best practice maneuvers, this model will not require manipulation of the patient, have less rigid criteria for reliable interpretation, and not require as specific of a technical skillset to interpret. Furthermore, it will include many common categories of resuscitative therapies (eg, vasopressors, inotropes, fluids) and will allow effects of a combination of interventions to be predicted while making no assumptions of interdependence between said interventions. This study will also contribute a novel process of sequence prediction using RNNs by incorporating an element of context on top of the sequential data in every training step. An RNN learning the sequence of hemodynamic data comprising a patient's hemodynamic state would, alone, fit into the realm of sequence prediction. Our innovation is the addition of treatment information with each temporal division of the hemodynamic data. The result is an RNN that combines the task of sequence prediction with sequence translation, the 2 major use cases for RNN learning algorithms.

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Immune stress biomarkers correlate to violence and internalization of violence in African American young adults

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OBJECTIVES/SPECIFIC AIMS: Allostatic load, the chronic stress-induced wear and tear on the body, has a cumulative deleterious effect in individuals over their lifetime. Recent studies have suggested that socio-economic status, psychological determinants, and biomedical health cumulatively contribute to allostatic load in young adults. Although these finding individually suggest that African American children may be particularly susceptible to the effects of allostatic loading due to racially-based discrimination and economic instability, few studies have shown the effect of exposure to violence on the allostatic load carried by young African Americans. METHODS/STUDY POPULATION: The Biological and Social Correlates of Drug Use in African American Emerging Adults (BADU) data set is composed of young African Americans (n = 557 individuals) living in the Washington, DC area, collected from 2010 to 2012. Study participants were sought equally between males and females (n = 283, n = 274, respectively). This data set provides a rich source of information on the behavioral, mental, and physical health of African American young adults (18–25 year olds) living in the Washington, DC area. Analysis of 6 biomedical markers were measured in BADU study participants: C-reactive protein, cortisol, Epstein-Barr virus IgG, IgE, IgA, and IgM, known to be markers of immune stress and allostatic load. Naive Bayes was used to identify participant responses that were correlated to elevated stress biomarker levels. RESULTS/ANTICIPATED RESULTS: Violence was most closely correlated to elevated EBVVCA IgM and IgE levels. Elevated IgE levels correlated to increased experience of familial violence and sexual abuse; familial drug abuse and depression; violence and community violence. Cortisol is positively correlated to reported emotional state ($R = 0.072$) and perceived individual discrimination ($R = 0.059$). DISCUSSION/SIGNIFICANCE OF IMPACT: Allostatic load appears to be high in individuals who self-report exposure to violence. Both perceived mental health and violence were correlated to elevated stress biomarkers. When Epstein-Barr virus viral capsid antigen IgM was compared with violence features characterized in the data set, we found that internalization of environmental stressors were most strongly correlated to elevated allostatic load markers. This work suggests that internalization of experienced violence may be as important as the actual violence experience.

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A machine learning pipeline to predict acute kidney injury (AKI) in patients without AKI in their most recent hospitalization

