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Leveraging Artificial Intelligence to Predict Tumor Necrosis Factor-Alpha Activity for Enhanced Disease Diagnosis and Therapeutic Development

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ABSTRACT

Tumor Necrosis Factor-Alpha (TNF-α) is a key pro-inflammatory cytokine involved in autoimmune disorders, cancer, and chronic inflammatory diseases. Accurate prediction of TNF-α activity is vital for understanding disease mechanisms and advancing targeted therapies. This review highlights the emerging role of Artificial Intelligence (AI), particularly Machine Learning (ML) and Deep Learning (DL) techniques, in predicting TNF-α activity. Recent advancements are discussed, including AI-based analysis of multi-omics data, clinical biomarkers, and patient records for disease diagnosis, treatment response prediction, and drug discovery. The AI models such as random forests and support vector machines have demonstrated improved accuracy in classifying TNF-α activity and supporting personalized treatment strategies. The integration of AI in inflammatory pathway modeling has accelerated the development of TNF-α inhibitors and optimized therapeutic outcomes. Despite these advancements, challenges remain in data standardization, model transparency, and ethical considerations. Future directions emphasize the need for incorporating real-world clinical data and enhancing model robustness to fully realize AI's potential in TNF-α-related research and precision medicine.

KEYWORDS

Tumor Necrosis Factor-Alpha (TNF-α), Artificial Intelligence (AI), Machine Learning (ML), Deep Learning (DL), inflammatory diseases, drug discovery, personalized medicine

INTRODUCTION

Tumor Necrosis Factor-Alpha (TNF-α) plays a crucial role in immune regulation, inflammation, and cellular homeostasis. Dysregulated TNF-α signaling is implicated in chronic inflammatory diseases, necessitating predictive models for early detection and targeted treatment[1].

The crucial role of TNF-α in inflammatory diseases such as rheumatoid arthritis has been highlighted by studies demonstrating its involvement in persistent immune activation and tissue damage, particularly among elderly populations in Nigeria[2].

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Tumor Necrosis Factor-Alpha (TNF-α), a pro-inflammatory cytokine, plays a pivotal role in the pathophysiology of numerous diseases, including rheumatoid arthritis, inflammatory bowel disease, and certain cancers[3]. Understanding its activity is vital for both diagnosing disease states and designing effective therapeutic interventions.

One of the key challenges of TNF-α research is its dual role in both normal immune response and pathological conditions. For instance, while TNF-α is essential for defending against infections, its dysregulation is implicated in chronic inflammation and autoimmune disorders[1]. Accurate prediction of TNF-α activity, therefore, requires sophisticated computational models capable of distinguishing between physiological and pathological conditions. Artificial Intelligence offers tools to address these challenges by developing predictive models that integrate diverse datasets, including genomic variants, patients' histories, and environmental factors[4].

Artificial Intelligence (AI) has changed and evolved biomedical research by enabling accurate prediction and analysis of Tumor Necrosis Factor-Alpha (TNF-α) activity. Artificial intelligence has emerged as a transformative tool in biomedical research, which has changed how we approach complex problems in medicine and life science. Among the many areas where artificial intelligence demonstrates potential, its activity of critical inflammatory mediators such as Tumor Necrosis Factor-Alpha (TNF-α) is particularly significant[4].

The integration of AI methodologies into the domain is driven by their ability to analyze vast amounts of biological data, identify hidden patterns, and predict complex interactions. Traditional experimental methods for studying TNF-α activity, while highly specific and reliable, are often resource-intensive and time-consuming. The AI-driven approaches, such as Machine Learning (ML) and Deep Learning (DL), analyze multi-omics datasets to model TNF-α behavior in disease states, thus enabling precision medicine[4].

In contrast, AI techniques such as machine learning and deep learning can process multidimensional datasets generated from transcriptomics, proteomics, and imaging studies to uncover the regulatory networks involving TNF-α[5].

Furthermore, AI-driven approaches hold a promise in therapeutic interventions targeting TNF-α. Monoclonal antibodies and receptor antagonists, such as infliximab and etanercept, have been used to inhibit TNF-α activity[6]. However, the clinical efficacy of these treatments varies among patients due to differences in genetic makeup, disease stage, and co-morbidities. By leveraging AI to predict patient-specific response to TNF-α inhibitors, personalized treatment regimens can be optimized, potentially improving outcomes and reducing adverse effects[7].

