46]. *Cohen S. et al.* (2021) created a molecular signature classifier to identify likely non-responders to TNF-α inhibitors, achieving AUC > 0.70 based on ACR50/70 criteria [12].

These findings highlight the potential of AI-driven personalized treatment approaches in RA. However, they also underscore the need for external validation, standardized evaluation metrics, and integration into clinical workflows.

Predicting progression and exacerbations

AI-based models, particularly those using recurrent neural networks (RNNs) and time series analysis, show promise in predicting RA progression and flares. These models leverage longitudinal data - including demographic, clinical, and laboratory variables - to anticipate disease trajectory and optimize treatment plans.

Kalweit M. et al. (2021) developed a DL model (AdaptiveNet) using data from over 9,500 patients in the Swiss SCQM registry. The model achieved an AUC of 0.73, sensitivity of 84.2%, specificity of 61.5%, and 75.6% classification accuracy for disease activity (DAS28-ESR > 2.6). The average error in DAS28-ESR prediction was 0.9. Key predictors included the number of tender joints, patient age, and disease duration [24].

Norgeot B. et al. (2019) evaluated gradient-boosted decision tree models using data from EHRs of 820 patients across two centers. These models outperformed traditional methods in predicting disease activity and identified over 20 relevant clinical variables. The study suggested that similar approaches could be extended to other chronic diseases with measurable outcomes [38].

Ankylosing spondylitis

Image Interpretation

Recent advancements in medical imaging analysis have seen a growing application of ML techniques, particularly in improving the diagnostic and prognostic accuracy for musculoskeletal diseases. A prominent area of research is the use of CNNs to classify the severity of sacroiliitis based on the modified New York criteria.

Multiple studies have demonstrated that CNNs can reliably differentiate between normal and pathological cases of sacroiliitis on radiographs (e.g., grade ≥2 bilaterally or grade ≥3 unilaterally), achieving diagnostic accuracy ranging from 89% to 97%, sensitivity from 79% to 91%, and specificity from 79% to 96%. These performance metrics are comparable to those achieved by experienced rheumatologists. In addition to classification tasks, CNNs are increasingly used to localize structural lesions such as erosions, subchondral sclerosis, and ankylosis in the sacroiliac joints [7].

On MRI of the sacroiliac joints, ML algorithms have shown capability in detecting bone marrow edema—a key imaging marker of active inflammation [8, 42]. A German study (*Bressem K.K. et al.,* 2022) reported that CNNs achieved diagnostic sensitivity and specificity comparable to expert readers, and in some cases, outperformed general radiologists without specific expertise in musculoskeletal imaging [7]. However, variability in reported diagnostic performance across studies may reflect heterogeneity in MRI acquisition protocols, reference standards, and patient sampling, particularly in single-center settings.

Beyond diagnostic tasks, CNNs have also been utilized for prognostic modeling, including the prediction of radiographic progression [3], and for generating synthetic MRI and CT images [23]. Notably, synthetic CT generated from MRI data has emerged as a promising tool, providing enhanced visualization of erosions, sclerosis, and ankylosis compared to conventional MRI. These synthetic images have shown strong concordance with reference (true) CT and offer a radiation-free alternative for early detection of structural changes in axial AS.

Dynamic monitoring of patients

Beyond traditional imaging analysis, AI - including large language models (LLMs) such as GPT-4, LLaMA, Bard, and Claude - has emerged as a promising tool for the dynamic monitoring of patient-reported outcomes (PROs). These models can generate structured textual summaries based on patients' descriptions of their symptoms and lived experiences, facilitating more granular and longitudinal tracking of disease dynamics.

By automating the interpretation and synthesis of subjective reports, LLMs offer potential advantages including reduced patient burden, streamlined data collection, and improved consistency in symptom monitoring over time. However, several challenges remain. These include the accurate extraction and contextualization of nuanced patient-reported symptoms from natural language input, the difficulty of mapping free-text data to standardized quantitative metrics, and the need for rigorous validation of such approaches against established PRO instruments [53, 54].

Predicting response to therapy

The selection and evaluation of treatment efficacy, particularly for biologic and targeted synthetic DMARDs in AS, remains a clinical challenge. This is due to the individual variability in treatment response, the absence of robust predictive biomarkers, and the substantial costs associated with advanced therapies. In this context, the application of AI-based predictive models represents a rapidly evolving and promising area of research [29, 30, 57].

