

Poster Presentation : Augmented Intelligence, Digital Health, and Data Science
Poster No. : B0063
Abstract Submission No. : APCN20250222

AI-Driven Modeling of Aquaporin-Mediated Water Transport and Volume Regulation in Renal Epithelia: A Systems Approach for Drug Discovery

Chitaranjan Mahapatra¹

¹ Bio Sciences & Bio Engineering, Indian Institute of Technology Bombay, Mumbai, India

Abstract

Introduction: Maintaining water homeostasis is vital to renal physiology, and aquaporin (AQP) channels, particularly AQP2, play a central role by facilitating rapid, selective water transport in the kidney's collecting ducts. Their regulation, often mediated by vasopressin, remains an active area of study due to its implications in disorders such as nephrogenic diabetes insipidus and SIADH. While AQP function has been structurally characterized, its real-time dynamic behavior and interaction with ion channels under osmotic stress are still poorly understood. To address this, we developed an AI-assisted computational model that couples water transport through AQPs with cell volume and membrane tension, aiming to uncover mechanisms relevant for drug innovation and systems-level nephrology.

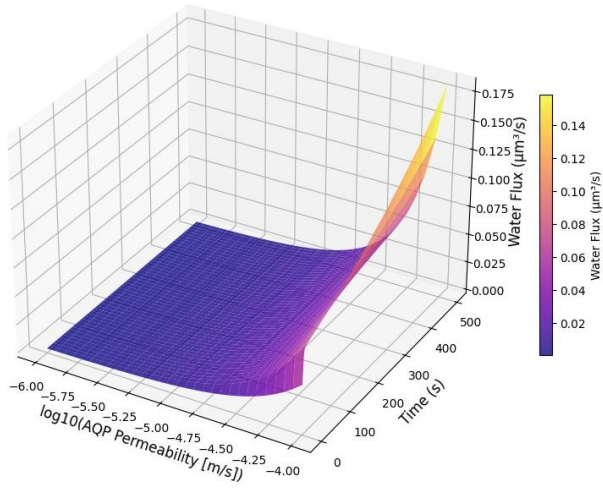
Methods: We constructed a system of nonlinear ordinary differential equations to model cell volume, AQP gating, membrane tension, intracellular osmolarity, and stretch-sensitive potassium (K⁺) channel gating. Water flux was modeled as a function of both osmotic gradient and AQP permeability, while K⁺ efflux responded to membrane tension. We used Python's odeint for numerical integration and incorporated machine learning approaches to optimize biophysical parameters based on physiological datasets. This framework allows simulation of dynamic cellular responses under various osmotic loads.

Results: Simulation outcomes revealed a self-regulating feedback system: increased AQP permeability led to rapid water influx and cell swelling, which elevated membrane tension and activated K⁺ channels. The resulting K⁺ efflux lowered intracellular osmolarity, dampening further water entry and stabilizing cell volume. Figure 1 presents a 3D visualization of this interaction, showing water flux and cell volume as nonlinear functions of AQP permeability. Notably, the stretch-activated K⁺ channels exhibited threshold-dependent activation behavior, acting as key modulators in reversing osmotic swelling and restoring homeostasis. The model demonstrates threshold-like behavior in response to changes in channel gating—insights which could aid in AI-driven drug screening of AQP modulators.

Conclusion: This AI-enhanced visualization provides insights into the coordinated roles of aquaporins and stretch-activated potassium channels in maintaining renal epithelial cell volume under osmotic stress. Our results underscore the dynamic feedback between AQP-mediated water influx and K⁺-channel-driven osmolyte efflux as a critical homeostatic mechanism. It highlights both AQP channels and mechanosensitive K⁺ channels as promising therapeutic targets: AQP antagonists could be employed to limit excessive water reabsorption in conditions like SIADH, while AQP agonists may help restore function in nephrogenic diabetes insipidus. Similarly, K⁺ channel agonists may enhance compensatory osmolyte flux during cellular swelling, whereas channel blockers could reduce maladaptive ion loss in hypotonic stress.

Keywords : Drug Target Discovery in Nephrology, AI-Driven Computational Modeling, Aquaporin Channel Regulation, Renal Cell Volume Homeostasis

3D Visualization of Water Flux Dynamics



Poster Presentation : Augmented Intelligence, Digital Health, and Data Science
Poster No. : B0065
Abstract Submission No. : APCN20250513

Evaluating Generative Artificial Intelligence (AI) Models for Patient Education on Renal Diet: A Comparative Study of ChatGPT, DeepSeek, Gemini, and Grok Models

WONG WEI KEI¹; LIM SOO KUN¹

¹ Department of Medicine, University Malaya, Kuala Lumpur, Malaysia

Abstract

Introduction: Generative artificial intelligence (AI) models are increasingly used for patient education, yet their reliability in delivering personalised, evidence-based dietary advice for chronic kidney disease (CKD) remains uncertain. This study aims to evaluate and compare the performance of four more accessible AI models, i.e. ChatGPT, DeepSeek, Gemini, and Grok, in addressing common renal diet questions to determine their suitability for clinical use in patient communication.

