



NIAGADS Update for the ADRC Data Core Meeting

Engaging ADRC Researchers and Understanding Genetic Data Analysis Needs

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University of Pennsylvania

RECAP: ADSP 2024 Releases



Released in 2024

October

Additional files added for R2, R3, and R4 releases

Structural Variant joint genotype calls, multi-allelic / chrX quality control results

Coming Soon in 2024

November

R5 Whole Genome Sequencing for ~24K new samples

Individual sample raw data (CRAMs)

Joint genotype calls preview pVCF across all ~60k genomes released by ADSP

December

Additional cohorts from the **Phenotype Harmonization Consortium (PHC)** released

RECAP: Next ADSP Data Release (Pending Nov 2024)

ADSP R5 – Up to 60K Whole Genomes

ADSP Release	Primary Ancestry/Ethnicity	Cases	Controls	Other	Totals
GCAD Release 5	Black/African American	2,646	5,608	777	9,031
	Asian	1,273	4,083	5	5,361
	Latino/Hispanic	4,488	10,248	2,777	17,513
	Non-Hispanic White	9,124	14,459	6,067	29,650
	Total	17,531	34,398	9,626	61,555

ADRC samples in R5

12,629
genomes
20% of total ADSP WGS




4,590
Exomes (previously released)
22% of total ADSP WES

ADRCs can get WGS/WES data from their own samples from us!
Send an email to niagads@penntermedicine.upenn.edu to initiate.

RECAP: Next ADSP Data Release (Pending Dec 2024)

Additional Clinical Data from the Phenotype Harmonization Consortium (PHC)

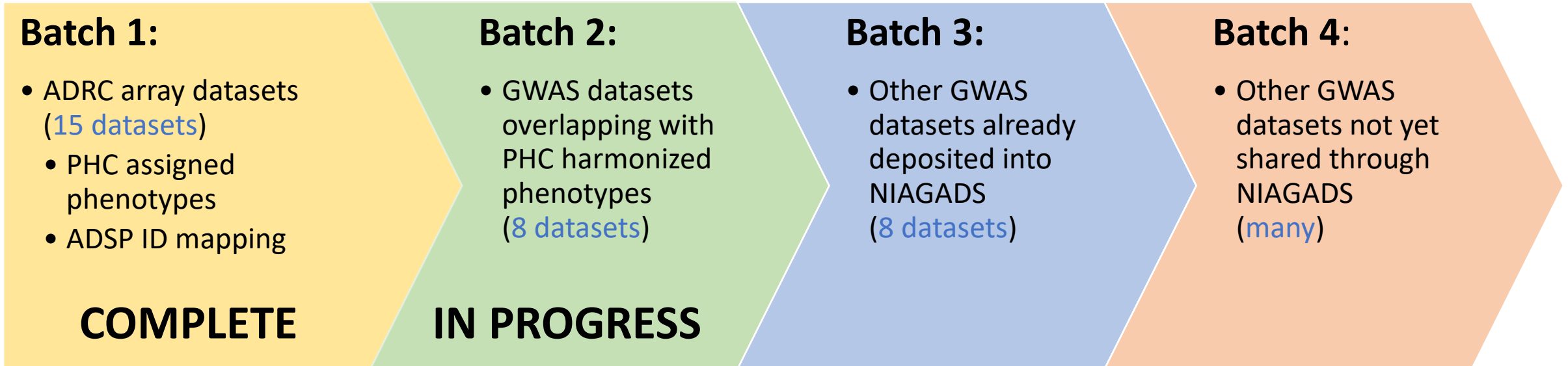
Cohorts	Cognition	Fluid Biomarkers	Neuro-pathology	Vascular Risk Factors	Imaging - DTI	Imaging - FLAIR	Imaging - T1	Imaging - PET
ADNI			N/A					
WHICAP		N/A						N/A
EFIGA		N/A			N/A	N/A	N/A	N/A
NIA-AD FBS		N/A			N/A	N/A	N/A	N/A
WRAP			N/A			N/A		
ROS/MAP/MARS		N/A						N/A
ACT		N/A			N/A	N/A	N/A	N/A
NACC								
WashU (Knight ADRC)								
A4		N/A	N/A					
KBASE								
TARCC		N/A	N/A					
HABS-HD		N/A	N/A					
Miami Brain Bank	N/A	N/A		N/A	N/A	N/A	N/A	N/A
HIHG Brain Bank	N/A	N/A		N/A	N/A	N/A	N/A	N/A
Case Western	N/A	N/A		N/A	N/A	N/A	N/A	N/A