In a retrospective study by Wang *R.* et al. (2022), data from 1,899 patients with active AS were used to develop predictive models for treatment response to TNF- α

inhibitors at 12 weeks. The most significant predictors of therapeutic response included C-reactive protein levels and patient-reported activity based on the Bath Ankylosing Spondylitis Disease Activity Index (BASDAI)—particularly item 2, which assesses the general level of pain in the neck, back, or hips.

In contrast, factors such as elevated body mass index (BMI), older age, and higher scores on the Bath Ankylosing Spondylitis Functional Index (BASFI) were associated with reduced likelihood of response. The developed models demonstrated moderate to high predictive performance and could serve as useful tools for the individualization of treatment strategies in clinical practice [57].

Psoriatic arthritis

Differential diagnosis, prognosis

PsA is a chronic inflammatory disease characterized by lesions of joints, skin and entheses, and is characterized by clinical polymorphism, which complicates diagnosis. In this regard, AI methods aimed at improving the accuracy of differential diagnosis and identifying phenotypes with different prognosis are being actively developed. A number of studies have proved high efficiency of AI algorithms in differentiating PsA from seropositive and seronegative RA according to MRI and US of joints [16, 17]. In a prospective cohort study based on Clinical Practice Research Datalink (UK), which included data from more than 120 thousand patients, models were developed to predict joint lesions in psoriasis patients. The models demonstrated high accuracy (AUC up to 0.851), and among the most significant predictors were highlighted the duration of psoriasis, intake of nonsteroidal anti-inflammatory drugs (NSAIDs), the presence of arthralgias, and an increase in the level of C-reactive protein [44].

Monitoring and evaluation of activity

A study by *Huang K.* (2023) used a neural network model trained on more than 14,000 images from 2367 psoriasis patients, capable of automatically calculating the Psoriasis Area and Severity Index (PASI) with accuracy better than the average of 43 experienced dermatologists. The developed system was integrated into the SkinTeller mobile application available on the WeChat platform and successfully tested in 18 clinics [19].

Systemic lupus erythematosus

Diagnosis, forecasting and monitoring

SLE is a chronic multisystem autoimmune disease characterized by pronounced clinical and serological heterogeneity. Diagnostic challenges stem from the overlap of SLE manifestations with those of other autoimmune conditions, as well as the temporal variability of clinical symptoms. These complexities have stimulated growing interest in the application of AI to enhance diagnostic accuracy and improve disease monitoring.

One prominent example of AI integration into clinical diagnostics is the SLE Risk Probability Index (SLERPI), a ML-based algorithm developed to aid in the binary classification of SLE (lupus vs. non-lupus). In a recent study, the model achieved a high overall accuracy of 94.8%, with strong performance across different clinical subtypes: early-stage SLE (93.8%), lupus nephritis (97.9%), neuropsychiatric SLE (91.8%), and severe SLE requiring immunosuppressants or biologic therapies (96.4%) [2].

Usategui I. et al. (2024) further demonstrated the potential of AI for prognosis, achieving predictive accuracies of up to 94% for the development of lupus nephritis and disease flares using clinical and laboratory data extracted from EHRs [52]. Similarly, *Ceccarelli F. et al.* (2021) developed a ReliefF-based ML model that achieved excellent diagnostic accuracy (AUC = 0.94) using only the three most informative clinical features: anti-double-stranded DNA (anti-dsDNA) positivity, reduced complement C3/C4 levels, and the presence of a malar or maculopapular rash [10].

Neural network models have also been widely employed to analyze complex, high-dimensional biomedical data, including cytokine profiles, genetic signatures, transcriptomic data, and serological biomarkers. These models facilitate early organ-specific diagnosis, disease phenotyping, patient stratification, and prediction of therapeutic response [11].

Efforts to improve real-time disease monitoring are ongoing. *Jorge A.M. et al.* (2022) applied a Random Forest (RF) classifier to predict hospitalizations in SLE patients, achieving an AUC between 0.751 and 0.772. The most informative variables included anti-dsDNA titers, serum complement levels C3, complete blood count parameters, inflammatory markers, age, and serum albumin [23]. In another application, researchers in China used the same model architecture to predict adverse pregnancy outcomes in women with SLE. Significant predictors included alanine aminotransferase (ALT), gamma-glutamyltranspeptidase (GGT), antinuclear antibody (ANA) titers, and platelet counts [18].

Osteoarthritis

Phenotyping

In recent years, AI-based approaches have been actively developed to identify OA phenotypes that differ in clinical and structural characteristics, prognosis, and potential response to therapy. *Nelson A.E.* (2022) applied the biclustering method (simultaneously clustering knees and clinical features to account for their interaction) to describe OA subgroups, two of which demonstrated a worse prognosis: more frequent total joint replacement and more pronounced structural progression [36].

