University of Florida Integrated Data Repository and One Florida, we will develop machine learning models suitable for sequential data to predict NEC. Our inclusion criteria include very low birth weight (VLBW; <1500g) infants born <32 weeks gestation and EHR data availability from the first 14 days of life. We will include infants with NEC and infants without NEC to train our ML model. Exclusion criteria include infants diagnosed with spontaneous intestinal perforation and severe congenital anomalies/defects requiring surgery. RESULTS/ANTICIPATED RESULTS: We anticipate that our model will provide an accurate and dynamic prediction for the risk of NEC in neonates using data up to the first 14 days of life. Our model will be interpretable to identify key risk factors and can integrate real-world clinical insights to increase early detection and improve patient outcomes. DISCUSSION/SIGNIFICANCE OF IMPACT: The development of a model to predict NEC could be used in neonatal intensive care guidelines and protocols and could ultimately decrease mortality, reduce complications, improve the overall quality of care, and lower healthcare costs associated with NEC.

384

A systematic approach to understanding nursing documentation tasks

Victoria Tiase, Varun R. Selvam, Julio Facelli and Katherine A. Sward
University of Utah

OBJECTIVES/GOALS: Healthcare organizations must track electronic health record (EHR) activity at the user level, including logons, accessed records, and viewed or entered documentation. There is little standardization in EHR audit logs and nurse workload has not been explored using these data. In this project, we characterized nurse actions from EHR audit logs. METHODS/STUDY POPULATION: We performed an analysis of EHR audit log data collected from 8,149 nurses over 5 years at University of Utah Health. We preprocessed nursing-centric EHR audit logs from the Epic EHR by cleaning and preparing the data for analysis. We calculated basic statistics for the variables labeled user_id (nurse) and metric_id (action). We reviewed the actions used by nurses and categories the actions as navigation, view, and entry. To capture the clinical context of the actions, two nurses categorized each action. A third nurse resolved any discrepancies. RESULTS/ANTICIPATED RESULTS: We found that of the 4,419 available metrics, nurses used 1,461 unique metrics during the timeframe. The actions most used by nurses were 1) report with patient data viewed, 2) inpatient system list, and 3) storyboard viewed. Most of the metrics were categorized as navigation. The number of nurses interacting with the EHR increased each year and on average, we found that 1000 unique metrics were used by each nurse user in a 24-hour period. The expected outcome is a set of actions that can be mapped to higher level nursing interventions and in the future contribute to models for nursing workload measurement. DISCUSSION/SIGNIFICANCE OF IMPACT: We found great value in using EHR audit logs to provide insights into nursing actions. Information gleaned can benefit organizations that are crafting interventions to decrease workload. Ultimately, the goal is to ensure that nurses have an appropriate workload allowing for safe and high-quality patient care while maintaining their well-being.

385

Impact of skin pigmentation on genomic alterations and mutation load

Rojina Nekoonam, Aravind K. Bandari, Delahny Deivendran, Bishal Tandukar, Harsh Sharma and Alan Hunter Shain
University of California San Francisco

OBJECTIVES/GOALS: Despite the documented link between ultraviolet (UV) exposure and skin cancer, the potential protective role of pigmentation in preventing skin carcinogenesis is not fully understood. This project will test the hypothesis that individuals with light skin tones are more susceptible to skin cancer due to a higher accumulation of somatic mutations from UV exposure. METHODS/STUDY POPULATION: Skin biopsies were collected from various anatomical sites of seven donors aged 70 to 80 years with dark skin tones and used to generate clones of normal skin cells. The clones were then subjected to whole-exome and RNA sequencing. We developed a workflow that allows us to accurately detect somatic mutations in clonal expansions of individual cells with high specificity and sensitivity. For comparison, we also analyzed mutations in skin cells obtained from individuals with light skin tones, who served as our control group. In the future, we plan to employ admixture analysis to clarify the impact of race on somatic mutations by examining ancestral genetic contributions. RESULTS/ANTICIPATED RESULTS: Our preliminary analysis of the existing data supports our hypothesis. The average mutation burden in individuals with light skin tone was found to be 3.778 Mut/Mb, whereas in those with dark skin tones, was only 0.818 Mut/Mb. These findings align with the prevailing hypothesis that melanin acts as a protective factor against skin cancer, as it appears to reduce the mutagenic effects of UV radiation. This suggests that individuals with darker skin may have a lower cumulative mutational load, potentially contributing to their reduced risk of developing skin cancers such as melanoma. Similarly, our results showed variations in mutational burdens across different anatomical sites, which seemed to be influenced by differing levels of UV exposure, with the highest burdens observed in areas with the greatest exposure. DISCUSSION/SIGNIFICANCE OF IMPACT: Understanding how skin cancer operates in darker-skinned individuals is imperative for tailoring effective screening and targeted therapies to meet their specific needs. In the long run, elucidating the mechanisms underlying skin cancer development in this demographic will help refine screening protocols and prevention recommendations.