This article aimed to review the application of artificial intelligence in predicting TNF-α activity, exploring its implications for disease understanding and therapeutics innovation. It will highlight advancements in computational biology, discuss current challenges in modeling inflammatory pathways, and propose future directions for integrating AI into personalized medicine. The integration of AI into TNF-α research not only underscores the potential of computational technologies in biomedicine but also paves the way for a deeper understanding of inflammatory diseases and their treatment strategies.

TNF-α structure: Tumor necrosis factor-alpha is a potent pro-inflammatory cytokine that plays a pivotal role in regulating immune responses, apoptosis, and inflammation. The TNF-α exists in both a membrane-bound precursor form and a soluble active form, with a well-defined structure that underpins its biological functions. Tumor Necrosis Factor-Alpha (TNF-α) is a trimeric cytokine belonging to the TNF superfamily. Each monomer of TNF-α consists of approximately 157 amino acids and adopts a beta-sandwich structure composed of two antiparallel beta-sheets. These beta-sheets form a characteristic "jelly roll" topology, which is a hallmark of TNF family proteins[1].

Mature form: The TNF-α is initially synthesized as a 233-amino acid transmembrane protein (pro-TNF-α). This membrane-bound form can act locally, but it is often cleaved by TNF-α converting enzyme (TACE) to release a 157-amino acid soluble form[8].

Primary structure: The TNF-α is initially synthesized as a 26 kDa type II transmembrane protein comprising 233 amino acids. This precursor protein has three key domains:

- **Cytoplasmic domain (N-terminal):** Located intracellularly and plays a role in intracellular signaling
- **Transmembrane domain:** Anchors the protein to the cell membrane, facilitating local signaling and cell-cell interactions
- **Extracellular domain (C-terminal):** Contains 157 amino acids that form the biologically active cytokine after proteolytic cleavage by TNF-α converting enzyme (TACE/ADAM17)

The Soluble Form of TNF-α (sTNF-alpha), with a molecular weight of approximately 17 kDa, is the active form responsible for systemic inflammatory effects[8].

Secondary structure: The secondary structure of TNF-α primarily consists of antiparallel beta-strands organized into a characteristic beta-sandwich motif:

- **Antiparallel beta sheets:** Beta sheets form the core of the molecule, providing structural stability
- **Loops and turns:** Connect beta strands, allowing flexibility and interaction with receptors

The beta-sandwich structure, also referred to as a "jelly roll" fold, is a defining feature of TNF superfamily[9].

Trimeric structure: The functional form of TNF-α is a non-covalent homotrimer. This trimerization is crucial for its interaction with TNF receptors and for initiating downstream signaling pathways[10].

TNF-α function: The TNF-α binds to TNF receptors (TNFR1 and TNFR2) to initiate inflammatory and apoptotic signaling[3].

The TNF-α plays a critical role in immune regulation, inflammation, apoptosis, and cellular homeostasis. Its functions are mediated through two distinct receptors: The TNF Receptor 1 (TNFR1) and TNF Receptor 2 (TNFR2), which trigger diverse biological responses[3].

Pro-inflammatory response: The TNF-α is a key mediator of inflammation. It promotes the production of other pro-inflammatory cytokines (e.g., IL-1 and IL-6) and chemokines, recruits immune cells to inflammation sites, and increases vascular permeability[1].

Recent studies have explored various inflammatory markers, including C-Reactive Protein (CRP), about disease progression and severity. The CRP levels demonstrate a distinct pattern to alcohol consumption, suggesting a potential link between lifestyle factors and inflammatory responses. Their findings highlight the modulatory effect of CRP, which could be significant in AI-driven predictive models for TNF-α, as both markers play roles in systemic inflammation and immune regulation[11].

Apoptosis and cell survival: The TNFR1 signaling can lead to apoptosis by activating caspase pathways.

The TNFR2 predominantly mediates cell survival and proliferation by activating the Nuclear Factor Kappa B (NF-κB) pathway[5].

TNF-α clinical significance: Aberrant TNF-α activity contributes to autoimmune diseases, sepsis, and cancer progression, making it a prime therapeutic target[9].

The TNF-α is a validated therapeutic target. Inhibitors, such as monoclonal antibodies (e.g., infliximab, adalimumab), and soluble TNF receptors are widely used to manage TNF-α-driven diseases[3].

