

illness (saw a doctor, visited the ER, or were hospitalized for a respiratory symptom). We examined the interaction of PM<sub>2.5</sub> with spending time outdoors during the wildfires. Poisson regression models with robust standard errors were adjusted for age, sex, race, smoking, allergies, and education. RESULTS/ANTICIPATED RESULTS: Among 337 adults with asthma in the WHAT-NOW cohort, one standard deviation higher smoke-driven PM<sub>2.5</sub> was associated with higher risk of any persistent respiratory symptom (risk ratio (RR) 1.38, 95% CI 1.07 – 1.78) and having at least one medically attended respiratory illness (RR 1.33, 95% CI 1.07 – 1.65), but not significantly associated with repeated asthma exacerbations (RR 1.30, 95% CI 0.92 – 1.81). However, there was a significant interaction between PM<sub>2.5</sub> and outdoor activities during the wildfire on the outcomes of any persistent respiratory symptoms ( $p = 0.041$ ) and repeated asthma exacerbations ( $p = 0.028$ ). The association between PM<sub>2.5</sub> and repeated asthma exacerbations was greater among people who spent time outdoors (RR 3.36, 95% CI 1.47 – 10.23) than those who did not (RR 1.00,  $p = 0.99$ ). DISCUSSION/SIGNIFICANCE OF IMPACT: This study provides evidence that exposure to wildfire smoke increases respiratory morbidity among adults with asthma beyond the acute wildfire period. Additionally, it suggests that avoiding outdoor activities on smoky days can significantly decrease the risk of future repeated asthma exacerbations associated with smoke exposure.

## 79

### How do you share documents with collaborators external to your institution?

Shokoufeh Khalatbari<sup>1</sup>, Susan Perkins<sup>2</sup>, Sally Thurston<sup>3</sup>, Jane Bugden<sup>4</sup> and Cathie Spino<sup>4</sup>

<sup>1</sup>Michigan Institute for Clinical & Health Research (MICHHR);

<sup>2</sup>University of Michigan (Indiana University School of Medicine);

<sup>3</sup>University of Rochester Medical Center and <sup>4</sup>University of Michigan

OBJECTIVES/GOALS: Using secure systems for sharing documents with external collaborators is essential for all researchers. These documents may include protected health information (PHI) or sensitive materials like protocols, study reports, DSMB reports, publications, presentations, abstracts, and statistical analysis plans (SAPs). METHODS/STUDY POPULATION: We surveyed the ACTS Biostatistics, Epidemiology, and Research Design Special Interest Group (BERD-SIG) to gather information about the systems they are currently using or have used in the past for document sharing with external collaborators. The survey focused on the security of these systems, particularly in relation to sharing documents containing PHI. In addition, the survey included questions about various system features of interest. These features included version control, simultaneous editing by multiple users, and access rights management, such as the ability to assign different permissions (e.g., read-only, write, and download) to different individuals. We also invited participants to provide feedback on any additional positive or negative aspects of the systems they use. RESULTS/ANTICIPATED RESULTS: We received 28 completed survey responses. Respondents had an option for choosing more than one system. The top current systems reported were Microsoft Teams (OneDrive, SharePoint) ( $n = 16$ ), Box ( $n = 11$ ), Google Docs/Drive ( $n = 10$ ), and Dropbox ( $n = 6$ ). Among other systems listed individually were Filelocker, REDCap, Slack, Website,

Significant Media Shuttle, and Zulip. Notably, 15 responses indicated the respondents were unsure if their system is secure for sharing documents containing PHI. Respondents also offered feedback on both the positive and negative aspects of these systems. For example, a key advantage of Box was its password-controlled access. However, its incompatibility with office tools and the challenges for external collaborators attempting to access the system were noted as drawbacks. DISCUSSION/SIGNIFICANCE OF IMPACT: Utilizing secure institutional document-sharing systems and understanding their features significantly affects the effectiveness and security of collaborations among researchers, particularly with external partners. This knowledge is especially crucial when sharing documents containing sensitive patient and study data.