Methods: Ten standardised CKD diet-related questions were input into each AI model with a response word limit of 300. Responses were collected on two occasions, 14 days apart, to assess consistency. The outputs were anonymised and independently evaluated by three nephrologists and one dietitian using a 5-point Likert scale across five domains: appropriateness, clarity and comprehensiveness, personalization and relevance, consistency, and human-like empathy. Data were analysed using Friedman's test for ranked data and post-hoc pairwise comparisons via the Nemenyi test. Inter-rater reliability was assessed using Kendall's W.

Results: Descriptive analysis has shown that ChatGPT scored the highest mean score in most domains (Appropriateness 4.32+/-1.00, clarity and comprehensiveness 4.28+/-1.00, personalization and relevance 4.05+/-0.93, consistency 4.40+/-0.55) while Grok has the highest mean score in human-like empathy domain (4.08+/-0.66).

Upon further analysis, Friedman test has shown there was significant difference between AI models in appropriateness ($\chi^2 = 10.86$, $p=0.013$), clarity and comprehensiveness ($\chi^2=18.21$, $p\text{-value} <0.001$) and consistency ($\chi^2=16.22$, $p\text{-value}=0.001$) domains. Post-hoc comparison also showed that ChatGPT performed significantly better than DeepSeek in clarity and comprehensiveness domain ($q=4.164$, $p=0.017$), supported by its superior average rank (1.95 vs 2.80). There were no significant differences between AI models in the personalization and relevance and human-like empathy domain.

Overall performance also differed significantly ($\chi^2=14.49$, $p=0.002$), with ChatGPT ranking higher than Gemini and DeepSeek. The average ranks of ChatGPT(best), DeepSeek and Gemini (worst) were 1.91, 2.71 and 2.80 respectively. Inter-rater agreement was weak across domains, reflecting the inherent subjectivity in evaluating AI-generated content.

Conclusion: This study highlights notable differences in the quality of AI-generated responses to renal diet questions. ChatGPT demonstrated superior overall performance over DeepSeek and Gemini, and was also significantly better than DeepSeek in terms of clarity and comprehensiveness. These findings support further integration of advanced AI models in nephrology patient education, with continued human oversight to ensure contextual relevance and personalisation.

Keywords : Artificial Intelligence , Patient Education , Renal Diet, Comparative Study

Poster Presentation : Augmented Intelligence, Digital Health, and Data Science

Poster No. : B0066

Abstract Submission No. : APCN20250653

Integrating Multi-Biomarker Profiles with Machine Learning to Enhance Risk Stratification in Chronic Kidney Disease Progression

Rickie Isahdie Ahmad Mulyadi Lai^{1,2}; Henkie Isahwan Ahmad Mulyadi Lai³; Suci Ventasamia⁴

¹ Department of Medical Science and Technology, Faculty of Health Sciences, University College of MAIWP International, Kuala Lumpur, Malaysia

² Lablink, KPJ Selangor Specialist Hospital, Selangor, Kuala Lumpur, Malaysia

³ School of Biosciences, Faculty of Health & Medical Sciences, Taylor's University, Selangor, Malaysia

⁴ Faculty of Medicine, Universitas Kristen Indonesia, Jakarta, Indonesia

Abstract

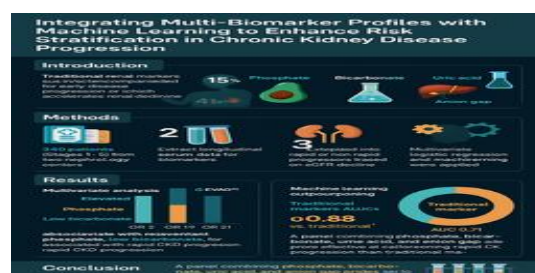
Traditional renal markers such as serum creatinine and urea often fail to detect early disease progression or subtle pathophysiological changes in chronic kidney disease (CKD). In Malaysia, where CKD affects an estimated 15.5% of adults, early and accurate risk stratification tools are crucial. This study investigates whether a panel of multiple non-traditional biomarkers, including phosphate, potassium, bicarbonate, uric acid, and anion gap can better predict rapid CKD progression than conventional indices.