ARTIFICAL INTELLIGENCE IN BIOMEDICAL RESEARCH

Artificial Intelligence (AI) has revolutionized biomedical research by enabling faster data analysis, improving disease diagnosis and facilitating drug discovery. The AI techniques, such as Machine Learning (ML) and Deep Learning (DL), help analyze large databases and identify patterns in disease outcomes with high accuracy[12]. In the identification of potential drug candidates by stimulating molecular interactions and predicting their effects[13]. Furthermore, AI-powered tools enhance medical imaging analysis, allowing for early detection of diseases like cancer and neurological disorders[14].

PREDICTING TNF-α ACTIVITY USING ARTIFICIAL INTELLIGENCE

Machine Learning (ML) approach: Artificial intelligence, particularly Machine Learning (ML), has become an invaluable asset in biomedical research, offering sophisticated predictive capabilities for analyzing Tumor Necrosis Factor-Alpha (TNF-α) activity. The TNF-α, a pro-inflammatory cytokine, is pivotal in autoimmune diseases, cancer, and inflammatory disorders, making it a significant target for therapeutic interventions. The ML techniques enable researchers to uncover patterns, predict outcomes, and enhance drug development by leveraging large and complex biomedical datasets. Recent studies have demonstrated the efficacy of ML models in predicting TNF-α inhibitors. For instance, Prabha *et al.*[15] developed classification algorithms; naïve Bayes, random forest, k-nearest neighbor, and support vector machine to identify TNF-α inhibitors, achieving an accuracy of 87.96% with the random forest model. Additionally, Nabi *et al.*[16] employed deep learning-based predictive modeling to screen natural compounds against TNF-α, identifying potential natural inhibitors with significant binding affinities.

Predicting TNF-α activity in disease states: The ML algorithms analyze omics data (e.g., genomics, transcriptomics, and proteomics) to predict TNF-α activity in diseases such as rheumatoid arthritis, Crohn's disease, and sepsis.

Example: Supervised learning models, such as Support Vector Machines (SVMs) and random forests, have been applied to classify TNF-α expression profiles in patient datasets, improving diagnostic accuracy for inflammatory diseases[4].

Predicting response to anti-TNF therapies: The ML enables personalized medicine by predicting patient-specific responses to anti-TNF therapies, such as infliximab and adalimumab. These predictions optimize treatment plans, minimizing side effects and improving outcomes.

Example: Logistic regression and gradient boosting models have been used to analyze genetic and clinical data to predict therapeutic efficacy in patients with rheumatoid arthritis[17].

Drug discovery and development: The ML accelerates the drug discovery process by screening large molecular libraries to identify potential TNF-α inhibitors. It also aids in predicting the pharmacokinetics and toxicity of new compounds.

Example: Gradient boosting algorithms and neural networks have been employed to predict molecular binding affinities, identifying small molecules with high specificity for TNF[18].

PREDICTING TNF-α IN DISEASE-SPECIFIC APPLICATION USING ARTIFICIAL INTELLIGENCE

AI-driven prediction of TNF-α and haemostatic changes in disease applications: Recent research has underscored the role of haemostatic alterations in cancer pathology, particularly in lymphoid malignancies. Onuoha *et al.*[19] investigated the haemostatic changes in patients undergoing chemotherapy, revealing significant disruptions in factor V activity and platelet count. The study highlighted how chemotherapy influences coagulation parameters, reinforcing the need for predictive modeling to assess these variations for optimal patient management. The interconnection between TNF-α and coagulation is well documented, with elevated TNF-α levels linked to hypercoagulability and endothelial dysfunction. The AI-driven models can analyze TNF-α fluctuations alongside haemostatic markers to predict thrombosis risks, ensuring timely interventions for patients undergoing chemotherapy or dealing with lymphoid malignancies. By integrating AI-based predictive analytics with haemostatic research findings, clinicians can refine therapeutic approaches, tailoring interventions that mitigate TNF-α-induced coagulation disorders.

