

PODIUM PRESENTATIONS

Kanchan Chowdhury
Marquette University



“Querying LLMs for Answering Geospatial SQL: Few-Shot Learning for Geospatial Objects and Operators”

AUTHORS

Samya Acharja, Marquette University
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ABSTRACT

Querying pre-trained LLMs using physical SQL operators to answer SQL queries by treating LLMs as large data repositories with rich information has recently gained the attention of researchers. This idea is still nascent and has not been extended to geospatial databases, largely due to two challenges. Firstly, LLMs have difficulty representing and reasoning over geometric primitives—points, lines, polygons—and associated coordinates, shapes, and topologies. Secondly, geospatial queries rely on spatial relationship operators (e.g., distance, intersects, overlaps, contains) in addition to standard SQL operations (selection, projection, join). This abstract proposes a new research direction with a vision to querying LLMs to answer geospatial database queries. We employ few-shot learning in two sequential phases: (1) learning embeddings that encode geospatial objects and topological context; and (2) learning representations for spatial relationship operators. In both phases, we use chain-of-thought prompting with question decomposition and intermediate reasoning steps. Regular SQL operators are handled using existing methods. Experiments on real-world SQL datasets indicate that carefully designed few-shot prompts can yield competitive performance, suggesting a promising path toward LLM-assisted geospatial querying. We outline evaluation protocols, including robustness to projection changes, and compositional generalization across spatial joins, to guide future LLM-based geospatial data management research.

Savannah Duenweg, PhD
Medical College of Wisconsin



“Quantitative assessment of prostate MRI intensity changes between sequential pre-surgical timepoints with post-surgical whole-mount pathological validation”

AUTHORS

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ABSTRACT

Background: Prostate cancer is the leading male cancer in the U.S. While prevalent, not all cases are high risk and can be managed through active surveillance. PI-RADS has standardized acquisition of prostate MRI; however, lesions are often described by hypointensity and “smudged” appearance, which may lead to inconsistencies in reads.

Aim: We sought to determine if intensity differences are observable between sequential prostate MRIs and if they correlate with pathological findings.

Methods: We analyzed data from 28 patients undergoing clinical and a subsequent research MRI prior to surgery. A prostate mask was delineated on T2WI and used to normalize images. Images were manually aligned, then automatically fine-tuned using ITK Snap. T2 subtraction maps were created by subtracting clinical (TP1) from research images (TP2). Post-surgical tissue was sliced using custom jigs created to align tissue sections to MRI. Tissue sections from 15 patients were H&E-stained, digitized, Gleason pattern annotated, and manually co-registered to T2WI using in-house software. Intensity differences across the prostate and within annotations were compared using paired t-tests.

Results/Conclusions: Across the prostate, normalized intensity significantly decreased by an average of 0.06 ($p < 0.001$). Across pathological annotations, atrophy, G3, and G4CG intensities increased, though not significantly. All other annotations decreased, though only HGPIN was significant (mean difference=0.17, $p=0.02$). In all noncancerous regions, there was a trending decrease in intensity (mean difference=0.04, $p=0.056$).

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PODIUM PRESENTATIONS

Anand George

Medical College of Wisconsin



“Neural Network and Ensemble Approaches to Predict Sepsis Risk in Multiple Myeloma Patients Receiving Bispecific Antibody Therapy”

AUTHORS

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ABSTRACT

Background: Treatment of Multiple Myeloma (MM) with bispecific antibodies (bsAb) results in an increased risk of infection, and predicting this risk is a significant unmet need.

Aim: Develop machine learning models to predict risk of infection in MM patients receiving bsAb therapy.

Methods: Clinical data was retrospectively collected in a multi-institutional cohort study (n=336), enrolling patients treated with at least one full dose of teclistamab or talquetamab. Using Python, AutoGluon-Tabular and PyTorch, neural networks were developed considering infection and severe infection ($\geq$ CTCAE Grade 3) as binary problems. To avoid overfitting and address imbalanced data, we used k-fold bagging, automatic sample weighting, and out-of-fold predictions. Feature importance was assessed using SHapley Additive exPlanations.

