imaging, and medication variables; disease diagnosis, procedure, and billing codes) and qualitative data extracted from an integrated health system electronic health record. The heart failure subphenotypes we identify from the integrated health system electronic health record will be replicated in other heart failure population datasets using unsupervised learning approaches. We will explore the potential to establish associations between identified subphenotypes and clinical outcomes (e.g. all-cause mortality, cardiovascular mortality). RESULTS/ANTICIPATED RESULTS: We expect to identify < 10 mutually exclusive phenogroups of patients with heart failure that have differential risk profiles and clinical trajectories. DISCUSSION/SIGNIFICANCE OF FINDINGS: We will attempt to derive and validate a data-driven unbiased approach to the categorization of novel phenogroups in heart failure. This has the potential to improve our knowledge of heart failure pathophysiology, identify novel biomarkers of disease, and guide the development of targeted therapeutics for heart failure.

44499

Heterogeneity of treatment effect among patients with type 2 diabetes and body mass index >=27kg/m^2 in the Jump Start Study

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ABSTRACT IMPACT: This is the first study to use QUINT analyses to examine heterogeneity of treatment effect for group medical visits among individuals with type 2 diabetes. QUINT is a data driven method that assumes no a priori assumptions regarding effect moderators - an important step in the path towards personalized medicine. OBJECTIVES/GOALS: To examine heterogeneity of treatment effect (HTE) in Jump Start, a trial that compared the effectiveness of group medical visits (GMVs) focused on medication management only versus the addition of intensive weight management (WM) on glycemic control for patients with type 2 diabetes and body mass index >=27kg/m^2. METHODS/STUDY POPULATION: Jump Start patients (n=263) were randomized to a GMV-based medication management plus low carbohydrate diet-focused WM program (WM/GMV; n = 127) or GMV-based medication management only (GMV; n = 136) for diabetes control. We used QUalitative INteraction Trees (QUINT), a tree-based clustering method, to determine if there were subgroups of patients who derived greater benefit from either WM/GMV or GMV. Subgroup predictors included 32 baseline demographic, clinical, and psychosocial factors. Outcome was hemoglobin A1c (HbA1c). We conducted internal validation via bootstrap resampling to estimate bias in the range of mean outcome differences among arms. RESULTS/ANTICIPATED RESULTS: QUINT analyses indicated that for patients who had not previously attempted weight loss, WM/GMV resulted in better glycemic control than GMV alone (mean difference in HbA1c improvement = 1.48%). For patients who had previously attempted weight loss and had lower cholesterol and blood urea nitrogen levels, GMV alone was better than WM/GMV (mean difference in HbA1c improvement = 1.51%). Internal validation resulted in moderate corrections in the mean HbA1c differences between arms; however, differences remained in the clinically significant range. DISCUSSION/SIGNIFICANCE OF FINDINGS: Among patients with diabetes and BMI>=27kg/m^2, a low-carbohydrate, weight loss focus may better improve HbA1c in those who have never attempted weight loss. A medication management focus may be better in those who have attempted weight loss and have lower cholesterol and blood urea nitrogen.

89976

ASSESSING PROTEIN BIOMARKERS ROLE IN CVD RISK PREDICTION IN PERSONS LIVING WITH HIV (PWH)

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ABSTRACT IMPACT: Our findings could potentially identify CVD at-risk persons living with HIV who might benefit from aggressive risk-reduction. OBJECTIVES/GOALS: PWH have higher rates of CVD than the general population yet CVD risk prediction models rely on traditional risk factors and fail to capture the heterogeneity of CVD risk in PWH. Here we identify protein biomarkers that are able to discriminate between CVD cases and controls in PWH, and we assess their added benefit beyond traditional risk factors. METHODS/STUDY POPULATION: We analyzed 459 baseline protein expression levels from five OLINK panels in a matched CVD (MI, coronary revascularization, stroke, CVD death) case-control study with 390 PWH from INSIGHT trials (131 cases, 259 controls). We formed 200 datasets via bootstrap. For each bootstrap set, a two-component partial least squares discriminant model (PLSDA) was fit. The importance of each variable in the discrimination of cases and controls in the PLSDA projection was assessed by the variable importance in projection (VIP) score. Proteins with average VIP scores > 1 were used in penalized logistic regression models with elastic net penalty, and proteins were ranked based on the number of times the protein had a nonzero coefficient. Proteins in the top 25th percentile were considered to have high discrimination. RESULTS/ANTICIPATED RESULTS: Participants had mean age 47 years, 13% were females, 4.9% had CVD at baseline and 69% were on ART at baseline. Eight proteins including the hepatocyte growth factor and interleukin-6 were identified as able to distinguish between CVD cases and controls within PWH. A protein score (PS) of the top-ranked proteins was developed using the bootstrap (for weights) and the entire data. The PS was found to be predictive of CVD independent of established CVD and HIV factors (Odds ratio: 2.17 CI: 1.58-2.99). A model with the PS and traditional risk factors had a 5.9% improvement in AUC over the baseline model (AUC=0.731 vs 0.69), which is an increase in model predictive power of 18%. Individuals with a PS above the median score were 3.1 (CI: 1.83- 5.41) times more likely to develop

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CVD than those with a protein score below the median score. DISCUSSION/SIGNIFICANCE OF FINDINGS: A protein score developed improved discrimination of PWH with CVD and those without, and helped identify PWH with high risk for developing CVD. If validated, this score and/or the individual proteins could be used in addition with established factors to identify CVD at-risk individuals who might benefit from aggressive risk-reduction.

