ABSTRACTS OF INVITED LECTURES – ISABS

Presentation number: IL 01 Abstract number: 147-ISABS-2026

FROM SCREENING TO ACTION: AI FOR DETECTING AND MANAGING ASYMPTOMATIC CARDIAC DISEASE

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Artificial intelligence (AI) is transforming cardiovascular medicine by expanding the role of the electrocardiogram (ECG) from a tool for rhythm interpretation to a scalable platform for disease detection, risk prediction, and population screening. In this presentation, we showcase how deep learning applied to raw ECG signals enables detection of conditions that are not traditionally identifiable from ECGs. We present AI models capable of identifying left ventricular systolic dysfunction, predicting atrial fibrillation even during normal sinus rhythm, and detecting systemic diseases such as liver cirrhosis. These approaches demonstrate strong diagnostic performance and highlight the ability of AI to extract clinically meaningful signals beyond human perception. We further discuss real-world implementation, including integration into clinical workflows and deployment at scale across primary care, wearable devices, and diverse global settings. Evidence from pragmatic clinical studies suggests that AI-guided screening can improve disease detection while maintaining efficient use of healthcare resources. Finally, we explore future directions, including multimodal AI, point-of-care imaging, and novel data sources such as voice, alongside key challenges related to validation, bias, and ethical deployment. Together, this work illustrates how AI can augment clinical decision-making and enable earlier, more effective detection of disease at scale.

Keywords: artificial intelligence (AI), electrocardiogram (ECG), deep learning, disease detection, risk prediction

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DATA-DRIVEN DISCOVERY OF LATENT ALS PHENOTYPES THROUGH +ICA AND EHR-BASED AI MODELING

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Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease characterized by progressive motor neuron loss, diagnostic delay, and substantial clinical heterogeneity. Current diagnostic and prognostic approaches rely largely on predefined clinical features and often fail to capture subtle, evolving patterns that precede diagnosis or distinguish biologically meaningful disease subgroups. We apply Independent Component Analysis (ICA) and supervised machine learning to large-scale electronic health record (EHR) datasets to identify latent ALS phenotypes that may improve early diagnosis, prognostic prediction, and patient stratification. We analyze two complementary EHR resources: the Vanderbilt University Medical Center Synthetic Derivative, which includes more than 3.9 million records and over 1,200 clinically confirmed ALS cases, and the NIH All of Us Research Program, a diverse national cohort with harmonized EHR and genomic data. Longitudinal clinical variables, including diagnoses, laboratory values, medications, and other structured features, are transformed into smoothed clinical trajectories suitable for ICA. ICA-derived components are then integrated into machine learning models to predict ALS diagnosis, disease progression, and survival, with model interpretability assessed using feature attribution approaches. Latent phenotypes are evaluated for associations with known clinical and genetic features, including ALS subtype, cognitive involvement, progression rate, and pathogenic variants. This work generates a scalable, data-driven framework for uncovering hidden clinical structure in ALS. By identifying early clinical signatures and biologically meaningful patient subgroups, this approach supports earlier diagnosis, more precise risk assessment, improved cohort enrichment for clinical trials, and more personalized care for individuals living with ALS.

Keywords: amyotrophic lateral sclerosis, electronic health records, independent component analysis, machine learning, precision medicine

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ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING IN BIOMANUFACTURING

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This presentation discusses strategies for the application of artificial intelligence and machine learning (AI/ML) to bioprocess development and manufacturing. While machine learning methods can outperform traditional data analytics tools, a limitation of applying machine learning has been that the selection of the best ML method requires a substantial level of expertise. In practice, methods are chosen based on familiarity, which limits performance, or on cross-validation results from a large candidate model pool, which overfits data. Some reasons are discussed for why commercial Automated ML tools for building models fail when applied biomedical and bioprocess data. Then an AI/ML approach for building data driven models is described that empowers the users to focus on the goals of the intended application rather than on method selection. The approach is based on domain knowledge, the specific data characteristics, and next cross-validation procedures. For some industrial bioprocess datasets, the approach selects symbolic learning methods that produce more accurate models that are also interpretable by humans. The frontier of AI/ML methods, which is the incorporation of mechanistic knowledge, is also briefly discussed.

Keywords: artificial intelligence, machine learning, biomanufacturing, symbolic learning, interpretable machine learning

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FROM CODE TO CLINIC: CHALLENGES AND OPPORTUNITIES IN TRANSLATING AI INTO RADIOLOGY PRACTICE

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The integration of artificial intelligence into radiology practice presents challenges that extend well beyond model development and validation. This lecture addresses the gap between research-grade AI and clinically deployed tools, focusing on project prioritization, feasibility assessment, and organizational readiness. Drawing from operational experience building and deploying AI solutions in a large radiology department, we examine how the criteria used to evaluate project value differ fundamentally between a research context and a clinical translation context. In research, feasibility centers on data availability, model performance, and scientific novelty; in clinical translation, feasibility must also account for regulatory pathways, system integration, maintenance burden, and sustainable adoption. We describe how misapplying research -oriented prioritization criteria to clinical deployment decisions leads to resource misallocation, project stagnation, and a growing gap between what is technically possible and what is operationally viable. Our experience supports a structural distinction between discovery and validation work on the one hand, and implementation -ready projects on the other, each governed by distinct intake criteria, success metrics, and ownership pathways. We conclude that translating AI into radiology practice requires not only technical rigor but deliberate institutional design, including explicit triage frameworks, defined handoff structures, and a shared organizational language for what clinical readiness truly means.

Keywords: radiology AI, clinical deployment, AI translation, project prioritization, clinical feasibility

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FROM THE DOUBLE HELIX TO THE GENOMICS INFORMATION EXPLOSION

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The molecular biology era began with the publication in Nature of the Double Helix model by Watson and Crick and the resulting focus on how biological information is stored and transmitted. PCR uses the same strategy to amplify a target DNA sequence in vitro that the cell uses for DNA replication. The history of PCR development and applications to forensic genetics, medical genetics, and evolutionary genetics will be reviewed. The introduction of a heat stable DNA polymerase made PCR more specific, more efficient, and automatable. The ability to detect a single DNA molecule enabled the analysis of single sperm for measuring recombination, gene conversion, and de novo mutation, and enabled the clonal sequencing property of NGS. The massively parallel aspect of NGS has expanded genomic sequence information, but its clonal feature has made possible the analysis of mixtures. Moving from this historical review, our current project in non invasive prenatal testing by NGS analysis of maternal plasma (a mixture of fetal and maternal DNA) will be discussed. A plasma library encompassing 4 kb of the beta globin (HBB) gene region, prepared by capture hybridization, is sequenced (Illumina MiSeq). Counting single nucleotide polymorphism (SNP) allelic sequence reads yields an estimate for the fetal fraction (FF, typically 5-15%), and expected sequence read ratios at the mutation site for potential fetal genotypes, based on the FF, are compared to observed ratios to predict the genotype. Low FF and based solely on the mutation site limit statistical confidence. Since maternal sequence reads in plasma are slightly longer than fetal reads, we enrich the fetal fraction by excluding longer reads through in silico size selection. By PCR amplifying a 2.2 kb HBB fragment from parental DNA and sequencing the amplicon with the Oxford Nanopore platform, we determine haplotypes and use allelic ratios at linked SNPs to increase statistical confidence in fetal genotype predictions.