Results: Teclistamab, prior BCMA-directed therapy, and CRS were associated with highest risk of infection. Modeling identified patients at risk of $\geq$ Grade 3 infection within 90 days of bsAb with ROC/AUC of 0.71; accuracy was improved to AUC of 0.91 with an ensemble model, at risk of overfitting given cohort size.

Conclusions: To our knowledge, this is the first machine learning model that predicts infection risk within 90 days of initiating bsAb for MM, and will be validated in larger patient cohorts.

Tongjun Gu, PhD

Versiti



“Discovery of miRNA-RNA Biomarkers for Risk Stratification in Acute Myeloid Leukemia with Multi-Cohort Validation”

AUTHORS

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ABSTRACT

Acute myeloid leukemia (AML) is a clinically aggressive and molecularly heterogeneous malignancy. Current prognostic standards, such as the European LeukemiaNet (ELN) classification, do not fully capture the regulatory complexity underlying AML biology. We developed a novel framework integrating gene and microRNA (miRNA) expression across three AML cohorts, employing a two-step principal component analysis (PCA)-guided survival approach combined with support vector machine (SVM) classifiers. This strategy enabled rigorous cross-validation and improved capture of biological variation. Using this framework, we identified 19 prognostic genes, including established oncogenes (e.g., HMGA2, TAL1) and novel candidates (e.g., MLEC, NAGLU), achieving high ELN classification accuracy (AUC = 0.919). Parallel analyses yielded a 16-miRNA panel with AUCs up to 0.924. Notably, most AML genes functioned as oncogenes, whereas many miRNAs acted as tumor suppressors, underscoring their complementary roles. Integration of experimentally validated miRNA:gene interactions uncovered 10 biologically coherent regulatory pairs, most showing inverse and three showing positive correlations, that further improved risk stratification. Combined miRNA:gene SVM models achieved the best performance (AUC = 0.933), demonstrating the added value of regulatory integration. Overall, our framework yields compact, biologically coherent, and reproducible signatures with strong prognostic power and translational potential to refine AML risk stratification and support precision therapy.

PODIUM PRESENTATIONS

K M Sajjadul Islam

Marquette University



“multiMentalRoBERTa: A Fine-tuned Multiclass Classifier for Mental Health Disorder”

AUTHORS

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ABSTRACT

Background: Early detection of mental health disorders from social media text is essential for enabling timely support, risk assessment, and referral. Automated systems must balance accuracy with interpretability and safety to ensure responsible use in sensitive contexts.

Aim: This study introduces multiMentalRoBERTa, a fine-tuned RoBERTa model for multiclass classification of mental health conditions, including stress, anxiety, depression, posttraumatic stress disorder (PTSD), suicidal ideation, and neutral discourse.

Methods: Leveraging multiple datasets, the research involved data exploration to analyze class overlaps, revealing strong correlations between depression and suicidal ideation as well as anxiety and PTSD, with stress emerging as a broad, overlapping category. Comparative experiments evaluated traditional machine learning methods, domain-specific transformers, and prompting-based large language models. Explainability techniques, including Layer Integrated Gradients and KeyBERT, were applied to identify lexical cues driving classification, particularly in distinguishing depression from suicidal ideation.

Results/Conclusion: multiMentalRoBERTa achieved superior performance, with macro F1-scores of 0.839 in the six-class setup and 0.870 in the five-class setup (excluding stress), outperforming MentalBERT and baseline classifiers. The findings highlight fine-tuned transformers as reliable, interpretable, and deployable tools for mental health detection, while underscoring the importance of fairness, bias mitigation, and human-in-the-loop safety protocols.