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OBJECTIVES/SPECIFIC AIMS: Our objective was to develop and evaluate a machine learning pipeline that uses electronic health record (EHR) data to predict acute kidney injury (AKI) during rehospitalization for patients who did not have an AKI episode in their most recent hospitalization. METHODS/STUDY POPULATION: The protocol under which this study falls was given exempt status by our institutional review board. The fully deidentified data set, containing all adult hospital admissions during a 2-year period, is a combination of administrative, laboratory, and pharmaceutical information. The administrative data set includes International Classification of Diseases, 9th Revision (ICD-9) diagnosis and procedure codes, Current Procedural Terminology, 4th Edition (CPT-4) procedure codes, diagnosis-related grouping (DRG) codes, locations visited in the hospital, discharge disposition, insurance, marital status, gender, age, ethnicity, and total length of stay. The laboratory data set includes bicarbonate, chloride, calcium, anion gap, phosphate, glomerular filtration rate, creatinine, urea nitrogen, albumin, total protein, liver function enzymes, and hemoglobin A1c. The pharmacy data set includes, for each medication, a description, pharmacologic class and subclass, and therapeutic class. Data preprocessing was performed using Python library Pandas (McKinney, 2011). Top-level binary representation (Singh, 2015) was used for diagnosis and procedure codes. Categorical variables were transformed via 1-hot encoding. Previous admissions were collapsed using rules informed by domain expertise (eg, the most recent age or sum of assigned diagnosis codes were retained as elements in the feature vector). We excluded any patient without at least 1 rehospitalization during the time window. We excluded any admission with or without AKI where AKI was also present in the most recent hospitalization. For comparison, we do not exclude such admissions for an identical experiment in which we considered any AKI event as a positive sample (regardless of AKI presence in the most recent hospitalization). We defined an AKI event as an assignment of any of the acute kidney failure (AKF) ICD-9 codes [584.5, AKF with lesion of tubular necrosis, 584.6, AKF with lesion of renal cortical necrosis, 584.7, AKF with lesion of renal medullary (papillary) necrosis, 584.8, AKF with other specified pathological lesion in kidney, or 584.9, AKF, unspecified]. Since diagnosis codes are believed to be specific but not sensitive for AKI (Waikar, 2006), we supplemented them using creatinine for patients who had laboratory values. Diagnosis was made according to the Kidney Disease: Improving Global Outcomes (KDIGO) Practice Guidelines (AKI defined as a 1.5-fold or greater increase in serum creatinine from baseline within 7 d or 0.3 mg/dL or greater increase in serum creatinine within 48 h). We report preliminary model discrimination via area under the receiver operating characteristic curve (AUC) using k-fold cross validation grouped by patient identifier (to ensure that admissions from the same patient would not appear in the training and validation set). It was confirmed that the prevalence of positive samples in the entire data set was maintained in each fold. Python library Sci-kit Learn (Pedregosa, 2011) was used for pipeline development, which consisted of imputation, scaling, and hyper-parameter tuning for penalized (l1 and l2 norm) logistic regression, random forest, and multilayer perceptron classifiers. All experiments were stored in IPython (Pérez, 2007) notebooks for easy viewing and result reproduction. RESULTS/ANTICIPATED RESULTS: There were 107,036 adult patients that accounted for 199,545 admissions during a 2-year window. Per admission, there were at most 54 ICD-9 diagnoses, 38 ICD-9 procedures, 314 CPT-4 procedures, and 25 hospital locations visited. The admissions were 55% female, the average age was 46 ± standard deviation 20, and average length of stay was 2.5 ± 8.0 days. We excluded 2360 admissions that involved an AKI event that directly followed an admission with an AKI event and 4130 admissions that did not involve an AKI event but directly followed an admission with an AKI event. In total, there were 4561 (5.3%) positive samples (AKI during rehospitalization without AKI in the previous stay) generated by 3699 unique patients and 81,458 negative samples (non-AKI during rehospitalization without AKI in the previous stay) generated by 31,831 unique patients. When using any AKI event as a positive sample (regardless of whether or not AKI was in the most recent stay), the prevalence was 7.3% (6921 positive samples generated by 4395 unique patients and 85,588 negative samples generated by 33,287 unique patients). Best results were achieved with a code precision of 3 digits for which we had a total of 4556 features per patient. Fitted hyper-parameters corresponding to each classifier were logistic regression with l1 penalty C as 2×10^{-3}; logistic regression with l2 penalty C as 1×10^{-6}; random forest number of estimators as 100, maximum depth as 3, minimum samples per leaf as 50, minimum samples per split as 10, and entropy as the splitting criterion; and multilayer perceptron l2 regularization parameter α as 15, architecture as 1 hidden layer with 5 units, and learning rate as 0.001. Five-fold stratified cross validation on the development set yielded AUC for logistic regression with l1 penalty average 0.830 ± 0.006, logistic regression with l2 penalty 0.796 ± 0.007, random forest 0.828 ± 0.007, and multilayer perceptron 0.841 ± 0.005. In an identical experiment for which an AKI event was considered a positive sample regardless of AKI presence in the most recent stay, we had 4592 features per sample with the same code precision. Five-fold stratified cross validation on the development set with identical settings for the hyper-parameters yielded AUC for logistic regression with l1 penalty average 0.850 ± 0.004, logistic regression with l2 penalty 0.819 ± 0.006, random forest 0.853 ± 0.004, and multilayer perceptron 0.853 ± 0.006. DISCUSSION/SIGNIFICANCE OF IMPACT: Our objective was to investigate the feasibility of using machine learning methods on EHR data to provide a personalized risk assessment for "unexpected" AKI in rehospitalized patients. Preliminary model discrimination was good, suggesting that this approach is feasible. Such a model could aid clinicians to recognize AKI risk in unsuspicious patients. The authors recognize several limitations. Since our data set corresponds to a time-window sample, patients with high frequency of hospital utilization are likely over-represented. Similarly, our data set contains records from only 1 hospital

