Project Request

Project #12132 : Integration of CNV and SNV for gene mapping of psychiatric disorders: methods and data analysis



Project name Integration of CNV and SNV for gene mapping of psychiatric disorders:

methods and data analysis

Project ID 12132
Approved user name Xin He

Institute affiliation UNIVERSITY OF CHICAGO (Non-Profit)

Request date : Renewal date :

Applicant Organization

Legal Name : UNIVERSITY OF CHICAGO

Department: Human Genetics Division: Biological Sciences

Street 1 : 920 E. 58th Street CSLC 420

City : Chicago State : IL - Illinois Zip : Country : United States

PI Contact Information

Name : Xin He Position : Principal Investigator

Organization: UNIVERSITY OF CHICAGO

Street 1 : 920 E. 58th Street CSLC 420

City : Chicago State : IL - Illinois Zip : 60637 Country : United States

Phone : 773-834-7678 : Email : xinhe@uchicago.edu

SO Contact Information

Name : Istvan Fekete Position : Senior Contracts Manager

Organization: UNIVERSITY OF CHICAGO

Street 1 : 6030 S. Ellis Ave.

City : Chicago State : Zip : 60637 Country : USA

Phone : 773-702-8601 : Email : ifekete@uchicago.edu

IT Director Contact Information

Name : Samuel Volchenboum Position : Associate Professor

Organization: UNIVERSITY OF CHICAGO

Department : Pediatrics Division : Biological Sciences

Street 1 : The University of Chicago Medicine 5841 S. Maryland Avenue, MC 4060

City : Chicago State : IL - Illinois Zip : 60637 Country : United States

Phone : (773) 702-4303 : Email : svolchen@peds.bsd.uchicago.edu

Project Request

Project #12132 : Integration of CNV and SNV for gene mapping of psychiatric disorders: methods and data analysis



Approved Research Use Statement

Recent studies have indicated that SNVs and CNVs of psychiatric disorders converge on the same set of target genes, making joint SNV-CNV analysis an extremely attractive strategy. We recently developed a method for integrating autism CNV and SNV data (Sanders & He et al, Neuron, 2015). The method extracts gene level evidence from CNV data, and then combine with gene-level test from SNV data. The method, however, suffers from several limitations: for instance, it assumes one causal gene per CNV; and it assumes all CNVs are independent (this would be violated for overlapping CNVs). We will extend this work and develop a more rigorous statistical model to infer causal genes from CNV data. Our idea is that whether a CNV is associated with autism depends on whether it overlaps with autism genes. Thus we can use the Bayes rule to infer the most probable risk genes from observed CNVs. This model allows multiple causal genes in one CNV and can easily incorporate gene-level information from SNV data. To develop and test this method, we need access to individual-level genotype and phenotype datasets specific for autism (accession number: phs000267.v4) containing the CNV data from a recent paper by Pinto et al, in AJHG, 2014 (PMID: 24768552). Our method will generate summary statistics (e.g. odds ratio estimates, standard errors) from the CNV dataset and combine with summary statistics from SNV data. By using summary statistics the data integration project will not create additional risks to participants. We acknowledge the use restrictions of each dataset and will not use any of these datasets to seek to reveal the identity of individuals.

Non-Technical Summary

We seek to develop methods that leverage genome-wide copy number variations (CNVs) for gene mapping of psychiatric diseases. CNVs are large genomic insertion or deletion events, an important source of genetic variation affecting neuropsychiatric disorders such as autism and intellectual disability. Recent evidence has implicated that CNVs and single-nucleotide variants (SNVs) converge on the same set of genes in etiology of many psychiatric traits. However, current methods for gene mapping typically analyze one type of data at a time -- either focusing on SNV association mapping, or CNV based gene-set analysis. The fact that CNVs often spread multiple genes raises analytic challenge of identifying the causal genes among all genes involved. We will develop a principled statistical framework to integrate SNV and CNV data at the gene-level, accommodating both trio-sequencing and case-control studies, to increase power of psychiatric gene discovery.

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Date

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Project Request

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Consent Group Information

phs000267.v4.p2: AGP Consortium - GWAS and CNV - Stage I

Consent Group: 1

Name: Disease-Specific (Autism Spectrum Disorder)

Abbreviation: DS-ASD

Request Date:

Use Limitation : Use of the data must be related to Autism Spectrum Disorder.

Data Use Certification Agreement AGP Consortium - GWAS and CNV - Stage I National Institute of Mental Health

09/19/2011

Introduction and Statement of Policy

The National Institutes of Health (NIH) has developed central data repositories to archive and distribute the results of studies provided by Contributing Investigators examining the relationship between genomic data (e.g., genotype, sequence, or epigenetic information) and phenotype. Such studies include genome-wide association studies, medical sequencing, and molecular diagnostic assays. Implicit in the establishment of the NIH data repositories, for example the database of Genotypes and Phenotypes (dbGaP), is the view that scientific progress in this area will be greatly enhanced if the data produced by these studies are readily available to all investigators in the research community.