386

Developing an assessment tool for NIH data management and sharing plans to understand current data practices and needs

Michelle Yee, Alisa Surkis and Fred LaPolla
NYU Langone

OBJECTIVES/GOALS: NIH requires researchers submit Data Management and Sharing (DMS) Plans with their grant applications. Librarians developed an assessment tool for the plans and completed a pilot assessment in order to leverage the plans and understand current institutional research data management and sharing.

https://doi.org/10.1017/cts.2024.1009

METHODS/STUDY POPULATION: The assessment tool includes questions related to evaluations of DMS Plans as well as questions related to the content of the plans. Evaluation questions were adapted from the Federation of American Societies for Experimental Biology evaluation rubric developed for the DataWorks! Data Management Plan (DMP) Challenge. Fields were added to collect information on the content of DMS Plans, including data type, institutional resources, data repositories, data standards, and data dissemination timelines. The assessment tool was tested in a pilot implementation. Seven library workers were trained and completed paired review samples of 27 DMS Plans (54 evaluations total) in order to test for tool reliability. RESULTS/ANTICIPATED RESULTS: Results include findings on the reliability of the tool as well as preliminary results from an assessment of DMS Plans. Findings on the reliability of the tool include assessments of the paired reviewers for each question included in the tool. Paired reviewers generally agreed, but tended to differ on specific questions, including questions pertaining to the data types generated or used in a research project. Questions with high levels of agreement included subjects of study and code sharing practices. Results on the content of the DMS Plans include information such as data repositories used, data oversight responsibilities, and data and metadata standards employed. DISCUSSION/SIGNIFICANCE OF IMPACT: DMS Plans present an opportunity to better understand data management and sharing practices, and good data management supports high-quality, reproducible research. Developing and testing assessment tools for these plans is a key step toward understanding and improving current research data management practices.

388

Subtyping social determinants of health in cancer: Implications for health equity policies

Suresh Bhavnani[1], Suresh K. Bhavnani[1], Rodney Hunter[2], Susanne Schmidt[3], Brian Downer[4] and Jeremy Warner[5]
[1]University of Texas Medical Branch; [2]Texas Southern University; [3]University of Texas San Antonio; [4]University of Texas and [5]Medical Branch Brown University

OBJECTIVES/GOALS: Although several studies have identified significant associations between specific social determinants of health (SDoH) and adverse outcomes, little is known about how SDoH co-occur to form subtypes and their outcome-based risks. Here we analyze how SDoH co-occur across all participants with a cancer diagnosis in the All of Us program. METHODS/STUDY POPULATION: Data: All participants (n = 3361) with cancer and their responses to 110 survey questions related to SDoH. Independent variables: 18 SDoH factors aggregated from the questions to address uneven granularity. Dependent variables: depression, delayed medical care, and ER visits in the last year. Analytical Method. (1) Bipartite network analysis with modularity maximization to identify participant-SDoH biclusters, measure the degree of their biclusteredness (Q), and estimate the significance of Q. (2) Visualization of the results using the ExplodeLayout force-directed algorithm. (3) Multivariable logistic regression (adjusted for demographics and corrected through FDR) to measure the odds ratio (OR) of each bicluster compared pairwise with the other biclusters to estimate their risk for the 3 outcomes. RESULTS/ANTICIPATED RESULTS: As shown in Fig. 1A (http://www.skbhavnani.com/DIVA/Images/Cancer-SDoH.jpg), the analysis (n = 3361, d = 18) identified 4 biclusters with significant biclusteredness (Q = 0.13, random-Q = 0.11, z = 9.94, P DISCUSSION/SIGNIFICANCE OF IMPACT: Currently, many health equity policies allocate resources based on sociodemographic factors like race and income to address disparities. The 4 distinct subtypes and their outcome-based risks suggest that such policies could be more precise if they were based directly on combinations of need using SDoH subtypes and their risk stratification.

Other

391

Determining the effects of the pathogenic developmental and epileptic encephalopathy patient variant, SCN1B-p.R98C, on neuronal excitability

Amanda Catalfio[1], Daniel T. Kashima[2], Chunling Chen[1] and Lori L. Isom[1]
[1]University of Michigan and [2]Northwestern University

OBJECTIVES/GOALS: Dravet syndrome is a developmental and epileptic encephalopathy associated with refractory seizures and a high risk of sudden unexpected death in epilepsy. A pathogenic biallelic variant in SCN1B, SCN1B-p.R98C, was identified in three patients with Dravet syndrome. Here we investigate SCN1B-p.R98C on neuronal function in vivo. METHODS/STUDY POPULATION: Scn1b-p.R98C mice were previously generated using CRISPR-Cas9 gene editing. Homozygous animals exhibit increased susceptibility to hyperthermia induced seizures at postnatal day (P) 15, 100% expression of spontaneous generalized seizures by P30, and ~20% undergo SUDEP by approximately P60. Here we examined the neuronal phenotype of P17–28 male and female Scn1b-p.R89C mice. We used whole-cell patch clamp electrophysiology approaches to measure effects of the variant on passive membrane properties, intrinsic excitability, and single action potential properties of parvalbumin positive (PV+) interneurons and pyramidal neurons in layers 5/6 of the somatosensory cortex and CA1 region of the hippocampus. Wild-type littermates were used as controls. RESULTS/ANTICIPATED RESULTS: Our results show no differences between genotypes in any measure for somatosensory cortical PV+ interneurons or pyramidal neurons. In the CA1 region of the hippocampus, we found no differences for any measure in PV+ interneurons. In contrast, CA1 pyramidal neurons were hyperexcitable, however, with no changes in passive membrane properties or single action potential properties. DISCUSSION/SIGNIFICANCE OF IMPACT:

https://doi.org/10.1017/cts.2024.1009