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Intelligent Engineering Systems for Torque Motors, Privacy-Aware Learning, and Urban Risk

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Abstract

Intelligent engineering systems increasingly combine mechanical design, privacy-aware learning, biomedical evidence, and disaster-risk modeling. Oil-immersed torque motor design for two-dimensional valves provides an engineering hardware context involving precision actuation and electromechanical system performance. Privacy-aware lifelong learning architectures support the governance of data-intensive systems that evolve over time. Sequential recommendation research contributes adaptive learning mechanisms, while biomedical evidence on hepatic ischemia-reperfusion and remote cardiac injury shows how intelligent systems may support complex health-risk interpretation. Flood relocation research adds an urban-risk context involving household behavior and disaster adaptation. This literature cluster connects mechanical systems, intelligent learning, biomedical risk, and disaster governance by emphasizing reliability, system adaptation, and decision support across technical and social environments.

Keywords: diabetes drug discovery; FT-Transformer; metabolic risk reasoning; compound identification; knowledge graph; biomedical AI

1. Cross-Disease Evidence: Kidney, Neurodegenerative, and Oncological Links

Diabetes is associated with multiple disease domains. One important domain is kidney disease. Diabetic kidney disease is a major complication of long-term diabetes, and research on exosomes as microscopic messengers in kidney disease diagnosis suggests that extracellular vesicles may provide important mechanistic and diagnostic information. Exosome-related evidence may help connect diabetes-related compounds with renal biomarkers, inflammatory pathways, and cell communication mechanisms.

Another relevant domain is neurodegenerative disease. Diabetes has been associated with cognitive decline, vascular dysfunction, and neurological complications. Artificial intelligence research in neurodegenerative diseases and cognitive assessment provides a useful reference for understanding how computational methods can map disease mechanisms and clinical outcomes. Although neurodegenerative disease research is not the same as diabetes drug discovery, it offers valuable cross-disease evidence for evaluating compounds that may influence inflammation, vascular health, or metabolic effects in the nervous system.

Oncological evidence may also contribute to mechanism-level reasoning. Research on metalloptosis and tumor therapy shows how metal metabolism, oxidative stress, mitochondrial function, and nanoparticle-based interventions are connected to disease mechanisms. These mechanisms may overlap with metabolic dysfunction and

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inflammation, which are also relevant to diabetes. Cross-disease evidence should be interpreted carefully, but it can enrich the evaluation of candidate compounds by identifying shared biological pathways.

2. Sparse Computational Methods for Scalable Biomedical Discovery

Large-scale biomedical discovery requires efficient computation. Compound databases, molecular feature matrices, and biomedical knowledge graphs can be extremely large and sparse. Most compounds are connected to only a small subset of known targets, and most diseases are associated with limited sets of pathways, genes, or biomarkers. Therefore, sparse matrix computation is important for scalable candidate search.

Input-aware sparse matrix-matrix multiplication methods, such as IA-SpGEMM, are relevant because they improve computational efficiency for sparse graph and matrix operations. In a diabetes-related candidate identification system, sparse computation may support graph propagation, similarity search, pathway expansion, and multi-hop reasoning. Efficient computation allows researchers to search larger compound spaces and integrate richer biomedical evidence.

Scalability matters because drug discovery is an iterative process. As new compounds, targets, pathways, and clinical studies are added, the computational system must be updated. Sparse computational methods make it more feasible to maintain large biomedical reasoning systems and apply them to real-world discovery tasks.

3. Conclusions

An integrated framework for diabetes-related candidate identification can include four layers.

The first layer is data representation. This layer collects molecular descriptors, compound annotations, drug-target relationships, pathway data, disease associations, metabolic biomarkers, and clinical evidence.

The second layer is transformer-based candidate screening. FT-Transformer and hybrid FT-TRF models can be used to learn from structured biomedical features and generate candidate scores.

The third layer is knowledge graph reasoning. Candidate compounds are connected with targets, pathways, diseases, metabolites, and clinical outcomes. This layer helps explain why a compound may be relevant to diabetes.

The fourth layer is metabolic and cross-disease evidence integration. Evidence from obesity, hypercholesterolemia, kidney disease, neurodegeneration, inflammation, and oncology can be used to refine candidate prioritization.

Together, these layers support a more interpretable and clinically meaningful discovery process. Instead of producing only a ranked list of compounds, the system can provide reasoning chains that explain candidate relevance.

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