Keywords: PCR (Polymerase Chain Reaction), next-generation sequencing (NGS), fetal fraction (FF), haplotypes, beta globin (HBB) gene

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IMAGING-DRIVEN AI MODELS: PERSONALIZING CARDIOVASCULAR MEDICINE

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Ischaemic heart disease remains the leading cause of mortality worldwide. Coronary computed tomography angiography (CCTA) is the reference non-invasive modality for ruling out obstructive coronary artery disease (CAD) in symptomatic patients. However, in contemporary clinical practice, obstructive CAD is detected in only 15-25% of patients undergoing CCTA, leaving the vast majority classified within a heterogeneous spectrum of non-obstructive or subclinical coronary disease. This large and diverse patient population spans conditions ranging from the complete absence of detectable atherosclerosis to advanced coronary disease characterized by extensive plaque burden, adverse plaque phenotypes, vascular remodeling, and inflammatory activation. Importantly, cardiovascular risk in these patients is highly variable, ranging from negligible levels to a risk approaching or exceeding that of obstructive CAD. Conventional stenosis-based paradigms are insufficient to capture this complexity, underscoring the need for more refined, biologically informed risk stratification. Recent advances in artificial intelligence (AI) applied to CCTA have enabled the extraction of high-dimensional imaging biomarkers, including quantitative plaque burden, plaque composition, vessel wall remodeling, perivascular fat characterization, and hemodynamic descriptors. When integrated with clinical variables, laboratory biomarkers, genetic profiles, and environmental factors, these AI-derived imaging features allow the construction of individualized, predictive models of cardiovascular risk. Such imaging-driven AI frameworks represent a paradigm shift toward truly personalized cardiovascular medicine, enabling risk assessment and preventive strategies to be precisely targeted to the dominant pathophysiological mechanisms driving disease-related risk in each patient. By moving beyond luminal stenosis to a comprehensive, dynamic characterization of coronary atherosclerosis and vascular inflammation, AI-enhanced CCTA has the potential to transform prevention, guide therapy, and improve long-term cardiovascular outcomes.

Keywords: CAD, CCTA, atherosclerotic plaques, AI, prognosis

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INFLAMMAGING: IT IS TIME FOR CLINICAL APPLICATION

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Inflammaging describes a chronic, systemic, low-grade inflammatory state that is recognized as a major risk factor for age-related diseases (ARDs) and a pivotal convergence point of multiple biological mechanisms involved in aging. A major characteristic of inflammaging is its heterogeneity emerging as a consequence of each individual's lifelong exposures to inflammatory stimuli, shaped by a unique combination of genetics, lifestyle, socioeconomic conditions and environmental factors such as infections and pollution. Thus, a crucial problem is how to measure inflammaging. Two clocks addressed this topic. Both the first and the second clock are capable of quantifying inflammatory age and show strong association with ARD incidence, despite taking into account a different set of inflammatory markers. The second clock, based on just 10 immunological parameters (SImAge) and using explainable artificial intelligence methods, is able to explain the model solution for each individual participant. Moreover, we developed EpInflammAge, an explainable deep learning tool that integrates epigenetic and inflammatory markers to create a highly accurate, disease-sensitive biological age predictor. This novel approach bridges two key hallmarks of aging-epigenetic alterations and immunosenescence. Finally, we consider interventions that may counteract inflammaging, including nutritional interventions, physical activity and gerotherapies such as senolytics. We propose that deepening our knowledge of the individual nature of inflammaging stands to enhance our understanding of personalized aging trajectories and inform precision interventions.

Keywords: inflammaging, biological clocks, inflammatory age, explainable artificial intelligence

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REALIZING THE PROMISE OF DIGITAL BIOMARKERS: CHALLENGES AND PHARMA'S ROLE IN DEVELOPMENT

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Across many medical indications, disease diagnosis, monitoring of progression, and evaluation of treatment response are limited by the absence of clear, objective biomarkers. In their place, clinicians rely heavily on patient self report and clinical rating scales that, while indispensable, are subjective, prone to errors, sparsely sampled and present a burden on both patients and clinicians. This presentation examines digital biomarkers as a potential re imagining of how health and disease may be measured. Digital biomarkers leverage widely available technologies and sensors including smartphones, wearables, voice recordings, and video to capture continuous, objective signals of human physiology and behavior in real world settings. The talk introduces what digital biomarkers are, why they may meaningfully complement traditional clinical assessments, and how they may enable more sensitive, frequent, and personalized measurement. At the same time, their promise is balanced by substantial scientific and practical challenges, spanning clinical usability, interpretability, validation, and integration into pharmaceutical development. Rather than viewing digital biomarkers as a single end to end solution, this presentation frames them along a spectrum of clinical proximity, highlighting the importance of aligning specific digital measures with well defined components of the clinical phenomena. The presentation concludes with selected examples from Teva's ongoing digital biomarker initiatives across multiple disease areas, illustrating both tangible progress and the rigor required for successful translation. Together, these examples suggest how digital biomarkers may ultimately support earlier insight, more precise monitoring, and the delivery of better therapies for patients.

Keywords: digital biomarkers, clinical assessment, patient monitoring, digital health, drug development

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FROM PAPER CHARTS TO HOSPITAL-WIDE DETERIORATION DETECTION: AMP, CEDAR, AND SEPSIS SURVEILLANCE

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The transition from paper-based charts to electronic medical records (EMRs) has unlocked unprecedented opportunities to develop real-time systems that continuously monitor hospitalized patients for clinical deterioration. This presentation reviews the historical evolution of electronic surveillance platforms, highlighting the development and implementation of AMP, CEDAR, and the Sepsis Sniffer at Mayo Clinic. Drawing on decades of experience in critical care informatics and clinical event detection, the presentation examines how real-time analytics, automated alerts, and AI-enhanced tools identify physiological decline across the hospital continuum. Given that sepsis remains a leading cause of morbidity and mortality, early recognition and rapid intervention are critical to improving patient outcomes. Finally, we will address the practical limitations of current approaches, focusing on workflow integration, model generalizability, and the barriers to clinician adoption.