Demanse D. et al. (2023) applied DL methods and distinguished phenotypes with high body weight, comorbidities and low physical activity, as well as younger and more active groups [14].

In addition to clinical data, studies have begun to include molecular parameters. For example, *Steinberg J. et al.* (2021) evaluated gene expression in cartilage and synovial membrane of joints in 113 patients. Clusters differing in the activity of inflammation pathways, extracellular matrix remodeling, and cell adhesion were identified [47]. *Trajerova M. et al.* (2022) investigated the composition of immune cells in synovial fluid from patients with knee OA and identified four immune subtypes associated with different clinical outcomes after 3-6 months of NSAIDs therapy, which may have implications for predicting response to therapy [50].

Conclusion

A review of current literature highlights the growing potential of AI in the field of rheumatology, particularly for early diagnosis, disease progression forecasting, and

treatment personalization. Contemporary algorithms, including CNNs and multi-omics models, have demonstrated high diagnostic and prognostic performance—achieving AUC values of up to 0.85 in several studies. These results pertain to the analysis of various data modalities, including MRI, radiographs, and EHRs.

Despite these promising developments, widespread clinical implementation remains limited due to several key challenges: lack of standardized AI algorithms, insufficiently representative training datasets, and unresolved ethical considerations within medical practice.

In the context of Kazakhstan, the application of AI in rheumatology holds particular relevance. The country's vast geography, ethnocultural diversity, and unequal access to specialized care underscore the need for scalable digital and intelligent healthcare solutions. To fully harness the benefits of AI in national healthcare, several critical steps must be taken: enhancement of digital infrastructure, development of workforce competencies, establishment of clear legal and ethical frameworks, and active participation in international multicenter research collaborations. These initiatives will not only improve the accessibility and quality of rheumatologic care but will also position Kazakhstan as a meaningful contributor within the global scientific and medical community.

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Information about authors:

Petrova Yuliya Viktorovna – Master of Medicine,Department of Internal Medicine and Rheumatology NCJSC «Semey Medical University», 103 AbayStreet, Semey, 071400, Kazakhstan; Email: yuliya.petrova@smu.edu.kz; phone number: +7(771) 537 6060; https://orcid.org/0000-0003-1910-7169

Goremykina Maiya Valentinovna - Candidate of Medical Sciences, Associate Professor, Department of Internal Medicine and Rheumatology, NCJSC «Semey Medical University», 103 AbayStreet, Semey, 071400, Kazakhstan;Email: maya.goremykina@smu.edu.kz;phone number: +7 (777) 390 8234; https://orcid.org/0000-0002-5433-7771

Ivanova Raifa Latyfovna– Professor, Doctor of Medical Sciences, Department of Internal Medicine and Rheumatology NCJSC «Semey Medical University», 103 AbayStreet, Semey, 071400, Kazakhstan; Email: raifa.ivanova@smu.edu.kz; phone number: +7(777)147 2892; https://orcid.org/0000-0001-9851-2255

Kozhakhmetova Dana Kenzhebaevna – PhD, assistant of the Department of Internal Diseases and Rheumatology, NCJSC «Semey Medical University», Address: 071400, Republic of Kazakhstan, Abai Region, Semey, 103 AbayKunanbayev St., Email: dana_ken@mail.ru; phone number: +7(702) 705 1403; https://orcid.org/0000-0002-8367-1461

Botabayeva Ainur - MD, assistant of the Department of Internal Diseases and Rheumatology, NCJSC «Semey Medical University»,Address: 071400, Republic of Kazakhstan, Abai Region, Semey, 103 AbayKunanbayev St., e-mail: aibota7878@mail.ru Phone: +7 (701) 100 2098 https://orcid.org/0009-0008-9228-7788

Razvodova Alexandra – MD, Rheumatologist, LLP «Hippocrates», Address: 110000, Republic of Kazakhstan**,** Kostanay, 151, 1st May Street, Building 7**;** phone number:+7(705) 727 0571 https://orcid.org/0000-0002-8367-1461

Corresponding author:

Goremykina Maiya Valentinovna - Candidate of Medical Sciences, Associate Professor, Department of Internal Medicine and Rheumatology, NCJSC «Semey Medical University»

Address:103 Abay Street, Semey, 071400, Kazakhstan

E-mail: maya.goremykina@smu.edu.kz

Phone: +7 (777) 390 8234