Rheumatoid arthritis (RA): Artificial Intelligence (AI), encompassing Machine Learning (ML) and Deep Learning (DL), has been increasingly utilized to predict TNF-α activity, elucidate disease mechanisms, and optimize therapeutic interventions in rheumatoid arthritis (RA). For instance, Nabi *et al.*[16] employed a DL-based approach to virtually assess natural compounds against TNF-α, identifying potential natural inhibitors with significant binding affinities. Additionally, Bouget *et al.*[20] applied ML algorithms to predict patient responses to TNF inhibitors, utilizing clinical and biological data to enhance treatment strategies.

Predicting TNF-α levels in RA patients: AI models analyze clinical, genetic, and molecular data to predict TNF-α activity levels, enabling early diagnosis and monitoring of RA progression.

Applications: Supervised learning models, such as random forests and support vector machines, have been employed to predict TNF-α overexpression in RA patients based on gene expression profiles.

Example: An ML model analyzed multi-omics data to classify RA patients into high and low TNF-α activity subgroups, enhancing personalized treatment planning[4].

Identifying biomarkers for diagnosis and prognosis: The AI models integrate omics data to identify biomarkers associated with TNF-α activity, aiding in early RA diagnosis and predicting disease progression.

Applications: Deep Neural Networks (DNNs) have been used to identify TNF-α-related genetic variants and protein markers linked to disease severity.

Example: A DNN-based study identified biomarkers such as IL-6 and MCP-1 that correlate with TNF-α levels and RA progression[5].

Inflammatory bowel disease (IBD): Artificial Intelligence (AI) has been increasingly applied to predict TNF-α activity, improve diagnosis, and optimize therapeutic interventions in inflammatory bowel disease (IBD). For example, Bouwman *et al.*[21] developed a method to predict and monitor responses to anti-TNF-α treatment by measuring signal transduction pathway activity, aiming to enhance therapeutic outcomes in IBD patients. Additionally, Gubatan *et al.*[22] reviewed AI applications in IBD, highlighting the potential of machine learning algorithms to analyze genomic datasets, construct risk prediction models, and assess disease severity, thereby improving diagnosis and treatment strategies.

Predicting TNF-α levels in IBD patients: AI models utilize clinical, genetic, and molecular datasets to predict TNF-α activity, aiding in the assessment of IBD severity and progression.

Applications: Machine Learning (ML) algorithms like random forests and support vector machines have been used to predict TNF-α overexpression based on patient-specific data.

Example: A study utilized ML to classify IBD patients into low and high TNF-α activity groups using serum cytokine levels, achieving an accuracy of 88%[4].

Identifying biomarkers for early diagnosis: The AI-powered analysis of omics data identifies biomarkers linked to TNF-α activity, enabling early and accurate IBD diagnosis.

Applications: Deep Learning (DL) models, such as Convolutional Neural Networks (CNNs), have been applied to transcriptomics and proteomics data to uncover novel TNF-α-related biomarkers.

Example: A DL model identified TNF-α-induced IL-23 and IL-17 as critical biomarkers differentiating Crohn's disease from ulcerative colitis[23].

Optimizing anti-TNF therapy in IBD: The anti-TNF therapies, such as infliximab and adalimumab, are commonly used in IBD treatment. The AI models predict patient-specific responses to these therapies, optimizing treatment strategies.

Applications: Logistic regression and gradient boosting algorithms predict the likelihood of therapeutic success based on clinical and genetic data.

Example: The AI-based predictions of anti-TNF therapy response achieved a 92% accuracy, reducing unnecessary treatments and improving patient outcomes[17].

Drug discovery targeting TNF-α: The AI accelerates the discovery of novel TNF-α inhibitors by screening molecular libraries and predicting drug-target interactions.

Applications: Generative Adversarial Networks (GANs) and molecular docking algorithms aid in identifying and validating new drug candidates.

Example: The GAN-generated small molecules showed high specificity for TNF-α inhibition in preclinical IBD models, reducing inflammation by over 70%[18].

Role of TNF-α in cancer: The TNF-α has dual roles in cancer: Promoting tumor growth through chronic inflammation and contributing to tumor cell apoptosis under certain conditions. Predicting TNF-α activity in cancer is critical for understanding its role and optimizing therapy.

AI APPLICATIONS IN CANCER RESEARCH

Predicting tumor microenvironment dynamics: AI models analyze multi-omics data to predict TNF-α activity within the tumor microenvironment (TME).

Example: A deep learning model predicted TNF-α-mediated immune cell infiltration in breast cancer tumors, achieving 85% accuracy[4].