Keywords: clinical deterioration, artificial intelligence, clinical surveillance, hospital-wide monitoring, decision support systems

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AI IN PATHOLOGY: USE CASES FOR AND AGAINST – A FRAMEWORK FOR PRESERVING BRAIN CAPITAL IN THE DIAGNOSTIC APEX

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AI integration in pathology is hindered by a significant gap between technical validation and clinical adoption; many tools demonstrate strong performance metrics but fail clinically because they do not account for pathologist cognitive demands. This work presents a five-criterion calibration framework centered on preserving "brain capital" – the finite cognitive resources available to clinicians – and stabilizing the "diagnostic apex," where histological evidence meets clinical judgment. Using cognitive load theory and implementation science, we developed the Pathology AI Diagnostic Balance, a conceptual model mapping the physician-specimen interaction within working memory and IT infrastructure constraints, validated through case studies of implemented pathology AI tools. The framework identifies five evaluation criteria: Contextual Literacy (integration of clinical history), Responsibility (preservation of signing authority and prevention of chronic doubt through spatially localized outputs), Evidence Gap Analysis (closure of diagnostic uncertainty), Verification (feasibility and speed of quality control), and Opportunity Cost (net return on cognitive investment). Successful tools – such as Ki-67 quantification and breast cancer screening AI – reduce cognitive burden by automating routine tasks or enabling rapid verification; conversely, tools requiring exhaustive re-review or producing opaque recommendations deplete cognitive bandwidth and cause decision fatigue. This framework enables pathologists to assess whether AI tools genuinely enhance diagnostic capability or merely redistribute burden, shifting evaluation from purely technical metrics to clinically relevant measures of cognitive impact. By prioritizing cognitive sustainability and clinical utility over technical performance alone, the profession can ensure AI serves as a genuine diagnostic force multiplier rather than an additional burden.

Keywords: artificial intelligence, cognitive load theory, diagnostic workflow, pathology, precision medicine

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SPATIALLY INTELLIGENT ONCOLOGY: INTEGRATING MULTIMODAL AI TO DECODE AND TREAT TUMORS

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Spatially resolved transcriptomics and proteomics are transforming oncology by revealing how tumor ecosystems are organized across tissue architecture, immune niches, stromal programs, and treatment-associated states. Yet extracting insight from these multimodal data remains challenging, requiring programming expertise, spatial statistics, visual interpretation, and iterative hypothesis refinement. We present spatiAlytica, a viewer-centric multi-agent AI system embedded in the Napari spatial viewer that enables natural-language, stateful, and image-grounded spatial biology analysis. spatiAlytica coordinates agents for data resolution, code generation, error recovery, spatial visual question answering, and biological interpretation, supported by memory across multi-turn workflows. Across benchmarks in single-turn code generation, sequential multi-turn analysis, and image-grounded reasoning, spatiAlytica outperformed existing agentic baselines. In oncology case studies, spatiAlytica decoded tumor biology across modalities and disease contexts. In Kaposi's sarcoma, it mapped stage-dependent tissue remodeling, viral tropism, niche composition, and immune dysfunction, revealing progressive CD8 T-cell transition from early immune surveillance to tissue-retained dysfunction. In colorectal cancer CODEX data, it identified subtype-specific immune niches and linked reduced PD1 -positive CD4 T-cell localization in granulocyte-enriched neighborhoods to poorer overall survival. In high-grade serous ovarian cancer Visium da ta, it characterized chemotherapy-associated cancer-associated fibroblast remodeling, showing how treatment reshapes the spatial tumor microenvironment. Together, these results support spatially intelligent oncology, where multimodal AI helps decode tumor ecosystems, identify clinically relevant spatial immune states, and generate hypotheses for therapeutic stratification and intervention.

Keywords: spatial biology, multi-agent system, multi-modal AI, Kaposi's sarcoma, colorectal cancer

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TREATING THE COMPLEX BRAIN: HOW AI ENHANCES EXPERTISE IN DEMENTIA CARE

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Dementia diagnosis remains one of the most demanding tasks in clinical neurology. Overlapping syndromes, heterogeneous trajectories, and protein-centric diagnostic frameworks frequently obscure the underlying network failures that drive symptoms, leading to delayed or imprecise diagnosis, particularly outside specialized academic centers. The goal of this work is to demonstrate how AI can enhance, rather than replace, clinical expertise across the full dementia spectrum by reframing diagnosis around brain network dysfunction. We present StateViewer, an FDG-PET-based AI platform developed at Mayo Clinic and now advancing through an FDA Software as a Medical Device pathway. StateViewer was trained and validated on a large multi -center cohort spanning 14 dementia phenotypes including Alzheimer disease, dementia with Lewy bodies, frontotemporal dementia variants, and related disorders. The platform analyzes regional metabolic patterns and maps them onto phenotype -specific network signatures, producing interpretable outputs that support differential diagnosis at the point of care. Across validation cohorts, StateViewer achieved over 90 percent diagnostic accuracy, with performance stable across sites and scanners. Reader studies demonstrate that AI-assisted interpretation improves accuracy and confidence among both subspecialists and general neurologists, with the largest gains in atypical and early-stage cases. We further situate these findings within the Stochastic Latent Oscillatory Diffusion framework, which models dementia subtypes as selective failures of distinct computational components of a generative brain system, providing a mechanistic foundation for precision phenotyping. AI tools grounded in network neuroscience can extend specialist-level diagnostic reasoning into broader clinical practice and accelerate access to disease-modifying therapies.

Keywords: dementia, FDG-PET, Alzheimer's, brain networks, AI

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THE CHESSBOARD OF ARTIFICIAL INTELLIGENCE AND HUMAN CREATIVITY

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The ancient boardgame of chess has been considered a bellwether of intelligence, both human and machine, both rightly and wrongly, for centuries. It has been used as a testing ground and model for generations of psychologists and computer scientists, from Alfred Binet to Alan Turing. Chess has continued to be a useful drosophila melanogaster of cognition even today, almost 30 years since Garry Kasparov lost his famous rematch against the IBM supercomputer Deep Blue in 1997. One insight was that humans working together with intelligent machines using better collaborative processes produced superior outcomes compared to more knowledgeable humans or higher-powered computers. This was demonstrated in the Kasparov invention of Advanced Chess. In 2017, Demis Hassabis at Deep Mind's chess program AlphaZero demonstrated that reinforcement learning and virtualized data could produce an expert system – designs that went into AlphaFold, for which Hassabis received a 2024 Nobel Prize. With LLMs becoming the dominant face of AI and spreading with unprecedented speed, it is critical to keep humans in the chain of accountability and decision-making. Like any tech, from electricity to nuclear power, AI is not good or evil; it reflects its human creators and users. Human leadership and creativity are more important than ever in using these remarkable new tools to achieve great things. We must use it to augment our ambition and intelligence, not replace them, and to open up new challenges instead of simply performing old tasks more efficiently. In education, business, and everyday life, we must demand more from AI and its creators to emphasize human-centric goals and results.