Jeremy Kedziora, PhD

Milwaukee School of Engineering



“Surrogate Optimization for Direct Feature Selection”

AUTHORS

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ABSTRACT

In classical machine learning and data science feature selection is both a key decision impacting model performance and an intractable problem because the number of feature selections is exponential in the number of features. In this paper, we study the use of surrogate optimization (SO) techniques to learn the optimal feature selection. SO is a flexible method for optimizing black-box functions by: 1) building a probabilistic model (the surrogate) of the relationship between inputs and outputs of said function using observations of function evaluations and 2) proposing the next input to try (the acquisition). To apply SO to the feature selection context we propose a novel but simple sampling-based acquisition method to search the feature selection space directly for promising candidate feature selections to evaluate. We demonstrate the effectiveness of this approach empirically using Monte Carlo experiments and show: 1) that the number of iterations to find the optimal feature selection is linear in the number of features; 2) that it substantially outperforms alternative wrapper feature selection methods (e.g. the greedy algorithm) at finding the optimal feature selection in linear data; 3) that leads to significant performance increases over embedded feature selection methods (e.g. random forest) in non-linear data.

PODIUM PRESENTATIONS

Paraic Kenny, PhD
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ABSTRACT



“A user-friendly, no-code, application for HIPAA-compliant automated analysis of tabular data at scale”

AUTHORS

Paraic A. Kenny, PhD
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Background: Clinical research often requires reviewing large volumes of unstructured electronic medical record (EMR) data, a time-consuming task demanding skilled personnel. Large language models (LLMs) like ChatGPT can efficiently analyze and summarize text, potentially accelerating chart review research. However, concerns about personal health information (PHI) leakage limit use of commercial chatbots. Secure, in-house LLMs within fire-walled environments can address these concerns.

Aim: To develop a user-friendly, scalable application leveraging an in-house ChatGPT 4o-mini on Emplify Health’s Azure cloud to automate processing of tabular clinical data while protecting PHI.

Methods: The application imports tabular data (Excel or text), guides users through prompt engineering, and automatically submits data row-by-row to the LLM. It retrieves and tabulates results as specified by users, enabling both automated extraction of clinical parameters, as well as data summarization/interpretation.

Results/Conclusions: Initially designed to identify cancer cases and extract related parameters from pathology reports, a fully generalized application was developed which has found utility in analyzing diverse data sources including cancer registries, cardiology CT reports, imaging narratives, and clinical notes. This tool has significantly accelerated research by reducing data retrieval time, allowing staff to focus on higher-value tasks like data analysis, while maintaining PHI protection.

Soma Mohanty
University of Wisconsin - Milwaukee

ABSTRACT



“Hybrid Semantic-Graph Speech Analysis for Early Detection of Alzheimer’s Disease”

AUTHORS

Soma Mohanty, M.S. Student, Department of Computer Science, University of Wisconsin–Milwaukee (Presenting Author)
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Background: Detecting Alzheimer’s disease (AD) in its early stages remains a major clinical challenge, yet early intervention is critical for effective care. Speech offers a non-invasive signal for screening, but most prior studies emphasize basic acoustic cues such as pitch or intensity. Valuable markers in both what is spoken (semantic content) and how the audio signal evolves over time (structural dynamics) are often underexplored.

Aim: This project proposes a hybrid approach that integrates semantic, acoustic, and structural features to improve early AD detection from spontaneous speech.

Methods: We will analyze publicly available corpora such as the DementiaBank Pitt Corpus (over 250 participants, including individuals with AD and healthy controls). These datasets include both audio recordings and aligned transcripts, enabling multi-level analysis. From the audio, we will extract acoustic features (pitch, intensity, duration) and structural graph features using Natural and Horizontal Visibility Graphs (NVG, HVG). From transcripts, we will generate semantic embeddings using models such as Sentence-BERT or ClinicalBERT. These features will be fused and evaluated with hybrid classifiers, including BiLSTM with attention and ensemble methods, using cross-validation and, where possible, external validation.

Results/Conclusion: We anticipate the hybrid model will outperform acoustic-only baselines by capturing richer semantic and structural markers of decline. This low-cost, non-invasive approach could provide clinicians and even laypeople with an accessible tool for earlier AD screening.

