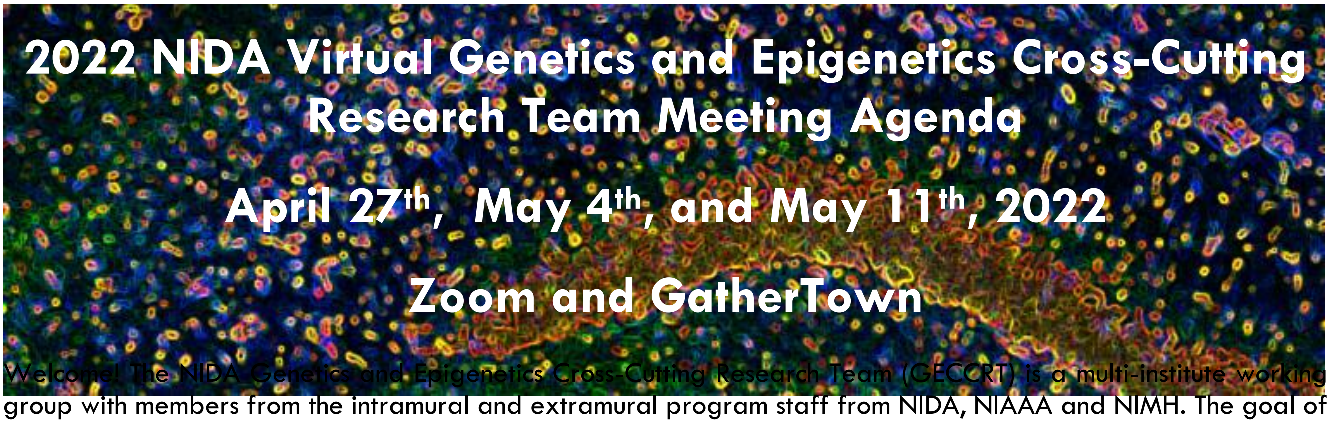

2022 NIDA Virtual Genetics and Epigenetics Cross-Cutting Research Team Meeting Agenda

April 27th, May 4th, and May 11th, 2022

Zoom and GatherTown

Welcome! The NIDA Genetics and Epigenetics Cross-Cutting Research Team (GECCRT) is a multi-institute working group with members from the intramural and extramural program staff from NIDA, NIAAA and NIMH. The goal of the GECCRT is to support the use of genetic and epigenetic tools to uncover new genetic, biochemical, and epigenetic pathways that contribute to substance use disorders. The GECCRT is hosting a multi-day annual meeting, attended by ~250 extramural and intramural investigators who will present their newest studies through talks (Zoom Webinar) and poster sessions (GatherTown). Join us on three consecutive Wednesdays: April 27th, May 4th, and May 11th!

Please register for the meeting here:
https://seiservices.zoom.us/meeting/register/tJcucO2qqTIsE9N_dnj_6Oq9vhuGnUMnhjNM

Day 1 **Link:**	**April 27, 2022**
10:30	**Welcome by Nora Volkow, MD, Director, National Institute on Drug Abuse**
10:45	**Welcome by Anthony K. Wutoh, PhD, RPh, Provost and Chief Academic Officer, Howard University**
11:00 to 12:30	**Session 1: Data Science in HBCUs: Leveraging Scientific Expertise to Tackle the Genetics of Addiction (Drs. Earl Ettienne and Evaristus Nwulia Co-chairs)**
11:00	William M. Southerland, PhD Howard University *The Howard University Center of Applied Data Science and Analytics (CADSA)*
11:15	Anil Shanker, MS, PhD Meharry Medical School *Genomics and Health Equity Research: Current Challenges and Opportunities*
11:30	Jennifer Troyer, PhD (video) Coordinator, Human Heredity and Health in Africa *Human Heredity and Health in Africa (H3Africa)*
11:45	Adaku Ofoegbu, PhD Howard University *The Role of Phase II Metabolic Enzymes and Drug Transporters on Buprenorphine Pharmacogenomics in Opioid Use Disorder Management*
12:00	Evaristus Nwulia, PhD Howard Universitiy *Comparative Response to Alcohol in Individuals with ADH1B*1 and ADH1B*3 Polymorphisms*
12:15	Discussion
12:30	**Break**
1:00 to 2:30	**Session 2: Tools and Methods to Visualize Genomic Signals in GWAS (Drs. Susan Wright and Amy Lossie, Session Chairs)**
1:00	Xiaoyu Liang, PhD University of Tennessee Health Science Center *A Mediating Role for Epigenetic Aging in the Relationship Between People Who Inject Drugs with HCV and All-Cause Mortality*
1:15	Luis FS Castro-de-Araujo, PhD Virginia Commonwealth University *Bidirectional causal modeling with instrumental variables and data from relatives*
1:30	Brittany Kuhn, PhD