We conducted a retrospective cohort study of 340 adult CKD patients (Stages 1–5) at two nephrology centers in Malaysia during 2024. Longitudinal serum data for creatinine, urea, phosphate, potassium, bicarbonate, uric acid, and anion gap were extracted from the laboratory information system. Patients were categorized as rapid progressors or non-rapid progressors based on an eGFR (estimated glomerular filtration rate) decline > 5 mL/min/1.73 m² per year. We applied multivariate logistic regression and machine learning algorithms (random forest and XGBoost) to identify the most predictive biomarker combinations for rapid progression.

Among the 340 patients, 29.7% experienced rapid eGFR decline. Logistic regression analysis showed that elevated serum phosphate (OR 2.3, 95% CI 1.4–3.7, $p = 0.001$), low bicarbonate (OR 1.9, 95% CI 1.2–3.1, $p = 0.007$), and a high anion gap (OR 2.1, 95% CI 1.3–3.3, $p = 0.004$) were independently associated with rapid CKD progression, even after adjusting for baseline kidney function. Machine learning models confirmed that the multi-biomarker panel achieved an area under the curve (AUC) of 0.88, substantially outperforming serum creatinine and urea alone (AUC 0.71).

Our findings demonstrate the clinical value of integrating non-traditional biomarkers into CKD monitoring. A combined panel of phosphate, bicarbonate, uric acid, and anion gap provides significantly better predictive power for identifying patients at risk of rapid progression than traditional markers alone. Implementing this multi-biomarker approach in routine care could enable earlier interventions and slower disease progression, which is especially important in high-burden populations like Malaysia.

Keywords : CKD progression, Machine learning, Random Forest, XGBoost, Non-traditional biomarkers, Predictive modeling



Poster Presentation : Augmented Intelligence, Digital Health, and Data Science

Poster No. : B0067

Abstract Submission No. : APCN20250943

Deep Learning Identifies Alternative Splicing Vulnerabilities Regulated by hnRNPF in Human Proximal Tubular Cells Under Diabetic Stress Conditions

Sahnaz Vivinda Putri¹; Rini Winarti²; Elfianny Syafruddin³; Prihantini⁴; Rifaldy Fajar

¹ Health Management Laboratory, International University Semen Indonesia, Gresik, Indonesia

² Department of Biology, Yogyakarta State University, Sleman, Indonesia

³ Computational Science Research Laboratory, BLK Muhammadiyah University, Bulukumba, Indonesia

⁴ AI-BioMedicine Research Group, IMCDS-BioMed Research Foundation, Jakarta, Indonesia

Abstract

Introduction: Diabetic kidney disease (DKD) is characterized by maladaptive tubulointerstitial responses to chronic hyperglycemia, including transcriptomic reprogramming in renal tubular epithelial cells. Alternative splicing (AS) has been increasingly recognized as a contributor to kidney disease progression, although its regulatory mechanisms under diabetic stress conditions remain insufficiently characterized. hnRNPF, a splicing factor responsive to osmotic stress, is overexpressed in diabetic kidneys and may modulate aberrant splicing in proximal tubule cells. This study aims to apply a deep learning framework to characterize hnRNPF-associated splicing alterations under hyperosmotic stress and assess their potential pathogenic relevance in DKD.

Methods: We retrieved transcriptomic data from the Gene Expression Omnibus (GEO), specifically dataset GSE299230, which profiles RNA-seq from HK-2 human proximal tubular cells overexpressing hnRNPF under 30 mM mannitol-induced hyperosmotic stress (n=3) and vector-only controls (n=3). Reads were aligned using STAR and quantified via Salmon. We implemented two deep learning architectures, SpliceFormer (transformer-based encoder) and DeepSpliceNet (multi-task CNN-RNN hybrid), trained on annotated splicing events from Gencode and VastDB, and fine-tuned to classify five AS event types: SE, A5SS, A3SS, MXE, and RI. Differential AS events were identified based on $\Delta\text{PSI} > |10\%|$ and $\text{FDR} < 0.05$. Functional relevance was inferred through g:Profiler and Reactome enrichment analysis. Splicing regulatory networks were reconstructed using integrated gradient-based attention inference, while unsupervised clustering of ΔPSI matrices was performed via UMAP to explore distinct splicing profiles in stressed versus control conditions.