Funding Source: None.

PODIUM PRESENTATIONS

Ronald Nowling

Milwaukee School of Engineering



“Microsecond Molecular Dynamics Simulations of an Alpha-Bungarotoxin Peptide Ligand”

AUTHORS

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ABSTRACT

HAPep and other short synthetic peptides are promising alternatives to anti-venoms for highly-toxic neuro-toxins like α -Bungarotoxin (α -BTX). Experimental work has demonstrated that HAPep binds to α -BTX with high affinity and resolved the static structure of the bound complex. The dynamics of HAPep, especially when not bound to α -BTX, have not yet been resolved. This work reports the achievement of extending previous 200 ns molecular dynamics simulations of HAPep in bound and unbound configurations to over 28 μ s (140 times longer than previous simulations) and the subsequent analyses of these simulations. Three macroscopic states were inferred using dimensionality reduction and clustering. Transition rates and times scales between the states were modeled using a Markov State Model (MSMs). The simulations indicate the presence of a stable state with non-native hydrogen bonds that may slow down and/or complicate folding pathways for reaching the β -hairpin structure observed in the bound complex with α -BTX.

Will Sebelik-Lassiter

Milwaukee School of Engineering



“THE ROLE OF ARTIFICIAL INTELLIGENCE IN VOCAL CORD ULTRASOUND INTERPRETATION”

AUTHORS

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ABSTRACT

The Role of Artificial Intelligence in Vocal Cord Ultrasound Interpretation (Project VIPR)

Introduction: Vocal cord paralysis (VCP) occurs as the result of anatomic or neurologic injury, primarily from thyroid and parathyroid surgery. The current standard of care for assessing VCP, endoscope-based laryngoscopy, is both invasive for the patient and expensive for the healthcare provider.

Vocal cord ultrasound (VCUS) has been suggested as an alternative to laryngoscopy, but is operator-dependent and may be difficult to interpret in some patients. In this research, we created an artificial intelligence (AI) model that can employ computer vision analysis to differentiate vocal cord motion from non-motion in ultrasound images captured under varying circumstances.

Methods: De-identified VCUS images were obtained from 30 healthy volunteers with clinically normal voice function, then synthetic models of VCP were created from these healthy images due to a lack of access to suitable clinical examples of pathology. We then trained a novel convolutional neural network (CNN), called VIPRnet, to differentiate between these healthy and synthetic VCP images.

Conclusion: We have shown through this promising proof-of-concept that vocal cord ultrasound is a non-invasive, inexpensive, and accurate alternative to laryngoscopy for evaluating vocal cord function. Additionally, augmenting VCUS with machine learning has the potential to reduce operator-dependence and provide consistent, accurate analysis of ultrasound imaging.

PODIUM PRESENTATIONS

Tyler Trask, MHA
Medical College of Wisconsin



“Enhanced Sampling Molecular Dynamics Reveals the Alternating Access Mechanism of a Prototypical SMR Transporter”

AUTHORS
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ABSTRACT

Antimicrobial resistance remains a critical and escalating public health threat. One major driver is the activity of multidrug-efflux pumps, like those in the small multidrug resistance (SMR) transporter family. Prototypical members of two SMR subtypes—Gdx (guanidinium exporters) and Qac (quaternary ammonium compound transporters)—exhibit strong structural similarity, with a Cα RMSD of just 1.2 Å. Interestingly, they display distinct substrate transport profiles, indicating divergent mechanisms of substrate selectivity.

To investigate, we employed a machine learning integrative approach developed in our lab (Marinelli et al., PNAS 2024), combining high-resolution X-ray crystallography with enhanced sampling molecular dynamics simulations. Using a specialized mean-force analysis, we quantified the free energy landscape governing protein conformational changes during transport. This computational framework enables us to resolve the complete transport mechanism in the presence of the native substrate, providing new insights into the molecular determinants of substrate specificity. The computational results were validated by single-molecule Förster resonance energy transfer (FRET) experiments, providing a molecular explanation of the single-molecule time traces. Our findings deepen the mechanistic understanding of SMR transporters and establish a generalizable simulation-based methodology suitable for other membrane transport proteins, especially when integrated with experimental data. Funding provided by MCW Start-Up Funds.