-  Coming in December 2024
-  Harmonization in Progress
-  Domain data not available

RECAP: ADGC GWAS Data Release



Leads: Adam Naj & Amanda Kuzma



Release Features

- All subject IDs standardized using updated schema
- PLINK files converted to forward strand and lifted to GRCh38
- Covariate files updated with consistent variables/formatting
- Standardized file naming schema

Challenges in Preparing Genetics Data for Researchers

Lessons learned from supporting the ADSP Artificial Intelligence and Machine Learning Consortium (AI-ML)

Analysis of imaging and genomic data

- Paul Thompson, **Ultrascale Machine Learning to Empower Discovery in Alzheimer's Disease Biobanks (AI4AD)**
- Degui Zhi, **Genetics of Deep-Learning-Derived Neuroimaging Endophenotypes for Alzheimer's Disease**

Analysis of gene expression data

- Towfigue Raj, **Learning the Regulatory Code of Alzheimer's Disease Genomes**
- Feixiong Cheng, **Alzheimer's MultiOme Data Repurposing: Artificial Intelligence, Network Medicine, Therapeutics Discovery**
- Wei Pan, **Causal and integrative deep learning for Alzheimer's disease genetics**
- Zhongming Zhao, **AIM-AI: an Actionable, Integrated and Multiscale genetic map of Alzheimer's disease via deep learning**

Developing and applying machine learning tools/platforms for AD research

- Olivier Lichtarge, **Cognitive Computing of Alzheimer's Disease Genes and Risk**
- Honghuang Lin, **Assessing Alzheimer Disease Risk and Heterogeneity Using Multimodal Machine Learning Approaches**
- Jason Moore, **Artificial Intelligence Strategies for Alzheimer's Disease Research**

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Data not properly integrated Lack of interoperability	<ul style="list-style-type: none">• Ensure all data are harmonized for interoperability. E.g. annotations/WGS calls are processed for the same genome build

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Data heterogeneity Different recruitment/DX criteria; different cognitive tests	<ul style="list-style-type: none">• Document design of cohorts• Go beyond just linking variables - harmonize clinical data by domain experts (e.g. PHC)• Test robustness of harmonization extensively

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Sample bias Case/control imbalance; age mismatch	<ul style="list-style-type: none">• Create virtual cohort for AI/ML analysis based on cohort characteristics; work with domain (AD and epi) experts

Example: Defining FunGen Data Standards

Project lead: Fanny Leung / UPenn



hipFG¹

Meta Data Schema Development



Define **meta-data** for describing various types of experimental data



Define **ontologies/open vocabularies** to be used for describing FunGen data attributes



Define **minimal information for standardization across data sources**: genome build, annotation, ontologies, file formats, etc.

Standardized Fields for Summary Statistics

- ✓ Variant position: chr, start, end
- ✓ Allele information: ref, alt, a1, a2
- ✓ Feature name (e.g. gene name, protein name)
- ✓ P-value and/or Q-value
- ✓ Effect size (Beta and Beta SE) or Spearman correlation p-value
- ✓ Detailed sample source, molecular trait and organism; provide protocol details if iPSCs
- ✓ Description of all the columns
- ✓ Software name and version used to perform the analyses

Harmonized Genomic Knowledge via NIAGADS Open Access Data and Annotation Resources

unrestricted data and annotations (variant, gene, sequence) available for immediate access



Open Access Portal

direct data downloads for
GWAS summary statistics
(p-values) and
ADSP Variant Annotations

<https://dss.niagads.org>



75,207
standardized, searchable
functional genomics tracks

<https://tf.lisanwanglab.org/FILER/>



curated AD-GWAS catalog,
documenting
>18k
published associations

<https://advp.niagads.org>



AD-genetics knowledgebase
and **Genome Browser**,
containing
>260M
annotated variants