## 80

### Genome-wide association study of visual memory and spatial organization in a community setting: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium\*

Alison Luckey<sup>1</sup>, Alison M. Luckey<sup>1</sup>, Qiong Yang<sup>2</sup>, Mohsen Sharifi, Tabar<sup>1</sup>, Sudha Seshadri<sup>1,2</sup>, Annette L. Fitzpatrick<sup>3</sup>, Claudia L. Satizabal<sup>1,2</sup> and NeuroCHARGE working group

<sup>1</sup>University of Texas Health Science Center at San Antonio, San Antonio, TX, USA; <sup>2</sup>Boston University's and National Heart, Lung, and Blood Institute's Framingham Heart Study, Framingham, MA, USA and <sup>3</sup>University of Washington, Seattle, WA, USA

OBJECTIVES/GOALS: Poor visual memory and perceptual organization task performance predicts cognitive decline and is sensitive to dementia severity. No genome-wide association study (GWAS) has assessed the genomic basis of cognitive visual-spatial phenotypes. We aimed to identify common genetic variants associated with visual memory and spatial organization. METHODS/STUDY POPULATION: We included dementia- and stroke-free participants aged 45 years or older from up to seven cohorts in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium, who performed cognitive tasks assessing delayed visual memory (e.g., Benton Visual Retention Test (BVRT,  $n = 10,934$ ) and visual reproductions (VR,  $n = 5,527$ )) or spatial organization (i.e., Hooper Visual Organization Test (HVOT,  $n = 5,024$ )). Each cohort used linear regression models to relate common genetic variants imputed to the 1000 Genomes panel to each cognitive phenotype, adjusting for age, sex, population stratification, and education. Summary statistics for the BVRT were meta-analyzed using METAL. Combined GWAS was used for a joint analysis of all traits. RESULTS/ANTICIPATED RESULTS: We identified a genome-wide significant variant related to BVRT performance located near the TSHZ3 gene (rs10425277,  $p = 6.76 \times 10^{-9}$ ). TSHZ3 is important for the development and function of cortical projecting neurons and may be implicated in Alzheimer's disease progression by repressing CASP4 transcription. Multitrait analyses, including BVRT, VR, and HVOT, identified two additional variants of interest in SMYD3 gene (rs10802275,  $p = 5.58 \times 10^{-7}$ ) and near ZFPM2 (rs2957459,  $p = 2.03 \times 10^{-7}$ ), both of which are overexpressed in the brain and have important implications for neurodevelopment. SMYD3 may be directly involved in synaptic dysfunction and has been shown to be upregulated in the prefrontal cortex of Alzheimer's disease patients. DISCUSSION/SIGNIFICANCE OF

**IMPACT:** Our findings suggest that variants related to visual memory and spatial organization are involved in neurodevelopmental and degenerative pathways. This GWAS adds to the growing body of GWAS literature on the genetic basis of cognitive function. Additional analyses are underway to replicate these findings and extend functional annotation.

### 81 **Fixing or mixing? Improving small sample size longitudinal microbiome models\***

Raunak Vijayakar, Jun Chen and Marina Walther-Antonio  
Mayo Clinic

**OBJECTIVES/GOALS:** Longitudinal studies capture dynamic host-environment interactions crucial to microbiome research. Commonly used mixed-effects models can struggle with small clinical samples, like many endometrial cancer studies. We will compare them to simpler fixed-effects models, aiming to develop a new fixed-effects differential abundance alternative. **METHODS/STUDY POPULATION:** Starting with simulated data for linear models with a single treatment effect, we will incrementally increase complexity to reflect real-world microbiome data. To observe conditions of misspecification, simulated data of repeated measures will be generated using different distributions, while varying parameters and inter-class correlation. In each condition, linear fixed- and mixed-effects models will be fitted 1000 times to empirically determine p-value, type 1 error rate, and power. We will increase the verisimilitude of our approach by using endometrial cancer data from our lab as a real background, while adding simulated signals. This data will be used to assess extant differential abundance models against our novel fixed-effects model. **RESULTS/ANTICIPATED RESULTS:** Our initial findings indicate that fixed-effects models maintain control over type 1 error rates in small samples, while mixed-effects models do not perform as reliably. We are now exploring the effects of confounders on type 1 error rates and power in linear models, while our next step will evaluate generalized linear models in a differential abundance context. We expect that the fixed-effects models will continue to be as reliable as mixed-effects models, while being less computationally complex. After establishing our theoretical basis, our novel model should perform comparably to mixed-effects models on pseudo-simulated endometrial cancer data and better at small sample sizes. We will finally apply our model to real endometrial cancer data to identify microbial markers of disease predisposition. **DISCUSSION/SIGNIFICANCE OF IMPACT:** By characterizing and improving these statistical tools, we seek to increase the robustness and power of microbiome study results (especially at small sample sizes), ultimately supporting better-informed translational research decisions. This work underscores the importance of statistical methods in advancing microbiome research.