Drug resistance and therapy optimization: Machine Learning (ML) identifies patterns of resistance to TNF-α-targeting therapies in cancers such as melanoma and pancreatic cancer.

Example: Gradient boosting algorithms predicted resistance to TNF-α inhibitors in melanoma based on genomic mutations[17].

Combination therapy design: The AI models simulate TNF-α dynamics to optimize combinations of immunotherapy and chemotherapy.

Example: The AI-guided simulations identified synergistic effects between anti-TNF drugs and checkpoint inhibitors in lung cancer[23].

Phytopreventive approaches targeting TNF-α in cancer: Emerging evidence suggests that natural products with phytopreventive properties can modulate inflammatory pathways, including TNF-α-mediated mechanisms, in cancer progression. For instance, a study demonstrated that tender coconut water possesses significant prophylactic effects against haematological disorders associated with benzene-induced lymphoid malignancy, partly by restoring normal immune cell profiles and inhibiting cancer biomarkers such as p53 and Bcl-2. These findings highlight the potential of integrating phytochemicals into AI-driven models for predicting TNF-α activity modulation in cancer therapies[24].

Relevance of natural therapeutic agents targeting TNF-α activity: Interestingly, natural products are gaining recognition for their potential to modulate TNF-α and related inflammatory pathways. In a related study, Emmanuel and Hallie[25] demonstrated that tender coconut water possesses ameliorative effects on benzene-induced lymphoid malignancy in Wistar rats by modulating cancer biomarkers such as p53 and Bcl-2. These findings underscore the broader potential of natural bioactive compounds in influencing TNF-α-driven disease processes, thereby suggesting possible integration into AI-assisted drug discovery platforms for cancer.

AI IN PERSONALIZED MEDICINE

Personalized drug selection: AI recommends the most effective anti-TNF therapy for individual patients based on their unique genetic and clinical profiles.

Applications: Ensemble learning models integrate patient data to rank potential therapies.

Example: An ensemble model identified etanercept as the optimal treatment for a subset of rheumatoid arthritis patients, reducing non-response rates by 20%[5].

Dose optimization: The AI determines optimal dosing regimens to balance efficacy and minimize adverse effects.

Applications: Reinforcement learning models simulate dose-response relationships.

Example: A reinforcement learning approach optimized infliximab dosing in ulcerative colitis patients, improving remission rates by 15%[23].

Predicting adverse effects: The AI predicts the likelihood of adverse effects from anti-TNF therapies, enabling safer treatment choices.

Applications: Neural networks analyze patient histories and pharmacogenomics data to predict side effects.

Example: An AI model predicted increased infection risk in 10% of anti-TNF therapy users, allowing preemptive interventions[26].

ROLE OF AI IN COMBINATION THERAPIES

Identifying synergistic drug combinations: The AI models predict drug synergy by analyzing multi-modal datasets, including genomic, proteomic, and clinical data, to identify interactions that enhance TNF-α modulation.

Applications: Generative Adversarial Networks (GANs), reinforcement learning, and deep learning models explore large drug libraries to propose optimal combinations.

Example: The AI-guided research identified a combination of anti-TNF agents and IL-17 inhibitors as highly effective for treating psoriatic arthritis[4].

Modelling drug-target interactions: The AI models analyze TNF-α signaling pathways and predict how different drugs modulate these pathways.

Applications: Neural networks and decision trees map interactions between TNF-α, downstream cytokines, and potential therapeutic targets.

Example: A deep learning framework predicted that combining anti-TNF drugs with JAK inhibitors could reduce inflammation more effectively in rheumatoid arthritis[17].

Dose and timing optimization: The AI refines dosing regimens and timing of combination therapies to maximize efficacy and minimize side effects.

Applications: Reinforcement learning models simulate drug pharmacodynamics and pharmacokinetics in patients.

Example: The AI optimized the timing of anti-TNF and methotrexate administration, improving remission rates in rheumatoid arthritis[23].

Transforming biomedical research: The AI has profoundly advanced biomedical research by accelerating biomarker discovery, enhancing our understanding of TNF-α-related pathways, and driving innovation in drug discovery. Through the application of machine learning and deep learning techniques, researchers can analyze multi-omics datasets, uncover novel regulatory mechanisms, and predict molecular interactions with unprecedented accuracy. For example, AI-driven analysis of genetic and proteomic data has identified novel TNF-α biomarkers and pathways, offering new targets for therapeutic intervention[4,17].

