concern, the geographic distribution of authors suggests under-investment in rural institutions.

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Mechanisms of exosome-mediated immunosuppression in IDH mutant gliomas*

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OBJECTIVES/GOALS: We aim to identify how IDH mutant (IDHm) gliomas use exosomes to modulate the local and systemic immune system. We will do so by characterizing differential miRNA expression between IDHm and IDH wild type (IDHwt) exosomes and identifying the specific immune cell population targeted by exosomes in vivo. METHODS/STUDY POPULATION: Exosome RNA will be isolated from cultured patient glioma samples and perform small RNA sequencing to investigate differential expression of miRNA between IDHwt and IDHm exosomes. We will then utilize miRNA target databases in conjunction with bioinformatic pathway analysis to generate potential target regulatory pathways. To identify the in vivo effect of tumor exosomes, we will generate a novel glioma mouse model that has been genetically engineered to release labeled exosomes using the RCAS retroviral system. We will collect peripheral blood and tumor tissue for flow cytometric immune profiling and single-cell RNA sequencing. The transcriptomic data will be analyzed to identify subsets of immune populations that have taken up the labeled exosomes and assess the resulting expression changes in those cells. RESULTS/ANTICIPATED RESULTS: From the small RNA sequencing and bioinformatics analysis, we expect to find several unique miRNA expressed in IDHm exosomes that induce immunosuppressive pathways in local and systemic immune cell populations when compared to IDHwt exosomes. Furthermore, using our novel murine model, we expect to be able to track endogenously released exosomes in the local tumor microenvironment and in the circulating blood. We hypothesize that IDHm exosomes specifically target precursor myeloid cells within the local and peripheral circulating immune populations and induce the expansion of monocytes, M2 macrophages, and mono-MDSCs. DISCUSSION/SIGNIFICANCE OF IMPACT: Immunosuppression in IDHm glioma has hindered the development of adequate therapies to treat this fatal disease. Our study will illuminate the mechanism by which tumor exosomes can suppress immune surveillance. These results will help identify new therapeutic targets to sensitize the immune system against glioma cells.

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Harnessing computational tools to rank vaccine targets in *Plasmodium falciparum* candidate antigens*

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OBJECTIVES/GOALS: We aim to predict and rank conserved, immunogenic targets within key malaria proteins using computational tools. These tools incorporate parasite protein diversity and regional HLA allele frequencies to prioritize antigens for further validation and inclusion in a malaria vaccine targeting circulating strains. METHODS/STUDY POPULATION: We identified 42 conserved malaria proteins with nonredundant functions for *P. falciparum* invasion and transmission as vaccine targets. Protein sequence datasets were constructed from samples collected in highly endemic areas. We predicted targets most likely to be presented to CD4+ and CD8+ T cells. We designed and used heuristic-based and AI-weighting models that integrated predicted binding affinities to HLA alleles, HLA allele frequency data, and sequence conservation to score and rank targets. We validated our model by comparing predicted epitope distributions with published in vitro and in vivo immunogenicity data available in the Immune Epitope Database and Tools repository. RESULTS/ANTICIPATED RESULTS: We successfully predicted and ranked targets within the vaccine candidate proteins, identifying conserved and HLA-nonspecific targets that correspond to positive immunogenicity data, validating our approach. We are currently analyzing model performance by comparing predictions to over 5,800 experimentally validated *P. falciparum* targets from clinical trials and immune assays. We will evaluate each models' accuracy and ability to prioritize targets and compare their performances as measured quantitatively by precision and area under the curve metrics. We expect the AI-based model to significantly outperform the heuristic approach, improving the identification of effective vaccine targets. DISCUSSION/SIGNIFICANCE OF IMPACT: By incorporating parasite diversity and regional HLA allele frequencies, our approach addresses the challenge of directing the human immune response against genetically diverse *P. falciparum* strains in highly endemic areas. This strategy could significantly enhance malaria vaccine efficacy and can be adapted for use against other pathogens.

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The role of artificial intelligence in translational science in oncology: A systematic review and meta-analysis

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OBJECTIVES/GOALS: This study aimed to investigate the role of artificial intelligence (AI) in translational science, including personalization of interventions and drug development. METHODS/STUDY POPULATION: A comprehensive literature search was conducted via PubMed, the Cumulative Index for Nursing and Allied Health Literature (CINAHL), Cochrane Library, Medline, and Web of Science. The risk of bias in the eligible studies was assessed using the risk of bias in nonrandomized studies. Data were systematically extracted and analyzed. RESULTS/ANTICIPATED RESULTS: The literature search yielded 2129 records, from which 20 studies that met the eligibility criteria were included. Meta-analysis demonstrated the high specificity of AI-based diagnostics,

reassuring the reliability of AI. Furthermore, AI applications significantly improved biomarker identification through machine learning algorithms, enhancing prognostic accuracy and treatment personalization. Moreover, AI showed enhanced diagnostic precision with high sensitivity and specificity in cancer detection, further validating its role in healthcare. AI-driven risk stratification was used in chemotherapy decisions. DISCUSSION/SIGNIFICANCE OF IMPACT: This study highlights the transformative power of AI in translational oncology research with applications in drug development and personalized patient care in cancer treatment and research.

