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Real-time data synchronization: Assessing the implementation of REDCap CDIS (Clinical Data Interoperability Service) for EHR systems

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OBJECTIVES/GOALS: This study tests the REDCap Clinical Data Interoperability Service (CDIS) for streamlined data extraction from electronic health records (EHRs) for research. Managed by Clinical and Translational Science Institute, IU Health, and Eskenazi Health, CDIS offers real-time data syncing, automated workflows, and HIPAA-compliant data security. METHODS/STUDY POPULATION: The REDCap CDIS uses the Fast Health Interoperability Resource (FHIR) Application Programming Interface (API) to extract data from EHRs. It includes the Clinical Data Pull (CDP), which automatically pulls EHR data into user-defined REDCap fields, and the Clinical Data Mart (CDM), which collects longitudinal patient data. Three use cases were selected to assess the CDIS's effectiveness in extracting data from the IUH Cerner and Eskenazi Epic EHR systems. The technical team set up clinical data mapping and adjudication processes, simplifying complex manual data extraction. RESULTS/ANTICIPATED RESULTS: The CDIS successfully achieved real-time data synchronization during pilot testing with each EHR system. We extracted demographics, drugs, procedures, labs, and conditions. The mapping interface supports many-to-one data point mapping for the study data dictionary, and the adjudication process ensures data quality before integration into the REDCap database. The CDIS also improved data security and HIPAA compliance. An implementation intake process was developed for Indiana University investigators, allowing them to use the service for affordable clinical data extraction from EHR systems. DISCUSSION/SIGNIFICANCE OF IMPACT: The implementation and testing of the REDCap CDIS demonstratesits effectiveness in streamlining EHR data extraction for research. The CDIS facilitates real-time data synchronization, automated workflows, and enhanced data security, offering a cost-effective solution through collaborative oversight with research teams.

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Rare Disease Alert System (RDAS) to promote rare disease research

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OBJECTIVES/GOALS: Rare disease patients often face lengthy delays in receiving accurate diagnoses or experience misdiagnoses due to a lack of available information. The NCATS Rare Disease Alert System (RDAS) is a public, comprehensive rare disease resource to collect and share accurate, up-to-date, and standardized data on rare diseases. METHODS/STUDY POPULATION: RDAS is composed of a frontend UI, Application Programming Interfaces, and backend Neo4j graph database. Each component of data collection, data annotation, data standardization, and data representation as steps were implemented during the process of each graph database creation. The UI allows users to search, browse, and subscribe to RDAS to receive the latest information and findings about their rare disease(s) of interest. The back-end data include four knowledge graphs built by integrating information from the NCATS Genetic and Rare Disease program, PubMed articles, clinical trials, and NIH grant funding. Ultimately, the integrative information pertinent to rare diseases from RDAS would advance rare diseases research. RESULTS/ANTICIPATED RESULTS: Of 5001 rare diseases belonging to 32 distinct disease categories, we identified 1294 diseases that are mapped to 45,647 distinct, NIH-funded projects obtained from the NIH ExPORTER by implementing semantic annotation of project titles. To capture semantic relationships presenting among mapped research funding data, we defined a data model comprised of seven primary classes and corresponding object and data properties. A Neo4j knowledge graph based on this predefined data model has been developed, and we performed multiple case studies over this knowledge graph to demonstrate its use in directing and promoting rare disease research. DISCUSSION/SIGNIFICANCE OF IMPACT: We developed an integrative knowledge graph with rare disease data and demonstrated its use as a source to identify and generate scientific evidence to support rare disease research. With the success of this study, we plan to implement advanced computation to analyze more funding related data and link to other types of data to perform further research.

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A half century of rural health research in the United States: the who, where, and what by bibliometrics

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OBJECTIVES/GOALS: As a priority area in translational science, rural health research can benefit from informatics methods for conducting thematic and environment scans. This study demonstrates an efficient approach to gaining insights about the rural health research literature by automated bibliometrics analysis. METHODS/STUDY POPULATION: We developed an automated pipeline to retrieve the 1972–2023 PubMed publications indexed with the MeSH terms "Rural Health" and "United States". The article metadata in XML format were downloaded and parsed, including title, year, journal, author institutions, and MeSH terms. Each institution address was augmented by Google Maps API to obtain the county and latitude/longitude coordinates. Summary statistics were computed for the publication years, journals, author departments, and locations. A topic network was generated from the frequent co-occurring MeSH terms. The institutions were linked to Rural-Urban Continuum Codes and labeled on a map to visualize their geographic distribution. RESULTS/ANTICIPATED RESULTS: A total of 4564 articles on rural health were analyzed. Two salient peaks of publications were revealed, one around 1978 and the other around 1993. The top author departments include Family Medicine, Nursing, Pediatrics, and Epidemiology. The five leading institutions reside in Chapel Hill, Minneapolis, Iowa City, Seattle, and Atlanta. The geographic distribution shows few institutions that reside in deep rural areas are well published on rural health, although the most scholarly productive institutions do seem adjacent to some moderately rural pockets. The frequently identified topics pertain to age group, study design, and specific concepts such as health services accessibility. DISCUSSION/SIGNIFICANCE OF IMPACT: The two publication peaks in history were likely linked to certain policy milestone or seminal publication. Primary care and epidemiology departments have been most active in rural health research. Of

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concern, the geographic distribution of authors suggests underinvestment 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,

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