Results: The ensemble deep learning model achieved an AUROC of 0.847 (95% CI: 0.818–0.876) across all AS categories. A total of 143 significant differential splicing events were detected, with 57.3% (82/143) being skipped exons (SE). Among these, 30.5% (25/82) involved genes linked to tubular epithelial polarity, including DAB2 and PARD6B. GO analysis indicated enrichment in epithelial morphogenesis (adjusted $p = 2.4e-6$), while Reactome pointed to splicing pathway perturbation ($p = 6.2e-5$). Regulatory inference identified SRSF3 and RBM47 as potential co-regulators under hnRNPF influence. UMAP clustering showed three discrete splicing signatures associated with maladaptive stress responses. Nineteen AS events corresponded to druggable exonic targets, suggesting opportunities for splicing-directed therapeutic strategies. Notably, aberrant exon inclusion in CFL1 and exon skipping in CLDN4 were predicted to alter cytoskeletal remodeling and paracellular barrier function, both validated across multiple splicing quantification algorithms.

Conclusion: This in silico study provides a computational characterization of hnRNPF-associated alternative splicing in proximal tubular cells under diabetic stress and identifies novel RNA-level mechanisms that may contribute to DKD pathogenesis and guide precision splicing-based interventions.

Keywords : Alternative Splicing, Diabetic Kidney Disease, Deep Learning, hnRNPF, Proximal Tubular Cells

Poster Presentation : Augmented Intelligence, Digital Health, and Data Science

Poster No. : B0068

Abstract Submission No. : APCN20250947

AI-Based Spatial Transcriptomic Mapping of Podocyte–Immune Crosstalk in Minimal Change Disease: A Predictive Model for Steroid Resistance

Sahnaz Vivinda Putri¹; Rini Winarti²; Elfianny Syafruddin³; Prihantini⁴; Rifaldy Fajar⁴

¹ Health Management Laboratory, International University Semen Indonesia, Gresik, Indonesia

² Department of Biology, Yogyakarta State University, Sleman, Indonesia

³ Computational Science Research Laboratory, BLK Muhammadiyah University, Bulukumba, Indonesia

⁴ AI-BioMedicine Research Group, IMCDS-BioMed Research Foundation, Jakarta, Indonesia

Introduction: Minimal Change Disease (MCD) is classically regarded as a steroid-sensitive nephrotic syndrome, although approximately 20–25% of patients experience steroid resistance or frequent relapses. Standard histopathological evaluation often fails to detect subtle molecular signals that precede treatment failure. Given the lack of reliable predictive biomarkers from baseline biopsy, there is a critical need for a computational framework that can predict resistance early by leveraging high-resolution spatial data. This study aimed to build an AI-driven model that predicts steroid resistance in MCD by analyzing spatial gene expression patterns of glomerular podocyte–immune cell interactions using biopsy-derived data.

Methods: We used spatial transcriptomic data from the Gene Expression Omnibus (GEO), dataset GSE277674, which includes digital spatial profiling of glomeruli from 10 patients with MCD and 4 controls, covering over 18,000 genes per region across 12 glomeruli per sample. Spatial graphs were constructed where each node represented microdomain transcriptomic profiles and edges were formed based on cellular proximity within 5–10 μm . Cell-type deconvolution was performed to annotate glomerular microdomains with podocyte, T cell, and macrophage identities using canonical marker gene sets. A spatial graph neural network (spatial-GNN) was developed to integrate spatial features and model directional signaling between podocytes and immune cells. An attention mechanism was incorporated to identify and prioritize microdomains most associated with resistance-related transcriptional activity. Labels for steroid resistance were computationally inferred based on transcriptional signatures, specifically upregulation of IFITM1, STAT1, HLA-DRA, and downregulation of podocyte integrity markers NPHS1 and SYNPO. Pathway enrichment was conducted to validate the biological plausibility of high-attention regions. Five-fold cross-validation was applied for model validation.

Results: The spatial-GNN model achieved an AUROC of 0.857, AUPRC of 0.802, and accuracy of 84.6% (95% CI: 78.1–91.0%) in identifying resistance-associated glomerular regions. High-attention microdomains were consistently enriched for CD80+ podocytes adjacent to CD68+ macrophages and CD3+ T cells. These regions showed a 2.3-fold increase in PD-L1 and CTLA4 expression, and a 1.7-fold reduction in NPHS1 and SYNPO. IL2/STAT5 and TNF- α /NF- κ B pathways were significantly enriched (adjusted $p < 0.001$). SHAP analysis ranked spatial podocyte–T cell proximity as the most influential feature (mean SHAP score 0.412), driven by microdomain-specific signaling gradients. Spatial correlation between CD86/CD80 density and glomerular injury score reached $r = 0.72$ ($p < 0.001$).