Dataset access will be provided to research investigators who, along with their institutions, have certified their agreement with the expectations and terms of access detailed below. It is the intent of the NIH and NIMH that Approved Users of NIH-provided datasets recognize any restrictions on data use delineated within the original informed consent agreements of contributing studies, as identified by the submitting institutions and stated on database websites.

Definitions of terminology used in this document are found in the Appendix.

The parties to this agreement include: the Principal Investigator (PI) requesting access to the genomic study dataset ("the Approved User"), his/her home institution as represented by the Institutional Signing Official designated through the eRA Commons system ("the Requester"), and the NIMH, NIH. The effective date of this agreement shall be the Project Approval Date, as specified on the Data Access Committee approval notification.

Terms of Access

1. Research Use

The Requester agrees that if access is approved, the Principal Investigator named in the Data Access Request (DAR) submitted to the NIH, those named in the "Senior/Key Person Profile" portion of the DAR, which should include the Information Technology Director or his/her designee, and any trainee or employee working on the proposed research project under the direct supervision of these individuals, shall become Approved Users of the requested dataset(s). Research use will occur solely in connection with the research project described in the DAR, which includes a 1-2 paragraph description of the research objectives and design. New uses of these data outside those described in the DAR will require submission of a new DAR; modifications to the research project will require submission of an amendment to this application (e.g., the addition of new aims related to the approved project, adding or deleting collaborators from the same institution, and the potential addition of new NIH genomic datasets to an approved project). The Requester and all Approved Users may use the dataset(s) only in accordance with the parameters described on the NIH database Web site for the appropriate research use, and any limitations on such use, of the dataset(s) and as required by law.

Research access to the requested dataset(s) is granted for a period of one (1) year as defined below.

Contributing Investigators, or their direct collaborators, who provided the data or samples used to generate an NIH genomic dataset and who have appropriate IRB approval, if applicable, for broader use of the data are exempt from the limitation on the scope of the research use as defined in the DAR.

2. Institutional and Approved User Responsibilities

The Requester agrees through the submission of the Data Access Request (DAR) that the PI named in the DAR has reviewed and understands the principles for responsible research use and data handling of the genomic datasets as defined in the NIH GWAS Data Sharing Policy and as detailed in this Data Use Certification (DUC) agreement and in the dbGaP Approved User Code of Conduct. The Requester and Approved Users further acknowledge that they are responsible for ensuring that all uses of the data are consistent with federal, state, and local laws and regulations and any relevant institutional policies. Through submission of the DAR, the Principal Investigator also agrees to submit annual data use reports to the appropriate NIH Data Access Committee (DAC) describing the research use of the Approved Users as described under "Research Use Reporting" below.

Approved Users who may have access to personal identifying information for research participants in the original study at their institution or through their collaborators, may be required to have IRB approval. By approving and submitting the attached Data Access Request, the Institutional Signing Official provides assurance that relevant institutional policies and applicable federal, state, or local laws and regulations (if any) have been followed, including IRB approval if required. The Institutional Signing Official also assures through the approval of the Data Access Request that other organizations within the institution with relevant authorities (e.g., the Office of Human Subjects Research, the Office of Information Technology, the Office of Technology Transfer, etc.) have reviewed the relevant sections of the NIH GWAS Data Sharing Policy and the associated procedures and are in agreement with the principles defined.

It is anticipated that, at least in some cases, these datasets will be updated with additional information. Unless otherwise indicated, all statements herein are presumed to be true and applicable to the access and use of all versions of these datasets.

3. Public Posting of Approved User's Research Use Statement

The Principal Investigator agrees that, if he or she becomes an Approved User, information about the PI and the approved research use may be posted on a public, US government web site that describes approved research projects. The information may include the Approved User's name and institution, project name, Research Use Statement, and a Non-technical Summary of the Research Use Statement. In addition, citations resulting from the use of NIH genomic datasets may be posted on NIH data repository websites.

4. Non-Identification

Approved Users agree not to use the requested datasets, either alone or in concert with any other information, to identify or contact individual participants from whom phenotype data and DNA samples were collected. This provision does not apply to research investigators operating with specific IRB approval, pursuant to 45 C.F.R. 46, to contact individuals within datasets or to obtain and use identifying information under an approved IRB research protocol. All investigators conducting "human subjects research" within the scope of 45 C.F.R. 46 must comply with the requirements contained therein.