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Validation of an artificial intelligence Algorithm for predicting diagnosis-related groups in a community health system

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OBJECTIVES/GOALS: This study aims to evaluate the performance of a third-party artificial intelligence (AI) product in predicting diagnosis-related groups (DRGs) in a community healthcare system. We highlight a use case illustrating how clinical practice leverages AI-predicted information in unexpected yet advantageous ways and assess the AI predictions accuracy and practical application. METHODS/STUDY POPULATION: DRGs are crucial for hospital reimbursement under the prospective payment model. The Mayo Clinic Health System (MCHS), a network of clinics and hospitals serving a substantial rural population in Minnesota and Wisconsin, has recently adopted an AI algorithm developed by Xsolis (an AI-focused healthcare solution provider). This algorithm, a 1D convolutional neural network, predicts DRGs based on clinical documentation. To assess the accuracy of AI-generated DRG predictions for inpatient discharges, we analyzed data from 930 patients hospitalized at MCHS Mankato between March 2 and May 13, 2024. The Xsolis platform provided the top three DRG predictions for the first 48 hours of each inpatient stay. The accuracy of these predictions was then compared against the final billed DRG codes from the hospital's records. RESULTS/ANTICIPATED RESULTS: In our validation set, Xsolis achieved a top-3 DRG prediction accuracy of 71% at 24 hours and 81% at 48 hours, which is lower than the originally reported accuracy of 81.1% and 83.3%, respectively. Interestingly, discussions with clinical practice leaders revealed that the most valuable information derived from the AI predictions was the expected geometric mean length of stay (GMLOS), which Xsolis was perceived to predict accurately. In the Medicare system, each DRG is associated with an expected GMLOS, a critical factor for efficient hospital flow planning. A subsequent analysis comparing predicted GMLOS with the actual length of stay showed variances of -0.10 days on day 1 and 0.14 days on day 2, indicating a high degree of accuracy and aligning with clinical practice perceptions. DISCUSSION/SIGNIFICANCE OF IMPACT: Our research underscores that clinical practice can leverage AI predictions in unexpected yet beneficial ways. While initially focused on DRG prediction, the associated GMLOS emerged as more significant. This suggests that AI algorithm validation should be tailored to specific clinical needs rather than relying solely on generalized benchmarks.

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Usability, acceptability, and future opportunities of mobile health (mHealth) apps for caregiver health decision making: A scoping review

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OBJECTIVES/GOALS: This study aims to evaluate common features of mobile health (mHealth) apps and their role in helping caregivers make health decisions for children. METHODS/STUDY POPULATION: A scoping review of literature on caregivers' use of mHealth apps (published since 2008) was conducted across 5 databases (i.e., Embase, PubMed, CINAHL, Clinicaltrials.gov, and IEEE Xplore). Selected papers were categorized based on app purposes, target users, and mHealth agile development phases. Common features were also identified and analyzed along with users' pros and cons. Further, primary feature requests were summarized to inform future development. RESULTS/ANTICIPATED RESULTS: This review included 62 studies. Most apps were about maternity and infant care and specific diseases. Major users were caregivers and pregnant women. Around 20% of papers covered multiple phases in the mHealth agile development lifecycle. The effectiveness/clinical trial (phase III) was the most common. E-learning, personalization and customization, and health tracking features were the three most common features of mHealth apps included in this review. More positive feedback was found regarding features than concerns. Caregivers perceived apps as helpful and empowered them to make informed decisions. Concerns were mainly over 1) technical issues, 2) inappropriate design, and 3) ambiguous terms. Requested new features included content comprehensiveness, user engagement, and usage flexibility. DISCUSSION/SIGNIFICANCE OF IMPACT: To our knowledge, this is the first review to investigate the usability of mHealth app features in this area. The results offer feasible strategies for developers to improve the effectiveness of apps for caregiver decision-making.

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On the completeness of medical records of patients with oral health records at three CTSA CORES Institutions: Iowa, Kentucky, and Utah

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OBJECTIVES/GOALS: Oral health is an important and understudied part of overall health. Poor oral health is linked to many systemic