Kevin Umba
Marquette University



“Quantum Meets Blockchain: Building Secure and Innovative Healthcare Solutions in Milwaukee”

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ABSTRACT

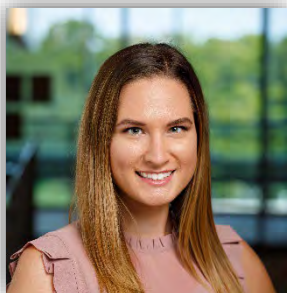
This research paper proposes a proof-of-concept that explores how hospitals can build unified prediction models using quantum machine learning (QML), Federated Learning (FL), and blockchain to address data security, privacy, and feasibility. The proof-of-concept uses post-quantum cryptography (PQC) to protect data in transit via quantum-resistant encryption, anticipating future threats. The system also uses Differential Privacy to anonymize patient data for privacy, and an experimental blockchain mechanism with Non-Fungible Tokens (NFTs) to transfer data ownership to patients while providing a reliable record of data access and transfer. Our approach provides an experimental proof of concept that can be expanded upon in a production iteration or through further research to maintain privacy and secure model sharing, thereby contributing to medical progress.

Despite limited equipment and scope, the PoC demonstrated that building a shared machine learning model while maintaining privacy, confidentiality, and transparency was feasible. Federated Learning and Differential Privacy anonymized patient data and only shared model parameters instead of identifiable patient data to preserve privacy. PQC encrypted data in transit and at rest in an off-chain database. The blockchain provided non-repudiation and transparency by recording each transfer on an immutable ledger. The system also transferred data ownership to patients via NFTs access management. Future directions include various considerations as this prototype was not meant for production. Critical improvements involve Identity and token lifecycle management, transitioning to a permissioned network for confidentiality, and performance improvements.

PODIUM PRESENTATIONS

Aleksandra Winiarz

Medical College of Wisconsin



“Association of FET PET tumor volume and radio-pathomic maps of cell density in newly diagnosed glioblastoma patients”

AUTHORS

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ABSTRACT

Glioblastoma is monitored with conventional MRI which lacks biological and metabolic information. O-(2-[¹⁸F]fluoroethyl)-L-tyrosine (FET) PET imaging addresses this by visualizing metabolically active tumor. We have a published machine learning algorithm that uses MRI data and autopsy tissue to generate radio-pathomic (RP) maps of cell density. This study investigated the hypothesis that regions of increased uptake of FET overlap with high cell density in areas of active tumor.

15 newly diagnosed GBM patients with FET PET and clinical imaging were included. We generated cell density maps for each patient and annotated for high cell density. FET uptake in healthy brain tissue as reference value was assessed by drawing a crescent-shaped region of interest on the contralateral side on 6 consecutive slices. FET PET tumor masks were created using clinically established tumor-to-brain ratio (TBR) ≥ 1.6 . Additional FET PET masks were created using a lower TBR ≥ 1.3 .

The overlap between cell density maps and FET PET tumor volumes based on TBR of ≥ 1.6 was low (Dice similarity coefficient (DSC), 0.26). Using the FET PET tumor volumes based on TBR ≥ 1.3 , greater spatial similarity was noted (DSC, 0.51). Patients with DSC ≥ 0.5 (n=9) between the RP cell density maps and the FET PET tumor volumes had a significantly higher FET uptake compared to the patients with DSC ≤ 0.5 (n=6; mean FET uptake, 2.24 ± 0.59 vs. 1.73 ± 0.23 ; p=0.04).

These findings demonstrate an association between metabolically active tumor regions and cellular tumor defined by FET PET and cell density maps. Lowering the FET PET threshold from a TBR of ≥ 1.6 to ≥ 1.3 , greater overlap was observed, suggesting cell density maps are more sensitive to tumor cells compared to FET PET, likely due to limited spatial resolution. Patients with greater overlap showed higher FET uptake suggesting greater metabolic activity. Further studies are warranted to better understand these results.