	Medical University of South Carolina *Network-based clustering approach models multi-symptomatic opioid use disorder vulnerability*
1:45	Kyle Sullivan, PhD Oak Ridge National Laboratory *Multi-omic network analysis identifies key neurobiological pathways in opioid addiction*
2:00	Andy Chen, PhD Indiana University School of Medicine *Functional Screening of 3'-UTR Variants Combined with Genome-wide Association Identifies Causal Regulatory Mechanisms Impacting Alcohol Consumption and Alcohol Use Disorder*
2:15	Discussion
2:30	**Lived Experiences (Drs. Denise Scott and Amy Lossie, Session Chairs)** Jessie Gambrell *Peer Recovery Coach* *Program Coordinator for Rusty Hound Wellness Program*
3:00	**Poster Session A (GatherTown)**
4:15	**Poster Session B (GatherTown)**
5:30	**Adjourn**

Day 2 **Link:**	**May 4, 2022**
10:45 AM	**Welcome**
11:00 to 12:30	**Session 3: Can Increasing Diversity Lead to Deeper Understanding of Addiction? (Dr. Jonathan Pollock, Session Chair)**
11:00	Xingyan Wang, Doctoral Candidate Penn State University *Trans-Ancestry Fine-Mapping and Ancestry Heterogeneity Analysis for Smoking & Drinking Addiction Phenotypes using 3.4 Million Individuals with Diverse Ancestries*
11:15	Alexander Hatoum, PhD Washington University School of Medicine *Cross-Ancestral Genome-wide analysis of Broad Addiction Vulnerability Leads to Additional Insight Over European GWAS Alone*
11:30	Hang Zhou, PhD Yale University School of Medicine *Advanced genetic study of problematic alcohol use in > 1 million subjects from multiple populations*
11:45	Discussion
12:00	**Break**
12:30	**Session 4: Leveraging Multi-Species Analyses (Dr. Amy Lossie, Session Chair)**
12:30	Andreas Pfenning, PhD Carnegie Mellon University *What can bats, capybaras, and tree shrews tell us about the genetic basis of addiction?*
12:45	Brenda Cabrera-Mendoza, PhD Yale University School of Medicine *Cross-tissue Evaluation of Epigenetic Clocks in Substance Use Disorder*
1:00	Abraham Palmer, PhD University of California, San Diego *Comparing polygenic signals across species*
1:15	Rohan Palmer, PhD Emory University *Molecular Brain Signatures of Chronic Alcohol Use Across Species*
1:30	Robyn Ball, PhD Jackson Laboratory *Integrating past, present and future mouse and human population genetics of addiction using multi-trait meta-analyses to identify conserved human polysubstance use genes*
1:45	Discussion
2:00 to 3:00	**Session 5: Understanding Comorbidities and Addiction (Drs. Naimah Weinberg and Udi Ghitza, Session Chairs)**

2:00	~~Amelia Cuarenta, PhD.~~ Talk Cancelled Temple University *The effect of resource scarcity early in life on the rat basolateral amygdala transcriptome*
2:15	Bonnie Alberry, PhD McGill University *Sex-specific prefrontal cortex gene networks moderate the effect of early adversity on childhood behavior and adult substance abuse*
2:30	Ditte Demontis, PhD Aarhus University *Genome-wide cross-disorder analysis of ADHD and cannabis use disorder and cannabis use*
2:45	Discussion
3:00	**Poster Session C (GatherTown)**
4:15	**Poster Session D (GatherTown)**
5:30	**Adjourn**
Day 3 Link:	**May 11, 2022**
11:00	**Welcome**
11:15 to 12:30	**Session 6: Epigenetics, Gene Regulation and the SUD Brain (Dr. Jean Lud Cadet, Session Chair)**
11:15	Consuelo Walss-Bass, PhD University of Texas Health Science Center at Houston *Postmortem brain multi-omic profiling and vertical data integration in cocaine and opioid use disorder*
11:30	Jessica Childs, PhD University of California, Irvine *Dominant negative of transcription factor NR4A2 in medial habenula attenuates reinstatement of cocaine self-administration in mice*
11:45	Delaney Fischer, Graduate Student University of Pennsylvania *Investigating the transcriptomic and epigenomic profile of the mouse striatum following cocaine exposure*
12:00	Erin Calipari, PhD Vanderbilt University *Histone acetyltransferase KAT2A is a critical epigenetic regulator of cocaine responses in the nucleus accumbens*
12:15	Discussion
12:30	**Break**
1:00	**Session 7: The Power of Single Cell Analyses (Dr. John Satterlee, Session Chair)**
1:00	ZhuZhu Zhang, PhD The Salk Institute *Single-cell characterization of epigenomic remodeling in cocaine self-administration in mice*
1:15	Ming-Fen Ho, PhD Mayo Clinic *Single cell transcriptomics reveals distinct transcriptional response to oxycodone and buprenorphine by iPSC-derived brain organoids from patients with opioid use disorder*
1:30	Francesca Telese, PhD University of California, San Diego *Computational analysis of snATAC-seq from amygdalae reveals cell type-specific chromatin regions associated with cocaine addiction*
1:45	BaDoi Phan, MSTP Student University of Pittsburgh *Single cell multi-omics of the rhesus macaque striatum reveal regulatory mechanisms underlying the genetic basis of addiction*
2:00	Discussion
2:15	**Wrap Up**
2:30	**Poster Session E (GatherTown)**
3:45	**Poster Session F (GatherTown)**
5:00	**Adjourn**