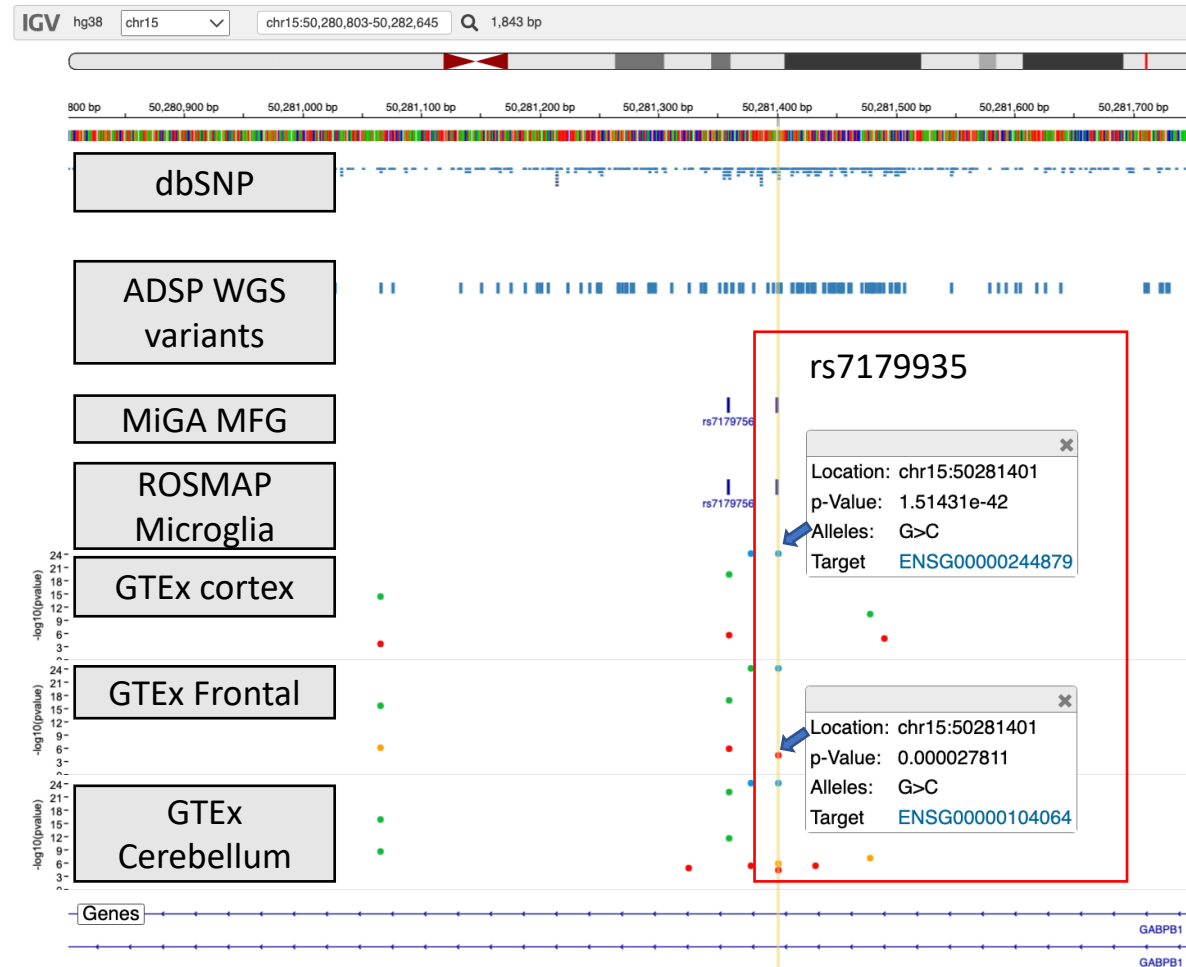
<https://www.niagads.org/genomics>

ASHG 2024 Platform Talk
Pavel Kuksa

Visualize and Explore Data

Lead: Emily Greenfest-Allen

Visualize Across Tracks



xQTL Track

Track in FILER
/GenomicsDB

Features

- Track selector
- Any QTL datasets
- FILER/user's own input tracks

<https://www.niagads.org/genomics/app>

1. Kuksa et al. *NAR Genom Bioinform* 2022. 2. Greenfest-Allen et al. *Alzheimers Dement* 2024.

NIAGADS Open Access NIAGADS API*

Lead: Emily Greenfest-Allen



Alzheimer's
Disease Variant
Portal



Functional
Genomics
Repository



Open Access Portal

GenomicsDB

Alzheimer's
Genomics Database



API
NIAGADS

- Programmatic access
- Bulk, ranged, and genome wide queries
- Integration into analysis pipelines
- Better support ADSP activities and AI/ML pipelines