Keywords: AI, artificial intelligence, chess, Deep Blue, cognition

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AI FOUNDATION MODELS FOR GENOMIC MEDICINE, DRUG DEVELOPMENT, PROTEIN STRUCTURE-TO-FUNCTION, AND PERSONALIZED THERAPEUTICS

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Generative AI is fundamentally reshaping our understanding of biology, medicine, and therapeutics elevating AI from an analytical tool to a true discovery partner. Here, I will present our work building foundational AI models spanning chemistry, protein structure, gene function, patient states, and therapeutic interventions, towards an integrated agentic-AI platform for precision medicine. In the domain of protein structure to function, I will introduce ProCyon, our multimodal foundation model that combines protein sequences, molecular functions, disease associations, therapeutic mechanisms, and structural information into unified representations, which enable zero-shot phenotype annotation, drug-binding prediction, and functional interpretation of disease variants, opening the door to functionally annotating the dark proteome and guiding therapeutic targeting. In the field of chemical space modeling, I will describe our embedding of molecular structures, integrated with global patent databases, drug-target interaction knowledge, and protein function, to create a chemically and functionally interpretable drug landscape, enabling generation of novel molecules, functional annota-tion of the chemical landscape using co-embedded drug patents, and discovery of structure function relationships for drug discovery. In the area of patient trajectory modeling, I will present our latent embedding of patient states, built from multimodal data spanning omics, clinical records, imaging, and treatment histories, inferring representations that enable improved diagnosis, detection of misdiagnosed cases through cross modal consistency, and personalized intervention strategies, tailored to individual patients' trajectories relative to previously treated populations. In the domain of personalized therapeutics, I will describe our work leveraging foundational models connecting molecular, cellular, and patient-level phenotypes to predict therapeutic responses and uncover mechanistic disease subtypes, by integrating molecular function, single cell expression, protein structure function, and chemical spaces, and constructing AI-driven models capable of proposing causally grounded therapeutic recommendations at patient specific resolution. Finally, I will present our AI-powered, human directed visual data science workbench, Mantis, that enables scientists to seamlessly navigate and interrogate these latent embedding landscapes across proteins, chemicals, patients, and therapies, through interactive and interpretable visualizations, agentic workflows where human intuition guides AI actions, uncovering latent patterns and steering the next generation of generative models for biomedicine. Together, these efforts are driving a new paradigm for AI-enabled science, combining mechanistic interpretability, predictive power, and human-centered discovery to transform biomedical research and precision therapeutics.

Keywords: generative AI, precision medicine, foundation models, protein structure–function modeling, personalized therapeutics

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ARTIFICIAL INTELLIGENCE AND ECHOCARDIOGRAPHY FOR CARDIOVASCULAR PROCEDURE PLANNING: FROM AUTOMATED QUANTIFICATION TO PATIENT-SPECIFIC DIGITAL TWINS

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Goal: To synthesize how artificial intelligence (AI) applied to echocardiography can strengthen cardiovascular procedure planning by improving measurement standardization, risk stratification, multimodal model building, and device-aware simulation. Material and methods: We propose a procedural-planning pipeline for AI-enabled echocardiography encompassing acquisition support and image quality assessment, automated segmentation and standardized quantification from 2D/3D echo, multi-view and multimodal fusion with CT/MRI to improve geometric fidelity, machine learning-based phenotype discovery and outcome prediction to inform patient selection, and patient-specific 3D modeling with virtual device placement to enable "what-if" testing. Key implementation requirements include cross-vendor data harmonization, uncertainty quantification, prospective validation in clinical workflows, and governance addressing privacy, safety, bias, and regulatory constraints. Results: Across valve and heart failure interventions, AI-based echo analysis demonstrates feasibility for rapid, reproducible chamber and valve quantification and supports risk stratification and patient selection through phenogrouping and outcome prediction. Automated 3D segmentation from TEE/ICE can reduce analysis time and variability for structural planning (e.g., annular sizing) and enables patient-specific digital models. Device-aware simulation can quantify procedure-relevant risks such as neo-left ventricular outflow tract reduction during mitral interventions by evaluating virtual prosthesis position within individualized anatomy. Data quality remains a critical limiter; multimodal fusion and standardized acquisition improve planning fidelity. Conclusion: AI-enabled echocardiography is moving from workflow automation toward decision-grade procedural planning. By combining robust segmentation, standardized measurements, predictive modeling, and multimodal digital twins with rigorous validation and governance, AI can improve patient selection, procedural strategy, and safety for complex cardiovascular interventions.

Keywords: echocardiography, artificial intelligence, procedure planning, digital twin, multimodal imaging fusion

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TOO MUCH, TOO SOON? THE IMPACT OF AI ON CLINICAL REASONING AND THE PHYSICIAN-PATIENT RELATIONSHIP

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Artificial intelligence (AI) is being rapidly integrated into medical practice across diagnostic, administrative, and documentation workflows. While AI promises efficiency gains and improved clinician experience, real - world evidence demonstrates that benefits are at times modest and highly dependent on governance, clinician oversight, and contextual integration. Recent multi-site observational and randomized studies of ambient AI documentation systems show limited time savings but substantial reductions in clinician burnout, cognitive load, and after-hours work. At the same time, technical limitations such as biased data, overfitting, and model drift intersect with cognitive risks including automation bias, alert fatigue, and erosion of clinical judgment. These challenges introduce ethical, legal, and regulatory complexities related to accountability, transparency, privacy, and patient autonomy. In addition, human factors research has shown that higher confidence in generative AI is associated with reduced critical thinking effort. Increased use of AI in clinical medicine also has the potential to reduce human interaction, increase reliance on AI for information gathering, and de-emphasize the physical examination, all of which can impact the physician patient relationship and the healing process in significant ways. This review synthesizes contemporary evidence on clinical AI applications, outlines major categories of risk, and provides best-practice recommendations for responsible deployment. Emphasis is placed on human-in-the-loop design, continuous validation, and professional stewardship, underscoring that AI in medicine should augment – rather than replace – clinical judgment.

Keywords: AI, critical thinking, clinical impact

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IMMUNOGLOBULIN GLYCANS AS BIOMARKERS AND FUNCTIONAL EFFECTORS OF INFLAMMAGING

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In the context of healthy aging, disease resilience – the capacity to withstand and rapidly recover from physiological stressors such as infection, injury, or chronic disease flares – emerges as a stronger determinant of outcome than disease prevention alone. As complete avoidance of such challenges becomes biologically implausible with advancing age, the difference between robust and frail trajectories hinges on an individual's ability to maintain physiological homeostasis under stress. Chronic low-grade inflammation ("inflammaging") is a central hallmark of diminished resilience. Glycosylation, the enzymatic attachment of complex glycans to proteins and lipids, is a key post-translational regulator of inflammatory pathways, immune function, and cellular stress responses. The human glycome integrates genetic, epigenetic, and environmental signals through hundreds of genes involved in glycan biosynthesis, exhibiting substantial heritability as a complex trait. Alternative glycosylation at individual sites dynamically modulates protein stability, receptor signalling, and immune recognition, thereby actively driving transitions from health to disease and frailty. Using high-throughput glycomics in >250,000 individuals across the lifecourse, we identified glycan signatures that robustly predict resilience to common age-related stressors. These signatures enable personalized risk stratification and reveal novel targets for pharmacological and lifestyle interventions aimed at preserving physiological reserve, attenuating inflammaging, and extending health span. Our findings position the glycome as a clinically actionable biomarker and therapeutic target for enhancing disease resilience and achieving compression of morbidity in aging populations.