Moreover, AI models facilitate the integration of diverse datasets, including genomic, transcriptomic, and clinical data, to create a holistic understanding of TNF-α activity in complex diseases such as rheumatoid arthritis, inflammatory bowel disease, and cancer. This data integration enhances reproducibility and provides actionable insights into disease pathophysiology, guiding research and innovation[5].

Advancing therapeutic interventions: In clinical practice, AI tools are reshaping therapeutic interventions by enabling personalized medicine. Predictive models of TNF-α activity allow for tailored treatment strategies that optimize therapeutic efficacy while minimizing adverse effects. For instance, AI-guided selection of anti-TNF therapies has improved treatment response rates in patients with inflammatory diseases[26].

The AI also facilitates early diagnosis and risk stratification, enabling proactive management of TNF-α-mediated diseases. Real-time monitoring tools powered by AI can track TNF-α activity and predict disease flare-ups, providing clinicians with actionable insights to adjust treatment plans dynamically[18]. Additionally, AI-driven approaches to combination therapies and drug repurposing have the potential to expand treatment options and improve patient outcomes, especially in diseases where TNF-α plays a central role[23].

Overcoming challenges for clinical translation: Despite its transformative potential, the clinical translation of AI models for TNF-α prediction faces several challenges. The lack of standardized validation protocols, limited generalizability across diverse patient populations, and ethical concerns surrounding data privacy and model interpretability remain critical barriers. Furthermore, regulatory frameworks must adapt to address the complexities of AI applications, ensuring safety and efficacy without impeding innovation[5].

Future research must prioritize the development of rigorous validation frameworks, the integration of real-world data, and the inclusion of diverse datasets to enhance model robustness and generalizability. Collaboration between researchers, clinicians, and regulatory agencies will be essential for addressing these challenges and ensuring the successful clinical adoption of AI tools[26].

Ethical and societal implications: The ethical implications of using AI in TNF-α research and clinical practice cannot be overlooked. Transparent and explainable AI models are essential for building trust among patients and clinicians, while robust data security frameworks are critical to safeguarding patient privacy. Efforts to democratize access to AI-driven tools will help bridge healthcare disparities and expand the benefits of precision medicine to underserved populations[17].

Future directions and challenges: The future of AI in TNF-α research is promising, with the potential to drive significant advancements in disease diagnostics, therapeutics, and personalized medicine. By addressing current challenges and fostering interdisciplinary collaboration, AI can revolutionize the management of TNF-α-mediated diseases and serve as a model for applying AI in other areas of biomedical research.

CONCLUSION

The integration of Artificial Intelligence (AI) in TNF-α research has revolutionized disease diagnosis, therapeutic development, and drug discovery. The AI-driven models enhance predictive accuracy, enabling personalized treatment strategies and optimizing anti-TNF therapies. Machine Learning (ML) and Deep Learning (DL) approaches have improved biomarker identification and drug screening, accelerating precision medicine. Despite its potential, challenges such as data standardization, model interpretability, and ethical concerns must be addressed.

Future research should focus on enhancing AI model interpretability, standardizing datasets, and integrating real-world clinical data to improve TNF-α activity prediction. Collaboration between AI researchers and biomedical scientists is essential for developing robust, clinically applicable models. Expanding AI applications in personalized medicine will optimize treatment outcomes for TNF-α-related diseases. Additionally, ethical considerations and regulatory frameworks should be established to ensure the safe and effective implementation of AI-driven healthcare solutions.

SIGNIFICANCE STATEMENT

This study discovered the potential of Artificial Intelligence (AI) to accurately predict Tumor Necrosis Factor-Alpha (TNF-α) activity, which can be beneficial for early disease diagnosis, patient-specific therapy, and the development of targeted TNF-α inhibitors. By integrating AI into biomedical research, this study enhances our ability to understand inflammatory mechanisms and optimize therapeutic strategies with

improved precision. The insights gained also address challenges such as model interpretability and data variability, promoting broader clinical adoption. This study will help the researchers to uncover the critical areas of inflammatory disease modulation and therapeutic response prediction that many researchers were not able to explore. Thus, a new theory on AI-guided immunological intervention may be arrived at.

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