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network. Although we supplement with laboratory-based diagnosis, using diagnosis codes as labels is problematic as numerous reports suggest low sensitivity of codes for AKI. Future work includes calibration analysis, incremental updating ("online learning"), and a representation learning-based ("deep learning") extension of the model.

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Genetic determinants of recovery after mild traumatic brain injury: Can study samples be identified from electronic medical records linked to DNA biobanks?

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OBJECTIVES/SPECIFIC AIMS: To develop an algorithm that identifies post-concussion syndrome (PCS) cases and controls from among patients with mild traumatic brain injury (mTBI) in a large academic biobank. METHODS/STUDY POPULATION: The Vanderbilt University Medical Center's (VUMC) electronic medical record (EMR) research database includes longitudinal medical record data on 2.5 million people. DNA and genotype data were also available for >225,000 of these individuals. Our algorithm used a combination of billing codes and natural language processing to apply inclusion and exclusion criteria. We defined PCS cases as those with a PCS billing code (ICD-9 310.2 or ICD-10 F07.81) and/or symptoms of PCS within 1–6 months of a qualifying mTBI. We will compare the positive predictive value of our algorithm to that of 2 simpler case selection schemes: (1) 1 instance of the PCS billing code anywhere in the medical record; and (2) 2 or more instances of the PCS billing code anywhere in the medical record. RESULTS/ANTICIPATED RESULTS: An mTBI was diagnosed in 28,720 patients regularly attending VUMC, and 528 of these patients were classified as PCS cases by our algorithm. The characteristics of our EMR sample reflected known risk factors for PCS. Our cases were more likely than controls to be female (49.4% vs. 38.4%), to have sustained a previous TBI (31.0% vs. 12.0%) and to have comorbid mood disorders. Our PCS cases were also more likely than controls to be <18 years of age (42.4% vs. 33.6%) and to have a sports-related keyword associated with the mTBI (44.1% vs. 25.2%), emphasizing the relevance of PCS to young athletes. Nonetheless, the number of PCS cases identified by our algorithm was small, and within the VUMC EMR, there were 5039 patients with 1 PCS billing code, and 2457 patients with 2 or more PCS billing codes anywhere in their EMR. Our next step is to calculate the positive predictive values of each selection scheme by manually reviewing the EMR of a selection of cases. Ultimately, we will implement the selection scheme that maximizes both positive predictive value and sample size, and in future work, we will genotype the selected patients to better understand the genetic architecture of PCS. DISCUSSION/SIGNIFICANCE OF IMPACT: EMR and biobanks are the future of human health research, and we asked whether complex algorithms or simple billing codes were best for studying the genetics of recovery after mTBI within the VUMC EMR. Our results are relevant to other studies of brain injury phenotypes within biobanks, including recovery from moderate or severe TBI, recovery from stroke, or the occurrence of delirium after routine surgery, and will help transform biobanks into fruitful research tools.

