ASHG 2020 Virtual Meeting

On October 27-30, data analyst Heather Issen and web developer Conor Klamann each presented their NIAGADS posters to the American Society of Human Genetics (ASHG) 2020 Virtual Meeting.

Heather Issen held a poster session on the NIA Genetics of Alzheimer's Disease Data Storage Site (NIAGADS), a rich resource for AD researchers to promote Alzheimer's genetics research advancements. NIAGADS enables AD researchers to achieve their research objectives more effectively through housing datasets from many projects and institutions.

Conor Klamann presented his poster on the NIAGADS Alzheimer's Genomics Database (GenomicsDB), an interactive knowledge base for AD genetics and related neuropathologies that provides unrestricted access to genome-wide association studies (GWAS) deposited at NIAGADS. These data are curated along with variant and gene annotations and AD-relevant functional genomics datasets, allowing AD researchers to quickly identify and interpret interesting genomic regions via interactive search strategies and the NIAGADS genome browser. \

In addition to the poster presentations, the ASHG virtual conference included a full schedule of plenary sessions, CoLabs, and invited sessions.

"The ASHG virtual conference provided a wonderful opportunity to share our work with other researchers in the field while learning about the work of other labs undertaking similar projects," said PNGC's Conor Klamann. "The virtual poster format turned out to be very efficient, and I was able to quickly find out a lot about the methods and technologies being used around the world." Those who registered for the ASHG virtual conference may find all these presentations and more through ASHG's website until October 2021.

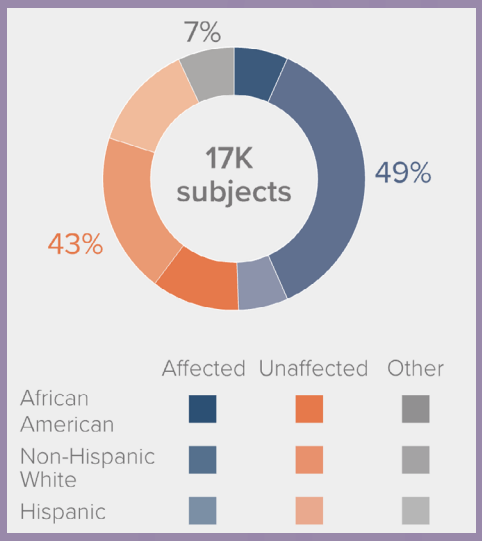
New Datasets available at https://www.niagads.org/datasets

NG00099 - Results of gene - based weighted burden analyses using SCOREASSOC and GENEVARASSOC and multivariate analyses of variants near APOE applied to the ADSP Discovery Case - Control Based Extension Study.

NG00102 - Genomic and multi-tissue proteomic integration for understanding the biology of disease and other complex traits

Future Datasets

17K whole-genomes



GCAD is currently processing an additional 13,000 whole-genomes to be joint-called with the first whole-genome dataset, totaling about 17,000 whole-genomes. Joint calling of this dataset will begin in March 2020. traits

74	90,743	12
DATASETS	SAMPLES	DATA TYPES