### 82 **Leveraging the biodesign process to create impactful medical technologies: A study in neurosurgery**

Arjun Menta<sup>1</sup>, Arjun K. Menta<sup>2,3</sup>, Ava Taylor<sup>3</sup>, Kenny Nova<sup>3</sup>, Sofia Garcia del Barrio Cervera<sup>3</sup>, Shreya Jindal<sup>3</sup>, Anders Sideris<sup>3</sup>, William S. Anderson<sup>2</sup>, Soumyadipta Acharya<sup>3</sup> and Youseph Yazdi<sup>3</sup>

<sup>1</sup>Johns Hopkins School of Medicine; <sup>2</sup>Department of Neurosurgery, Johns Hopkins University School of Medicine Baltimore and <sup>3</sup>Center for Bioengineering Innovation & Design (CBID) Whiting School of Engineering, Johns Hopkins University, Baltimore

**OBJECTIVES/GOALS:** This study demonstrates the utility of the CBID biodesign process for identifying and prioritizing high-impact neurosurgical needs. The research emphasizes the process's role in developing innovative medical technologies that align with the healthcare ecosystem's demands and stakeholder priorities. **METHODS/STUDY POPULATION:** The CBID Spiral Innovation Model, integrating clinical, technical, business, and strategic considerations across clinical challenges in neurosurgery was employed over a 15-week period at a tertiary care center. The process involved three phases: (1) needs identification through 8 weeks of clinical immersion, (2) 7–8 weeks of stakeholder engagement via informational interviews, surveys, and conferences, and (3) iterative refinement based on evidence generation and market value. Stakeholders included over 70 clinicians (neurosurgeons, neurocritical care specialists, neurologists, etc.) across 15 institutions as well as more than 10 payers and hospital administrators. Data collection encompassed direct observation, structured interviews, and comprehensive literature review. **RESULTS/ANTICIPATED RESULTS:** The initial list of 300+ identified neurosurgical needs was reduced to 271 after clinician and market input. High-level market and clinical evidence assessments further reduced this to 74 needs. Finally, through iterative evaluation of evidence generation, market opportunity, and stakeholder feedback, five critical unmet needs in stroke, traumatic brain injury, hydrocephalus, and epilepsy were identified for technological innovation. These needs met the criteria for clinical importance, economic viability, and market accessibility. The findings highlight the effectiveness of the biodesign process in creating a roadmap for innovation that is both clinically relevant and commercially viable. **DISCUSSION/SIGNIFICANCE OF IMPACT:** This study underscores the effectiveness of structured need-finding and prioritization within neurosurgery. Integrating stakeholder perspectives and rigorous analysis, it provides a replicable framework for medical innovation to accelerate the development of impactful solutions across medicine.

### 85 **Geographic landscape of US broadband availability from 2017 to 2020**

Jenna Rajczyk and Jeffrey Wing  
The Ohio State University

**OBJECTIVES/GOALS:** Telehealth is a key solution to improving access to healthcare and disease detection, especially in rural areas. Telehealth access relies on the presence of broadband in an area, which has shifted with the growing importance of internet. We aim to assess the distribution of US county-level broadband availability from 2017 to 2020 overall and by rurality. **METHODS/STUDY POPULATION:** We employed an ecologic study design to examine the distributions of two measures of broadband availability across all US counties from 2017 to 2020. Broadband presence was defined as counties meeting the Federal Communications Commission (FCC) definition of broadband with at least one high-speed internet provider and an average download/upload speed of at least 25/3 megabits per second using 2017–2020 FCC Broadband Deployment Data. Broadband access, or county-year proportion of households with broadband, was defined using 2017–2020 data from the American Community Survey. We used log-binomial and linear regression models and a difference-in-difference analytical approach to estimate the difference in the change in broadband presence and access from 2017 to 2020 between rural and urban counties. **RESULTS/ANTICIPATED RESULTS:** Overall, broadband presence increased