Keywords: disease resilience, inflammaging, glycosylation, glycome, healthy aging

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PRECISION GEROMEDICINE: CHANGING THE HEALTH NARRATIVE

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Precision geromedicine is reshaping medicine by positioning the biology of aging, geroscience, as a primary, modifiable clinical target. Rather than focusing solely on the treatment of established disease, this emerging medical discipline aims to optimize function and intrinsic capacity across the adult life course through mechanism-based gerodiagnostics and matched gerointerventions. The field integrates advances in geroscience, systems biology, digital health, and clinical medicine into a translational framework capable of addressing multimorbidity before overt disease develops. Central to precision geromedicine is the development of robust gerodiagnostics. These include molecular, clinical and digital biomarkers of aging that together characterise individual ageing trajectories and underlying biological mechanisms. Epigenetic clocks, inflammatory signatures, clinical measures of all organs, physical and psychological performance metrics and longitudinal digital phenotyping are increasingly being integrated to define "gerotypes" and stratify individuals according to biological rather than chronological age. However, the rapid clinical adoption of these tools requires rigorous evidence building, analytical validation, standardisation, and regulatory oversight. Gerointerventions in precision geromedicine extend beyond single-drug approaches. Multimodal interventions combining exercise, nutrition, sleep optimisation, behavioural strategies, nutraceuticals, and repurposed pharmacological agents are being evaluated to target shared ageing pathways and improve multi-system outcomes. Importantly, the field is moving towards adaptive and personalised intervention strategies informed by longitudinal gerodiagnostic profiling. To establish precision geromedicine as a recognised medical speciality, evidence generation frameworks must evolve. Conventional randomised controlled trials remain essential, but need to be complemented by longitudinal registries, registry-based randomised clinical trials, and real-world evidence platforms embedded within clinical care. Such infrastructures enable continuous learning, evaluation of long-term outcomes, and assessment of interventions across diverse populations. The establishment of international standards, accredited education pathways, clinical guidelines, and dedicated regulatory frameworks will be critical to ensure scientific rigour, patient safety, and responsible implementation. Precision geromedicine therefore represents not only a new clinical discipline, but a fundamental shift in the health narrative: from reactive disease management towards proactive maintenance of lifelong optimized health and function.

Keywords: geroscience, precision, geromedicine, aging, gerodiagnostics

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AI TOOLS FOR THE DIAGNOSIS AND MANAGEMENT OF PANCREATIC DISEASES

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AI is rapidly transforming the diagnosis and management of pancreatic diseases. Early advances are most notable in the domain of pancreatic imaging, where CT-based radiomics models have shown potential for improving early pancreatic cancer detection, risk stratification of pancreatic cystic lesions and enhancing the identification of small, visually occult tumors. In one study, researchers trained a 3 -dimensional convolutional neural network (CNN) for detection of pancreatic cancer in diagnostic CT scans and evaluated its ability to detect cancer before a visible tumor was clinically diagnosed. The model could detect occult pancreatic cancer on prediagnostic CTs with AUROC 0.91 at a median 475 days prior to clinical diagnosis. AI-based imaging tools have also enabled automated analysis of body composition and pancreatic fat. For example, a CNN-based model for quantification of whole-pancreas fat, has overcome the limitation posed by the heterogeneous distribution of pancreatic fat, which renders partial sampling susceptible to error and subjectivity. More recent developments involve AI applications within the electronic health record for individualized extraction of specific disease -related risk factors. In one study, researchers developed a rule -based natural language processing algorithm to identify familial and germline pancreatic cancer risk from unstructured clinical notes. In a test set of 807 subjects, it achieved an F1-score of 0.85 for detecting family history of pancreatic cancer. Currently ongoing work in this domain focuses on the use of longitudinal health records to predict future disease trajectories. Despite rapid progress in the technological aspects, significant challenges remain regarding clinical implementation, adoption, and regulatory approval. As the field continues to advance, it will be crucial to ensure the use of high -quality input data for training and validating models and focus on robust evaluation frameworks and explainability.

Keywords: artificial intelligence, pancreatic cancer, pancreatic fat, natural language processing, image analysis

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FROM IMAGES TO INSIGHTS: USING AI TO IDENTIFY THE RIGHT CELLS

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The development of new medicines is a multi-stage R&D process that begins with early drug discovery, continues through preclinical animal testing, and advances to clinical trials in humans. In the early discovery stage, large numbers of potential drug candidates are explored using in silico and in vitro techniques, even though only a small fraction will ultimately progress to later pipeline stages. This creates a highly selective filtering process in which most of the time, labor, and cost are invested in candidates that will eventually be eliminated. In this work, we demonstrate how artificial intelligence (AI) can be used to improve efficiency in early drug development, with a focus on antibody discovery. We present a tool designed to support the early identification of antibody producing B -cells that are predicted to yield active and developable antibodies in later stages. The tool applies computer vision and machine learning (ML) techniques to analyze cell and assay images and rank candidate cells based on their predicted likelihood of downstream success. Deployed within Teva's drug development workflow, the system prioritizes candidate cell subsets enriched for higher predicted likelihood of downstream success. This enables earlier focus on promising candidates and reduces the time and effort spent on low potential options, improving timelines and supporting more efficient allocation of resources in early-stage antibody discovery.

Keywords: drug discovery, antibody discovery, artificial intelligence, machine learning, biologic therapeutics

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REDUCING INFLAMMATION FOR THE PREVENTION OF CARDIOVASCULAR DISEASE

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Inflammation is a key element of atherosclerotic cardiovascular disease (CVD), contributing to all of its stages, from plaque initiation to subsequent growth and eventual rupture. Circulating downstream biomarkers of systemic inflammation (such as the acute phase reactant C-reactive protein (CRP)) are strongly associated with atherothrombosis, risk factors, and CVD events, but these biomarkers are largely reflective of the overall inflammatory state, and may not drive CVD -associated inflammation. This presentation will provide an overview of the role of inflammation in cardiovascular events and discuss biomarkers of inflammation and CVD risk. Recent evidence demonstrating that the resolution of inflammation is not a passive process but occurs in an active coordinated process will be reviewed, along with a focus on important signalling molecules and mediators. Human experimental and observational studies have shown that glycan posttranslational protein modifications and bioactive lipid mediators are key factors and signaling molecules that initiate and sustain CVD-associated inflammation. Certain protein glycan modifications as well as bioactive lipid mediators (e.g. specialized pro-resolving mediators and omega-3 derived mediators) play a pivotal role in CVD-associated inflammation and could have important public health significance since residual inflammatory risk is common and remains undertreated with current therapeutics.

Keywords: glycans, glycomics, bioactive lipids, specialized pro-resolving mediators

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AI MEETS THE NON-CODING GENOME: DECODING BIOLOGICAL FUNCTION AND DISEASE

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The non-coding genome, which comprises ~98% of human DNA, was long considered "junk." This view has shifted substantially, as non-coding regions are now known to harbor diverse functional elements, including enhancers, silencers, and multiple classes of non-coding RNAs. These elements play central roles in gene regulation, shaping development, cellular identity, and disease states. Remarkably, up to 75% of the genome is transcribed, underscoring the extensive activity of the non-coding landscape. Despite advances in multi-omics technologies, identifying functional non-coding regions and interpreting the impact of variation within them remain major challenges. Genome-wide association studies (GWAS) have identified thousands of disease-associated single nucleotide polymorphisms (SNPs), the majority of which lie in non-coding regions and lack clear mechanistic links to gene regulation. Current diagnostic pipelines, including whole-genome sequencing, still prioritize protein-coding variants, leaving most non- coding genes and variants unexplored. Addressing this gap requires systematic functional annotation and computational frameworks capable of predicting regulatory activity. Our work aims to decode the functional non-coding genome using integrated multi-omics approaches combined with artificial intelligence. Using these strategies, we have identified novel long non-coding RNAs, mapped regulatory elements across cellular contexts, predicted enhancer activity directly from DNA sequence features, and pinpointed critical nucleotides required for regulatory function. Collectively, these efforts uncover previously unrecognized genetic mechanisms underlying development and disease, providing a framework for interpreting non- coding variation and helping to resolve the missing heritability of complex diseases.