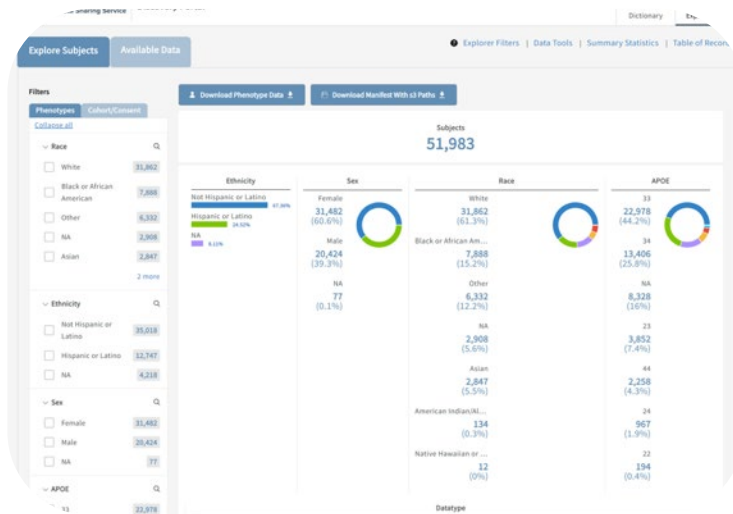
conforms to OpenAPI standards (& is FAIR)

Supporting FAIR Principles

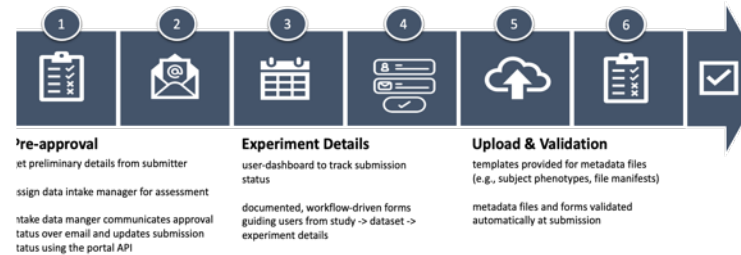


Initiatives	Findable	Accessible	Interoperable	Reusable
Gen3 Platform				
RAS Authentication				
Data Submission Portal				
DOI Implementation				
ADGC GWAS Standardization				
Outreach Initiatives				
NIAGADS Knowledgebases <small>(Alzheimer's Genomics Database, FILER, ADVP, VariXam)</small>				
NIAGADS Open Access				

Supporting FAIR Principles



ADSP Data Discovery Platform Integration powered by **Gen3 Technology**



Streamline data submission and validation using **DSS Data Submission Portal**



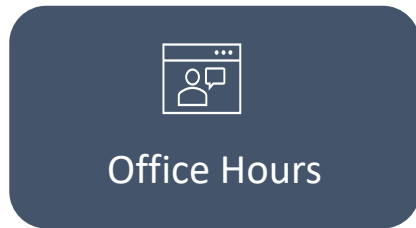
Digital Object Identifiers (DOI) Enabled through **NIH DataCite Consortium** membership

Supporting Data Use

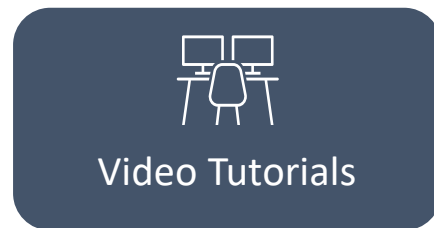


User Support

NIAGADS offers several support resources launched over the last year:



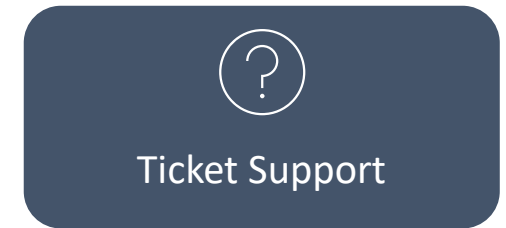
Held at least once a quarter



<https://www.youtube.com/@niagads>
1814



All NIAGADS documentation in one place, new informational pages to address user questions, dedicated FAQ page



Users can now submit a ticket to work on resolving technical issues with the NIAGADS team.