Team Science

10227

A Framework for Bringing Secondary Analysis of EHR Data to Geographically Dispersed Clinician Scientists

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ABSTRACT IMPACT: The described framework will enable other sites with a well-defined apparatus for enabling the secondary analysis of EHR data for research through education, team science, and resource consolidation. OBJECTIVES/GOALS: EHR's potential to improve healthcare outcomes extends far beyond the clinic. This vast repository of clinical insights has dramatic potential for biomedical research. To enhance accessibility for busy clinicians and underserved populations, we describe a framework for interfacing with EHR locally and through national network participation. METHODS/STUDY POPULATION: The Institutional Development Award (IDeA) program, which began in 1993, broadens NIH funding's geographic distribution for biomedical research. Included in this is the IDeA Networks for Clinical and Translational Research, which focuses on enhancing clinical and translational science across a network of IDeA-states with traditionally underserved communities and rural providers. A prior survey of the needs and capabilities of IDeA-CTR centers identified the need for improved research support. Based on our annual member survey we developed a process for supporting distributed research projects across the GP-CTR. NIH also recently made a funding announcement for the IDeA-CTR community identifying EHR research as a major priority in responding to the COVID-19 pandemic. RESULTS/ANTICIPATED RESULTS: Results from site interviews and member surveys show a clear need for dedicated resources to navigate the process of EHR-derived research. Most described a different set of requirements for increasing accessibility to EHR for research and a strong desire to participate in research networks. Local investigators cited a lack of tools, educational materials, and accessibility. Initial efforts demonstrate strong research questions but limited technical, statistical, and terminological capabilities to succeed. In response, a pipeline for team science and promotion of projects from local phenotypes to national studies. We created a facilitator training program to expand the number of facilitators (n=22), quarterly training for investigators (n=104), and ongoing efforts to advance COVID-19 research. DISCUSSION/SIGNIFICANCE OF FINDINGS: As evidenced in the expanding number of EHR-based research networks there is a need for a system to promote project development and best practices. The proposed model promotes education, resource sharing, and team formation to advance clinical questions from the idea stage toward national research network participation.

74123

A Learning Health Systems approach using health record data to construct patient frailty scores and predict safety events

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ABSTRACT IMPACT: Laying the groundwork for better predictive algorithms to inform clinical decisions and planning. OBJECTIVES/GOALS: Frailty scores predict poor patient outcomes. Validated against highly relevant outcomes, such scores can be used to inform clinical and resource utilization decisions. We generated and validated an electronic Frailty Index (EFI) from real-world EHR data using the Rockwood deficit-accumulation framework to predict patient safety events. METHODS/STUDY POPULATION: To assure that the research approach reflected perspectives of multiple stakeholders, our multidisciplinary group included an implementation scientist, a geriatrician, an internist, and an informatician. From our large academic health center, we accessed EHR data for 14,844 patients randomly sampled from the data warehouse underlying our ACT/SHRINE node. The per-visit EFI scores were calculated using EHR codes in a rolling 2-year time window. EFI was used as the predictor variable in the analytic design. The primary outcomes were preventable patient-safety events derived from ICD-10 codes including hospital-acquired infections, non-operative hospital-acquired trauma, and cardiac complications. Cox proportional hazard models were used to estimate risk for each outcome. RESULTS/ANTICIPATED RESULTS: We found statistically significant associations of EFI with clinically meaningful outcomes from EHR data. For most outcomes, we found significant correlation with EFI and c-statistics indicating good calibration of the models. The EFI was a strong predictor of clinically relevant outcomes without relying on any data other than diagnoses, vital signs, and laboratory results from the EHR. In contrast to previous studies, we treated EFI as a time-varying predictor with multiple follow-ups per patient, which is more realistic than relying on one static time-point. We used a representative sample of the adult patient population rather than limiting it to older individuals and found EFI to be a useful metric even at relatively young ages. DISCUSSION/SIGNIFICANCE OF FINDINGS: The EFI predicted safety events in adult patients using only routine, structured EHR data and can offer a low-effort, scalable method of risk assessment, valuable to clinical decisions. The capability to harness EHR data and rapidly generate clinical knowledge can be transformative for complex care and contributes to Learning Health Systems.

Translational Science, Policy, & Health Outcomes Science

21063

A Review of Novel Uses of REDCap in Clinical and Translational Science

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ABSTRACT IMPACT: This review will encourage further development of novel uses of REDCap for the benefit of the research

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