Keywords: non-coding genome, long non-coding RNA, regulatory elements, machine learning, artificial intelligence

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AN AI-ENABLED AUTOMATED TRIAGE SYSTEM FOR DIGITAL DERMATOPATHOLOGY

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The rise of digital pathology and the routine digitization of histopathology slides has ushered in a new era of modern practice, creating opportunities for computational approaches that can support diagnostic workflows. This presentation will describe work developing an AI-enabled triage system that can categorize WSIs into broad diagnostic groups in order to improve case prioritization and efficiency. We constructed a dataset of 40,684 whole slide images (WSIs) from routine dermatopathology practice, categorized into nine physician-developed diagnostic classes. A pipeline leveraging the Atlas v1.1 foundation model generated embeddings from 224×224 pixel tissue tiles exhaustively cropped at 10x magnification (1.05 µm/pixel). A slide-level classifier employing attention-based multiple instance learning (ABMIL) was trained using the tile-level embeddings as input. The current best model achieves 80% overall accuracy and 0.74 macro F1- score on the held-out test set. Performance varied by category, with Basaloid (F1=0.90) and Squamous (F1=0.87) leading while Inflammatory conditions trailed (F1=0.65). This study demonstrates the feasibility of foundation-model-based triage systems for dermatopathology. The pipeline shows promise for optimizing case read efficiency and highlights the benefits of using AI-based tools to improve pathology workflow.

Keywords: digital pathology, dermatopathology, multiple instance learning (MIL), foundation models, whole slide imaging (WSI)

Presentation number: IL 24 Abstract number: 160-ISABS-2026

THE SUGAR SWITCH: PRO- AND ANTI-INFLAMMATORY ACTIVITIES OF IGG REGULATED BY GLYCOSYLATION

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IgG antibodies are major drivers of inflammation but are also used in the form of intravenous immunoglobulins (IVIg) to suppress inflammatory processes. A key factor in modulating both, the pro- as well as the anti-inflammatory activity of IgG is the sugar domain attached to each IgG Fc-domain. The talk will discuss how specific IgG glycosylation variants affect IgG function and how this knowledge can be used to optimize the therapeutic activity of IgG antibodies in humans.

Keywords: IgG glycosylation, IVIg, therapeutic antibodies, inflammation, immunomodulation

Presentation number: IL 25 Abstract number: 143-ISABS-2026

ARTIFICIAL INTELLIGENCE–DRIVEN MULTI OMICS COMPARISON OF MICRO FRAGMENTED ADIPOSE TISSUE (MFAT) AND HYALURONIC ACID (HA) IN KNEE OSTEOARTHRITIS

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Osteoarthritis (OA) is the most prevalent musculoskeletal disorder worldwide, affecting more than 528 million individuals. Although traditionally regarded as a cartilage disease driven by mechanical overload, OA is now recognized as a whole joint disorder involving coordinated pathological changes in cartilage, subchondral bone, synovium, and periarticular tissues, resulting in profound alterations in tissue architecture, metabolism, and function. The knee is the most commonly affected joint, followed by the hip and hand. Previous investigations at St. Catherine Specialty Hospital have demonstrated the therapeutic potential of mechanically micro fragmented adipose tissue (MFAT) in knee osteoarthritis (KOA). MFAT is enriched with CD45 negative cell populations, including endothelial progenitors, mature endothelial cells, pericytes, transitional pericytes, and supra adventitial adipose stromal cells, supporting angiogenic, immunomodulatory, and regenerative processes within the joint microenvironment. In this study, we evaluated the clinical, radiological, and biological effects of MFAT in patients with KOA. Clinical outcomes were assessed using validated pain and function questionnaires (VAS, WOMAC, and KOOS). Structural cartilage changes were investigated indirectly through assessment of glycosaminoglycan (GAG) content using delayed gadolinium enhanced magnetic resonance imaging of cartilage (dGEMRIC). In parallel, comprehensive molecular profiling of plasma and synovial fluid was performed, including analysis of cytokines, chemokines, N glycans, and microRNAs. Given the lack of disease modifying therapies for KOA, MFAT was further compared with intra articular hyaluronic acid (HA), a widely used standard treatment primarily providing mechanical and symptomatic benefits. From a master cohort, individuals with an inflammatory KOA phenotype were selected and treated with MFAT or with follow up at baseline, one month, and six months. Blood samples were analyzed using a multi omics framework, and the resulting datasets were integrated using an interpretable artificial intelligence model to identify treatment specific biological pathways. At six months, HA treated patients demonstrated persistent molecular signatures associated with inflammation and cartilage degradation. In contrast, MFAT treatment was associated with activation of pathways related to tissue repair, inflammation resolution, and cartilage protection. These findings suggest that, beyond symptomatic relief, MFAT may favorably remodel the biological milieu of the osteoarthritic joint, supporting its potential role as a disease modifying therapeutic strategy in inflammatory KOA.

Keywords: artificial intelligence; knee osteoarthritis; micro fragmented adipose tissue; hyaluronic acid; multi omics data integration; regenerative medicine

Abstracts of Invited Lectures

Presentation number: IL 26 Abstract number: 141-ISABS-2026

MULTI-OMICS AI-DRIVEN DATA FUSION REVEALS DIVERGENT MOLECULAR SIGNATURES OF INTRA-ARTICULAR MICRO-FRAGMENTED ADIPOSE TISSUE AND HYALURONIC ACID TREATMENT IN INFLAMMATORY-PHENOTYPE KNEE OSTEOARTHRITIS

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Knee osteoarthritis (KOA) is a chronic, progressive joint disease with limited disease-modifying treatment options. In current clinical practice, intra-articular hyaluronic acid (HA) is widely used as a standard, primarily for its lubricating and shock-absorbing properties, providing symptomatic relief but with ongoing debate regarding its true biological impact on disease progression. In contrast, regenerative approaches such as micro-fragmented adipose tissue (MFAT), which contains mesenchymal stem cells, have shown superior clinical outcomes in selected patient groups. However, the biological mechanisms underlying these differences remain insufficiently understood. In this study, we aimed to compare the molecular effects of MFAT and HA in patients with the inflammatory phenotype of KOA, independent of clinical outcome scores. Out of a master cohort of over 18,000 patients, a total of 53 participants were selected based on specific inflammatory phenotype and treated with either MFAT (n=35) or HA (n=18) with a 6-month follow-up. Blood samples were analyzed using a multi-omics approach, including whole genome sequencing, microRNA expression profiling, proteomic analysis, and glycomic profiling. These data were integrated using an interpretable artificial intelligence framework to identify biological pathways that differ between treatments. At six months, clear differences emerged between the two groups. Patients treated with HA continued to show molecular patterns associated with ongoing joint degeneration and inflammation, including pathways linked to cartilage breakdown and inflammatory signaling. In contrast, MFAT-treated patients showed activation of pathways related to tissue repair, reduced inflammation, and cartilage protection. These findings were consistent across both gene-level and microRNA analyses. In conclusion, while HA remains a commonly used treatment for symptomatic management of KOA, our results suggest that its effects are largely mechanical and do not substantially alter the underlying molecular processes driving disease progression. In contrast, MFAT appears to shift the biological environment of the joint toward regeneration and inflammation resolution, supporting its potential as a disease-modifying therapy.