5. Non-Transferability

The Requester and Approved Users agree to retain control over the data and further agree not to distribute data obtained through this Data Access Request to any entity or individual not covered in the submitted Data Access Request. If Approved Users are provided access to NIH genomic datasets for inter-institutional collaborative research described in the Research Use Statement of the Data Access Request, and all members of the collaboration are also Approved Users through their home institution(s), data obtained through this Data Access Request may be securely transmitted within the collaborative group. All data security practices and other terms of use defined in this agreement and the <u>dbGaP Security Best Practices</u> for the raw data are expected to be followed for the derived data, including any transmission of the data.

The Requester and Approved Users acknowledge responsibility for ensuring the review and

agreement to the terms within this Data Use Certification and the appropriate research use of NIH genomic data by research staff associated with any approved project, subject to applicable laws and regulations. NIH genomic datasets obtained through this Data Access Request, in whole or in part, may not be sold to any individual at any point in time for any purpose.

Approved Users agree that if they change institutions during the access period, they will submit a new Data Access Request and Data Use Certification in which the new institution agrees to the NIH GWAS data use policy before data access resumes. Any versions of data stored at the prior institution for the approved use will be destroyed and documented through a final Data Use Report as described below. However, if advance written notice and approval by the JAAMH Data Access Committee is obtained to transfer responsibility for the approved research project to another Approved User within the same institution the data may not need to be destroyed.

6. Data Security and Data Release Reporting

The Requester and Approved Users, including the institutional Information Technology Director or his/her designee, acknowledge the intent of the NIH that they have reviewed and agree to handle the requested dataset(s) according to the current <u>dbGaP Security Best Practices</u>, including its detailed description of requirements for security and encryption. These include, but are not limited to:

- o all Approved Users have completed all required computer security training required by their institution, for example, the http://irtsectraining.nih.gov/, or the equivalent;
- the data will always be physically secured (for example, through camera surveillance, locks on doors/computers, security guard);
- o servers must not be accessible directly from the internet, (for example, they must be behind a firewall or not connected to a larger network) and unnecessary services should be disabled:
- o use of portable media, e.g., on a CD, flash drive or laptop, is discouraged, but if necessary then they should be encrypted consistent with applicable law;
- o use of updated anti-virus/anti-spyware software;
- security auditing/intrusion detection software, detection and regular scans of potential data intrusions;
- use of strong password policies for file access.
- all copies of the dataset should be destroyed, as permitted by law, whenever any of the following occurs:
 - the DUC expires and renewal is not sought;
 - access renewal is not granted;
 - the NIMH requests destruction of the dataset;
 - the continued use of the data would no longer be consistent with the DUC.

In addition, the Requester and Approved Users agree to keep the data secure and confidential at all times and to adhere to information technology practices in all aspects of data management to assure that only authorized individuals can gain access to NIH genomic datasets. This agreement includes the maintenance of appropriate controls over any copies or derivatives of the data obtained through this Data Access Request.

Requesters and Approved Users agree to notify the JAAMH Data Access Committee of any unauthorized data sharing, breaches of data security, or inadvertent data releases that may compromise data confidentiality within 24 hours of when the incident is identified. As permitted by law, notifications should include the known information regarding the incident and a general description of the activities or process in place to fully define and remediate the situation. Within 3 business days of the JAAMH Data Access Committee notification, the Requester, through the Approved User and the Institutional Signing Official, agree to submit to the JAAMH Data Access Committee a more detailed written report including the date and nature of the event, actions taken or to be taken to remediate the issue(s), and plans or processes developed to prevent further problems, including specific information on timelines anticipated for action.

All notifications and written reports of data security incidents should be sent to:

JAAMH Data Access Committee URGENT, <u>JAAMHDAC@mail.nih.gov</u>

The NIMH, the NIH, or another entity designated by the NIH may, as permitted by law, also investigate any data security incident. Approved Users and their associates agree to support such investigations and provide information, within the limits of applicable local, state and federal laws and regulations. In addition, Requesters and Approved Users agree to work with the NIMH and the NIH to assure that plans and procedures developed to address identified problems are mutually acceptable consistent with applicable law.

7. Intellectual Property

By requesting access to genomic dataset(s), the Requester and Approved Users acknowledge the intent of the NIH that anyone authorized for research access through the attached Data Access Request follow the intellectual property principles within the NIH GWAS Policy for Data Sharing as summarized below:

Achieving maximum public benefit is the ultimate goal of data distribution through the NIH genomic data repositories. The NIH believes that these data should be considered as precompetitive, and urges Approved Users to avoid making IP claims derived directly from the genomic dataset(s). However, the NIH also recognizes the importance of the subsequent development of IP on downstream discoveries, especially in therapeutics, which will be necessary to support full investment in products to benefit the public.