PODIUM PRESENTATIONS

Robert Wujek, PhD

Medical College of Wisconsin



“iTb Maps: Using Cnvolutional Neural Networks with Multiparametric MRI to Visualize Infiltrating Brain Tumor”

AUTHORS

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ABSTRACT

Background: MRI with contrast agent administration is considered the gold standard for detecting and evaluating brain tumors. However, this standard approach is incapable of showing brain tumor that infiltrates into non-enhancing lesion (NEL) beyond the bright contrast-enhancing regions. The inability to detect infiltrating tumor burden (ITB) is thought to be a primary reason why the most aggressive brain tumors are incurable.

Aim: As a solution, a CNN was trained, referred to as the iTB model, to classify tissue as tumor or non-tumor within NEL using multi-parametric MRI (mpMRI) inputs and image-localized biopsy tissue as ground truth labels.

Methods: The iTB model was designed using a 3D ResNet-type network incorporating ConvNeXt based modifications. A large, histologically validated dataset (N=233 samples, 71 patients) of stereotactically acquired biopsy samples that were spatially co-registered with mpMRI was used for model training (80%) and evaluation (20%). A novel forward selection augmentation optimization procedure was used to further improve iTB model performance. iTB maps were generated by per-voxel inference of segmented NEL.

Results/conclusion: Before augmentation optimization, the iTB model achieved an accuracy of 0.745 and an AUC of 0.859. After augmentation optimization, performance improved to an accuracy of 0.855 and an AUC of 0.942.

Josiah Yoder

Milwaukee School of Engineering



“Layer Streaming Distillation”

AUTHORS

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ABSTRACT

Distributed machine learning offers significant advantages over centralized approaches, including improved accessibility, memory efficiency, and performance. However, despite these benefits, distributed training remains underused, often sacrificed in favor of data security-centric methods such as federated learning. A major barrier to wider adoption is the lack of effective algorithms that efficiently leverage distributed compute. Current training methods often rely on bandwidth-heavy all-gather operations and global gradient dependencies, making distributed training challenging. In this paper, we propose a novel approach to distributing layer-wise knowledge distillation. By carefully routing data, passing layer parameters instead of activations, and eliminating cross-device gradient dependencies, our method significantly reduces training wall time compared to data-parallelization. Furthermore, our approach reduces communication bandwidth, improves memory utilization, and enables flexible resource allocation.

PODIUM PRESENTATIONS

Michael Zimmermann, PhD
Medical College of Wisconsin

ABSTRACT



*"Computational Structural Genomics is a New
Bioinformatics Frontier to Transform Diagnostics
and Therapeutics"*

AUTHORS

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We present a paradigm for better understanding and treating human diseases caused by epigenetic dysregulation. Our premise is that studying multi-protein complexes, rather than individual genes, provides better mechanistic understanding, improve diagnostics, define disease spectra, and build trajectories towards therapeutics. This paradigm emerged from our work in Genomic Odyssey Boards, where clinical and research teams integrate findings from classical genomics approaches with our calculations that leverage three-dimensional and time-dynamic modeling of gene products. This is important since current guidelines and data science methods for genetic diagnosis are primarily based on single genes, linear sequences, evolutionary conservation, and population-level empirical observations, rather than 3D features and calculations derived from gene products. We provide examples of this paradigm through studies of the BAF complex from the SWI/SNF family of chromatin remodeling enzymes, and the COMPASS complex from the histone methyltransferase family. These enzymes regulate genome accessibility and whose activity changes influence epigenatures, or the patterns of genomic accessibility that define cellular states and human diseases. The information we derive feeds back to our translational program to empower a positive cycle where we are discovering mechanisms of genetic diseases, expanding the numbers of patients that can be diagnosed, and identifying potential therapeutic paths.