Keywords: artificial intelligence; knee osteoarthritis; multi-omics data fusion; regenerative medicine

Abstracts of Invited Lectures

Presentation number: IL 27 Abstract number: 152-ISABS-2026

MULTI-OMICS DATA FUSION FOR PRECISION MEDICINE AND PRECISION THERAPEUTICS

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Large amounts of multi-omic data are increasingly becoming available. They provide complementary information about cells, tissues and diseases. We need to utilize them to better stratify patients into risk groups, discover new biomarkers and targets, re-purpose known and discover new drugs to personalize medical treatment. This is nontrivial, because of computational intractability of many underlying problems on large interconnected data (networks, or graphs), necessitating the development of new algorithms for finding approximate solutions (heuristics). We develop versatile artificial intelligence (AI) frameworks for multi-omics data fusion, constrained by the state-of-the-art network science methods, to address key challenges in precision medicine and pharmacology from time-series, multi-omics data, including patient-derived single-cell data, to better stratify patients, predict new biomarkers and targets, re-purpose existing and discover new drugs; we apply these to different types of cancer, Covid-19, Parkinson's, osteoarthritis, other diseases and longevity. Our new methods stem from graph-regularized non-negative matrix tri-factorization (NMTF), a machine learning (ML) technique for dimensionality reduction, inference, fusion and co-clustering of heterogeneous datasets, coupled with novel graphlet-based network science algorithms and generative models. We utilize our new frameworks for improving the understanding of the molecular organization of life and diseases from multi-omics data and to generate new precision therapeutics. The aim is to develop an overreaching framework encompassing all multi-omics data towards consumer-facing precision medicine and precision therapeutics products.

Keywords: multi-omics data fusion, precision medicine and therapeutics, network-based machine learning, biomarker and drug discovery, graph-regularized NMTF

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REIMAGINING PRECISION ONCOLOGY THROUGH AI-NATIVE WORKFLOWS

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Precision oncology has advanced rapidly through genomics and targeted therapies, yet clinical workflows remain fragmented, inefficient, and vulnerable to delays. A central challenge is transforming vast, heterogeneous data into timely, actionable decisions. AI in medicine is now evolving from isolated, single task tools into a connected infrastructure that supports the full continuum from diagnosis to treatment. Computational pathology and multimodal models are enabling integrated systems that span the entire cancer pathway. Emerging pathology foundation models can assist pathologists in diagnosis while simultaneously guiding oncologists by inferring molecular alterations, predicting prognosis, and estimating treatment response directly from tumor morphology on routine H&E slides. The lecture will explore the human-AI collaboration and examine how AI could function as the organizational operating system for cancer care by coordinating data, decisions, and clinical action across the diagnostic and therapeutic continuum.

Keywords: precision oncology, artificial intelligence, computational pathology, foundation models, clinical decision support

Presentation number: IL 29 Abstract number: 150-ISABS-2026

USING GENAI AND MACHINE LEARNING TO IDENTIFY SURGICAL CANDIDACY: AN OTOLARYNGOLOGY – HEAD & NECK USE CASE

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Surgical departments at tertiary referral centers face a persistent mismatch between referral volume and clinical capacity. Efficient triage – matching the right patient to the right provider – is essential but labor- intensive, requiring clinician review of heterogeneous records. AI-based systems offer an opportunity to support this process at scale. We developed and deployed two AI-driven triage systems in the Department of Otorhinolaryngology at a tertiary academic medical center. For Head & Neck Surgery, a large language model identifies and extracts relevant documentation from the patient record, then evaluates findings against a physician-authored policy document specifying criteria for surgical consultation. The system outputs a triage recommendation including appointment appropriateness, prerequisite or completed workup, and supporting evidence. For Rhinology, an LLM first extracts structured clinical findings from cross-sectional imaging reports (CT/MRI); these extracted features then serve as inputs to a supervised machine learning model trained to predict whether the patient will undergo surgery within six months of imaging. Both systems are in clinical production, with prospective evaluation underway. We present retrospective validation results demonstrating strong performance. These deployments demonstrate that existing generative AI models, when paired with well-defined clinical criteria, are capable of meaningfully supporting clinical decision-making – and that the optimal integration pattern may vary by subspecialty context and available data.

Keywords: otolaryngology, large language models (LLMs), surgical decision support, machine learning, healthcare workflow optimization

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ADVANCING PRECISION MEDICINE THROUGH INTEGRATIVE GENOMICS, TRANSCRIPTOMICS, EPIGENOMICS, AND ARTIFICIAL INTELLIGENCE

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Advances in next-generation sequencing (NGS) and computational biology are rapidly redefining precision medicine across oncology, inherited disorders, and complex human diseases. The clinical integration of whole-exome sequencing (WES), long-read whole-genome sequencing (lrWGS), and RNA sequencing enables comprehensive characterization of somatic and germline variation, transcriptomic landscapes, and epigenetic alterations with unprecedented resolution. An integrative multi-omic perspective is transforming molecular diagnostics and personalized therapeutic decision-making. Emphasis is placed on the combined application of WES/WGS and transcriptome sequencing for improved detection of clinically actionable variants, fusion transcripts, and pathway dysregulation, as well as the growing role of methylome profiling using long-read WGS technologies capable of simultaneously resolving structural variation and native epigenetic signatures. A central challenge in precision oncology remains tumor heterogeneity, which drives disease evolution, therapeutic resistance, and variable clinical outcomes. Integrating genomic and epigenomic data with advanced computational approaches is increasingly essential for overcoming these limitations and refining patient stratification. The expanding role of artificial intelligence and machine learning in the interpretation of large-scale multi-omic datasets is enabling improved biomarker discovery, predictive modeling, and clinically actionable insights that are shaping the future of precision and personalized medicine.

Keywords: precision medicine, multi-omics, whole-genome sequencing, tumor heterogeneity, artificial intelligence

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AI-ASSISTED BIOMARKER DEVELOPMENT IN HEAD AND NECK CANCER

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Apart from human papillomavirus (HPV), head and neck squamous cell carcinoma (HNSCC) has few biologically driven biomarkers that guide curative-intent treatment. Standard clinicopathologic features explain only part of the variability in response and outcome, leaving patients and physicians to make difficult treatment decisions while balancing cure, toxicity, and treatment burden. AI-based methods may help address this problem by integrating clinical, omic, and imaging data into more useful biomarkers and decision-support tools. Here, we describe linked clinical and translational projects in HNSCC. Clinically, we are harmonizing patient-level data across existing cohorts and using prognostic and treatment-effect modeling to estimate expected outcomes after curative radiation-based therapy while incorporating patient preferences. Translationally, LLM-assisted analysis of omic datasets has identified candidate biomarkers connecting tumor-intrinsic metabolism with antitumor immunity and therapeutic response. Early validation studies have generated new hypotheses about how tumor metabolic state influences treatment vulnerability. Together, these projects support a practical path toward more personalized therapy in HNSCC.