Awareness

Expanding NIAGADS reach through increased investigator awareness was accomplished through informational outreach sessions at AAIC and will continue at ASHG in 2024



Exhibit Hall Booth

Visit us at booth 1023 at ASHG!



Poster Presentations



ADRC workshop at AAIC in partnership with NACC, Sage, and NCRAD

ASHG 2024 Activities



ASHG Exhibit Hall Booth

Visit us at booth **1023D** at ASHG

See you this November in Denver!



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Posted October 09, 2024.

NIAGADS: A Comprehensive National Data Repository for Alzheimer's Disease and Related Dementia Genetics and Genomics Research

Amanda Kuzma, Otto Valladares, Emily Greenfest-Allen, Heather Nicaretta, Maureen Kirsh, Youli Ren, Zivadin Katanic, Heather White, Andrew Wilk, Lauren Bass, Jascha Brettschneider, Luke Carter, Jeffrey Cifello, Wei-Hsuan Chuang, Kaylyn Clark, Prabhakaran Gangadharan, Jacob Haut, Pei-Chuan Ho, Wenhwei Horng, Taha Iqbal, Yumi Jin, Peter Keskinen, Alexis Lerro Rose, Michelle K Moon, Joseph Manuel, Liming Qu, Flawless Robbins, Naveensri Saravanan, Jin Sha, Sam Tate, Yi Zhao, Laura Cantwell, Jake Gardner, Shin-Yi Chou, Jung-Ying Tzeng, William Bush, Adam Naj, Pavel Kuksa, Wan-Ping Lee, Yuk Yee Leung, Gerard Schellenberg, Li-San Wang, Alzheimer's Disease Sequencing Project

doi: <https://doi.org/10.1101/2024.10.07.24315029>

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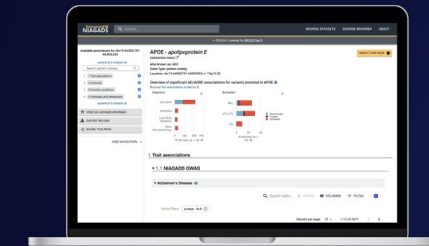
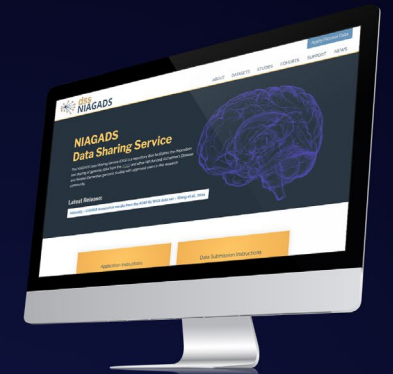
The National Institute on Aging Genetics of Alzheimer's Disease Data Storage Site

The NIAGADS is a collaborative agreement between the National Institute on Aging and the University of Pennsylvania that stores and distributes genetics and genomics data from studies on Alzheimer's disease, related dementias, and aging to qualified researchers globally.

Qualified Access

The NIAGADS Data Sharing Service (DSS) is home to genetics and genomics data from the Alzheimer's Disease Sequencing project and many other datasets that require qualified access for distribution.

[Learn More](#)



Open Access

In addition to qualified access data housed in the DSS, NIAGADS freely offers any ADRD data we can through our publicly available files portal and annotation resources.

[Learn More](#)

DOI: 10.1101/2024.10.07.24315029

We are forming a **Genetics Data Workgroup** within the ADRC Program

- NACC and NIAGADS are organizing the workgroup
- Currently in planning stage
- Primary goal: understand ADRC needs in accessing and using genetic data; inform and advise NIAGADS and NACC

Please contact **Sarah Biber** or **Li-San Wang** if you are interested in participating!!