Conclusion: This AI-driven spatial transcriptomic model offers a non-invasive, biopsy-based framework to predict steroid resistance in MCD. By mapping podocyte–immune cell interactions in situ, this approach may support early risk stratification and guide future personalized immunomodulatory therapies.

Keywords : Minimal Change Disease, spatial transcriptomics, artificial intelligence, podocyte–immune interaction, steroid resistance

Poster Presentation : Augmented Intelligence, Digital Health, and Data Science

Poster No. : B0069

Abstract Submission No. : APCN20251097

Artificial Intelligence in Analyzing Liver Disease , How The Process Works?

JUMRIANI JUMRIANI¹; Ade Kartika Sari Sebba²

¹ Sciences Education Department, Teacher Training and Education Faculty, Universitas Sulawesi Barat, Majene, Indonesia

² Public Health Department, Bina Bangsa College of Health Sciences, Majene, Indonesia

Abstract

Liver disease is a global health problem with high morbidity and mortality rates, mainly due to cirrhosis, chronic hepatitis and liver cancer. Liver disease management requires accurate diagnosis, careful therapy planning, and complex long-term monitoring. In recent years, the development of artificial intelligence (AI) has brought major breakthroughs in the field of medicine, including in liver treatment. This study aims to assess the role and contribution of AI in supporting the treatment of liver disease through literature analysis. This study employed a systematic literature review following the PRISMA guidelines to evaluate the role of AI in liver disease detection used the keywords 'Artificial Intelligence', 'Liver Disease', 'Liver Surgery', 'Machine Learning', and 'Deep Learning' in articles published in the last five years (2019-2024). The study results show that AI plays an important role in five main aspects. Firstly, AI helps early detection and diagnosis of liver disease through radiological image analysis (ultrasound, CT-scan, MRI) with higher accuracy than conventional methods. Secondly, AI is able to classify liver lesions and determine the stage of the disease automatically by considering clinical, laboratory, and radiological data. Third, AI is used in surgery and therapy planning through the creation of 3D liver models, simulation of safe resection limits, and prediction of postoperative liver function reserve. Fourthly, AI supports the prediction of complication risk, prognosis, and likelihood of recurrence after treatment. Finally, AI becomes an important component in clinical decision support systems (CDSS), assisting clinicians in selecting the most effective and safe therapy. In conclusion, the use of AI in liver medicine has the potential to improve the accuracy, speed, and personalization of treatment, thereby supporting more precise and efficient healthcare.

Keywords : Artificial intelligence (AI), Machine Learning, Liver Disease, Liver Treatment

Poster Presentation : Augmented Intelligence, Digital Health, and Data Science

Poster No. : B0070

Abstract Submission No. : APCN20251146

Evaluating whether the diabetes e-platform can meet user needs from the perspective of service design

Lu, chiao Hsin¹

¹ Nursing Department Ministry of Health and Welfare Taoyuan Hospital

Abstract

Objective: With the rapid development of digital health technology, smart health management platforms play an important role in self-care for chronic diseases. However, whether the existing system can truly meet the needs of users is a systematic test.

There are three questions to explore:

1. From the perspective of service design, what are the main demand factors that users expect from smart platforms?
2. Does the quality function deployment method (QFD) build a quality house model to clearly correspond to user needs?
3. What are the key gaps in the actual service of the "Diabetes E-platform"?

Method: From the perspective of service design, using the "Diabetes E-platform" as a research tool, combined with the quality function deployment method (QFD), importance-performance analysis method (IPA) and technology acceptance model (TAM), through 102 health management platform demand questionnaires and 100 user satisfaction questionnaires, quantitatively analyze the relationship between users' functional requirements, performance and willingness to accept.

Results: This study used a questionnaire survey method to collect 102 health management platform demand questionnaires and 100 diabetes E-platform questionnaires for statistical analysis. The research results show that: 1. QFD analysis confirms that "health monitoring" and "personalized health advice" are the core needs that users value most. 2. The IPA four-quadrant diagram positions the above two functions in the "high importance, low performance" area, and points out that the usability of the interface needs to be improved first. 3. The TAM test results verify that "perceived usefulness" has a significant positive impact on "user satisfaction" ($\beta=0.80, p<0.01$), and "perceived ease of use" can positively predict usefulness ($\beta=0.65, p<0.05$).

Conclusion: The study not only enriches the evaluation methods of health management platforms, but also provides specific optimization suggestions for developers and institutions. It is advisable to strengthen the immediacy of information, optimize personalization and continuously simplify the operation interface, and strengthen the feedback mechanism to improve user experience and long-term stickiness.

Keywords : Diabetes e-platform, health management platform, service design, quality function deployment (QFD), importance-performance analysis (IPA)