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The design of a patient-centered personal health record with patients as co-designers

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OBJECTIVES/SPECIFIC AIMS: The promise and potential of connected personal health records (PHRs) has not come to fruition. This may be, in part, due to the lack of user-centered design and of a patient-centric approach to curating personal health data for use by patients. Co-design with end-users could help mitigate these issues by ensuring the software meets user's needs, and also engages patients in informatics research. Our team partnered with patients with multiple chronic conditions to co-design a patient-centric PHR. This abstract will describe our experience with the co-design process, highlight functionalities desired by patients, and showcase the final prototype. METHODS/STUDY POPULATION: We conducted 3 design sessions (90 min per session) with patients as co-designers and employed an iterative process for software development. Patients were recruited from Chapel Hill and surrounding areas. The initial design session laid the foundation for future sessions, and began with brainstorming about what patients thought their ideal version of an engaging connected PHR would look like in terms of features and functionalities. After each software iteration, our entire design team, including our patient co-designers, was shown the prototype during a subsequent design session. Once the final prototype was developed, usability testing was conducted with patient participants. Our team then conducted a final design session to debrief about the final prototype. RESULTS/ANTICIPATED RESULTS: We started with an initial group of 12 patients (6 males) who all had diabetes and an additional comorbidity such as hypertension and hyperlipidemia. Age of participants ranged from 30 to 77 years with an average age of 56. The majority of participants were Caucasian with 1 Asian and 2 African Americans. Hemoglobin A1c values ranged from 6.0% to 9.2% with approximately half having A1c values less than the goal of 7.0%. Half the patients were aware of PHRs, majority had smartphones, and all participants had access to the Internet and used email. Two of the patients were retired engineers who had prior experience with software design. The other sessions had between 7 and 8 participants at each session, and 7 patients completed the 90-minute usability testing session. There was a core group of 7 patients who were engaged in the design and testing sessions throughout the entire 9-month study. Key features of the PHR that emerged from design sessions included the following: (1) allow for annotation of data by patients (particularly important for lab values like glucose or for physical activity); (2) calendars, to do list, and reminder functions should be linked so that an entry in one of these allows for auto-population of this data within the other sections; (3) notifications whenever new data from the electronic health record or other sources are pushed to the PHR account; (4) allow for drag and drop of photos of pills/medications taken via smartphone or from other sources so that medication list has photo of actual pills or pill bottle; (5) allow for patients to customize the order of sections in the PHR dashboard so that the sections most important to the individual patient can be displayed more prominently; (6) allow for notifications from pharmacies to be pushed to the PHR (eg, confirmation of receipt of prescription requests or alert that prescription is ready to pick up); and (7) graphical display of trends over time (patients would like to select the measures and time frames to plot for display). Patients cited the importance of data provenance so that patient-entered data Versus provider or electronic health record data could be easily differentiated. Patients also highlighted the importance of having this PHR be a "one-stop shop for all their health data" and to have meaningful data dashboards for the different types of information needed to comprehensively manage their health. Patients wished for a single PHR that could easily bring together data from multiple patient portal accounts to avoid having to manage multiple accounts and passwords. They felt that heat map displays such as those used on popular fitness tracking websites were not intuitive and that the color-coding made interpretation challenging. Participants noted that engagement in the design process made them feel that they contributed towards developing software that could not only positively impact them individually but others as well. Every patient indicated the desire to participate on future design projects. Of the 19 tasks evaluated during usability testing, only 5 tasks could not be completed (eg, adding exercise to the calendar, opening the heat map, etc.). Patients felt that the overall PHR design was clean and aesthetically pleasing. Most patients felt that the site was "pretty easy to use" (6 out of 7). The majority of participants would like to use this PHR in the future (5) and would recommend this PHR to their friends/family to use (6). DISCUSSION/SIGNIFICANCE OF IMPACT: Involving patients directly in the design process for creating a patient-centric connected PHR was essential to sustaining engagement throughout the software life cycle and to informing the design of features and functionalities desired by patients with chronic conditions.

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Streamlining study design and statistical analysis for quality improvement and research reproducibility

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OBJECTIVES/SPECIFIC AIMS: Key factors causing irreproducibility of research include those related to inappropriate study design methodologies and statistical analysis. In modern statistical practice irreproducibility could arise due to statistical (false discoveries, p-hacking, overuse/misuse of *p*-values, low power, poor experimental design) and computational (data, code and software management) issues. These require understanding the processes and workflows practiced by an organization, and the development and use of metrics to quantify reproducibility. METHODS/STUDY POPULATION: Within the Foundation of Discovery – Population Health Research, Center for Clinical and Translational Science, University of Utah, we are undertaking a project to

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