Keywords: head and neck squamous cell carcinoma, precision oncology, multi-omics integration, artificial intelligence, biomarker discovery

Presentation number: IL 32 Abstract number: 159-ISABS-2026

CUTTING-EDGE TOOLS FOR CRITICAL DIAGNOSES: DEEP LEARNING AND LARGE LANGUAGE MODELS IN SPINAL METASTASIS DETECTION

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The spine is the third most common site for metastatic disease, and radiographic detection remains challenging, with missed lesions risking pathologic fractures and spinal cord compression. Artificial intelligence (AI), particularly deep learning, has emerged as a promising decision-support tool by enabling automated lesion detection and segmentation, improving radiologist sensitivity while reducing interpretation time, differentiating metastatic from osteoporotic vertebral fractures, and facilitating early detection of metastatic spinal cord compression, with models reducing diagnostic delays by approximately 20 days. Meta-analytic data across imaging modalities report a pooled sensitivity of 88%, a specificity of 89%, and an AUC of 0.95. Despite these results, significant challenges remain: external validation AUC drops substantially compared to internal validation (0.819 vs. 0.947), and over half of published studies carry a high risk of bias. Multicenter prospective validation and standardized reporting frameworks are needed before widespread clinical adoption.

Keywords: artificial intelligence, spine metastasis, deep learning, imaging, diagnostic accuracy

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MULTIMODAL AI FOR PREDICTING RISK OF SUDDEN CARDIAC DEATH

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Sudden cardiac death (SCD) remains a leading cause of mortality worldwide, yet current risk stratification tools are inadequate, failing to identify a large proportion of individuals who would benefit from implantable cardioverter-defibrillator (ICD) therapy while exposing low-risk patients to unnecessary device implantation. Our team at Johns Hopkins University has pioneered a multimodal artificial intelligence framework that integrates complementary data streams to achieve unprecedented accuracy in predicting individualized SCD risk. Central to this approach is the fusion of cardiac imaging, electroanatomic data, and clinical variables within deep learning architectures. Late gadolinium enhancement MRI provides high-resolution characterization of myocardial scar geometry and heterogeneity, which serves as the structural substrate for life-threatening arrhythmias. These imaging features are combined with patient-level clinical data to train models that capture the multidimensional nature of arrhythmic risk. Validation across multicenter cohorts has demonstrated that the multimodal AI framework significantly outperforms established clinical criteria, including ejection fraction thresholds, in identifying patients at genuine risk of SCD. Importantly, the approach also identifies low-risk patients who may safely forgo ICD implantation, with meaningful implications for reducing procedural complications and healthcare costs. This approach represents a shift in cardiac risk stratification, moving from population-level guidelines toward precision, patient-specific prediction that integrates the full complexity of arrhythmic substrate.

Keywords: multimodal AI, imaging, sudden cardiac death, clinical variables

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APPLICATION OF AI TO PATHOLOGY

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The goal of this presentation is to demonstrate the applicability of artificial intelligence (AI) to the practice of pathology with an emphasis on anatomical pathology, whole slide images and multi -modal datasets. The presentation will review the conceptual space of digital whole slide images (WSI) and explore several diverse applications which have been developed at Dartmouth Health. The tasks which can be modeled using the features contained in WSI are surprisingly broad, despite the limitations of anatomic pathology tissue preparation techniques and WSI creation as they relate to dynamic biological processes. It is reasonable to attempt to create models for virtually any task which may be driven by tissue morphology regardless of whether the task is performable by a human.

Keywords: digital pathology, whole slide images, morphometry, multi-modal, machine learning, artificial intelligence

Presentation number: IL 35 Abstract number: 136-ISABS-2026

AI WON'T CURE CHILDHOOD CANCER, BUT IT WILL HELP THE PEOPLE WHO DO

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Artificial intelligence is reshaping oncology – not as a distant promise, but as a set of tools already changing how tumors are detected, how patients are matched to therapies, and how clinicians make decisions under uncertainty. The goal of this presentation is to provide a clinically-grounded assessment of where AI is delivering impact in cancer care today and where critical gaps remain. Drawing on real-world deployments across radiology, pathology, and clinical decision support, as well as data from the Pediatric Cancer Data Commons, a harmonized repository spanning 46,000 patients across 200 institutions globally, this talk examines three domains: early detection, where deep learning models match or exceed specialist performance in identifying malignant findings; precision oncology, where integration of genomic and clinical data at scale reveals patient subgroups whose outcomes differ in ways invisible to single-institution analysis; and workflow automation, where continuously-running predictive algorithms flag deterioration and treatment toxicity before clinical thresholds are crossed. Results from deployed systems demonstrate both the potential and the limits of these tools: adversarial vulnerabilities, dataset shift, and cognitive biases baked into training data remain real constraints. The conclusion is that AI will not replace the clinicians who cure childhood cancer, but it will make them faster, more accurate, and better equipped to act on the right information at the right time.

Keywords: AI, pediatric oncology, bioinformatics, machine learning, deep learning

Presentation number: IL 36 Abstract number: 148-ISABS-2026

REAL-WORLD APPLICATIONS OF AI IN RADIATION ONCOLOGY: PERSONALIZING TREATMENT AND IMPROVING EFFICIENCY

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Artificial intelligence (AI), particularly large language models (LLMs), is rapidly transforming radiation oncology by enabling more efficient workflows, enhanced data synthesis, and personalized patient care. This work highlights real-world clinical implementations of AI tools within a large academic radiation oncology practice, focusing on the impact on efficiency, quality, and decision-making. RadOnc-GPT, a Mayo Clinic AI-powered platform designed to address multiple data streams and "noise" present in modern electronic health records. By using RadOnc-GPT to access longitudinal oncology records with a multi-stage architecture, we can identify and synthesize clinically relevant information. This system supports multiple applications, including automated patient summaries, treatment documentation, and clinical decision support. One key implementation, "Daily Dose," generates concise, structured patient summaries by integrating data from electronic health records, treatment planning systems, and imaging platforms. Following deployment across more than 500 users, the system produces hundreds of summaries daily and saves an average of 11 minutes per clinician per day at low cost. Additionally, automated radiation treatment summary notes have eliminated manual workflows, reducing documentation burden while maintaining clinical accuracy. We further demonstrate AI applications in toxicity assessment through automated extraction of CTCAE adverse events from clinical notes and ambient audio transcripts. These approaches achieve performance comparable to human reviewers, with improved consistency and reduced inter-observer variability. Emerging tools such as OncoTimeline integrate AI-driven data visualization and interaction to support longitudinal patient management and decision-making. These real-world implementations illustrate how AI is enhancing efficiency, reducing administrative burden, and enabling personalized care in radiation oncology.

Keywords: artificial intelligence, radiation oncology, clinical workflows, large language models, personalization