It is expected that these NIH-provided data, and conclusions derived therefrom, will remain freely available, without requirement for licensing. The NIH encourages broad use of genomic datasets coupled with a responsible approach to management of intellectual property derived from downstream discoveries in a manner consistent with the NIH Research Tools Policy.

8. Research Dissemination and Acknowledgement of NIH Genomic Study Datasets

It is the intent of the NIH to promote the dissemination of research findings from NIH genomic dataset(s) as widely as possible through scientific publication or other appropriate public dissemination mechanisms. Approved Users are strongly encouraged to publish their results in peer-reviewed journals and to present research findings at scientific meetings, etc.

In accord with the <u>NIH GWAS Policy for Data Sharing</u>, and as expressed through the submission of the DAR, Approved Users acknowledge the NIH's expectation that they will not *submit* findings using the AGP Consortium - GWAS and CNV - Stage I dataset(s), or updated versions thereof, for publication or presentation for a period of exclusivity for Contributing Investigators concluding with the Embargo Date identified on the <u>dbGaP</u> or other NIH genomic data repository homepage.

Approved Users agree to acknowledge the NIH data repository, the Contributing Investigator(s) who contributed the phenotype data and DNA samples from his/her original study, and the primary funding organization that supported the contributing study in all oral and written presentations, disclosures, and publications resulting from any analyses of the data. Approved Users further agree that the acknowledgment shall include the dbGaP accession number to the specific version of the dataset(s) analyzed.

A sample statement for the acknowledgment of the dataset(s) follows:

The datasets used for the analysis described in this manuscript were obtained from dbGaP at http://www.ncbi.nlm.nih.gov/gap through dbGaP accession number, phs000267.v1.p1. Submission of the data, phs000267.v1.p1, to dbGaP was provided by Dr. Bernie Devlin on behalf of the Autism Genome Project (AGP). Collection and

submission of the data to dbGaP were supported by a grant from the Medical Research Council (G0601030) and the Wellcome Trust (075491/Z/04), Anthony P. Monaco, P.I., University of Oxford. AGP project references:

- 1) "Functional impact of global rare copy number variation in autism spectrum disorders", The AGP Consortium, *Nature*, 466(7204):368-72 (2010), PMID: 20531469.
- 2) "A genome-wide scan for common alleles affecting risk for autism", The AGP Consortium, *Human Molecular Genetics*, 19(20):4072-82 (2010), PMID: 20663923.
- 3) "Mapping autism risk loci using genetic linkage and chromosomal rearrangements", The AGP Consortium, *Nature Genetics*, 39(3):319-328 (2007), PMID: 17322880.

9. Research Use Reporting

To assure that NIH policies and procedures for genomic data use are adhered to, Approved Users agree to provide to the JAAMH Data Access Committee annual feedback on how these data have been used and any results that have been generated as a result of access to the data, including patents and publications. This information will be used by the JAAMH Data Access Committee staff for program evaluation activities, and may be considered by the NIH GWAS Governance committees as part of the NIH effort to provide ongoing oversight and management of all NIH genomic data sharing activities.

Approved Users thus agree to provide a brief Annual Data Use Report on the research specified within the DAR submitted with this DUC. Approved Users who are seeking renewal agree to provide specific information in a renewal DAR. Those not seeking renewal agree to provide specific information to the Data Access Committee via the contact information below. Annual Data Use Reports will provide information regarding potentially significant findings and publications or presentations that resulted from the use of the requested dataset(s), a summary of any plans for future research use, any violations of the terms of access described within this Data Use Certification and the implemented remediation, and information on any downstream intellectual property generated as a result of the data. Approved Users also may include general comments regarding topics such as the effectiveness of the NIH genomic data access process (e.g., ease of access and use), appropriateness of data format, challenges in following the policies, and suggestions for improving data access or the program in general if desired.

Approved Users agree to send the Annual Data Use Report prior to the anniversary of the Approved Access Date assigned by the DAC and specified within the manifest file provided to Approved Users by the NIH Data Repository at the time that data access is provided. It is agreed that the Annual Data Use Report will be shared with the NIH within the context of a renewal Data Access Request, or via a letter signed by the Institutional Signing Official and the Approved User.

Annual Data Use Reports should be submitted to:

Email: JAAMHDAC@mail.nih.gov

Provide in the report:

Project Identifiers:

- Approved User Name
- Institutional Affiliation
- Project Name
- · Report Date

Project update:

- Summary of research progress, including the potential significance of any findings.
- Proposed plans for further research utilizing currently approved NIH GWAS datasets (including any proposed plans to include analyses of additional NIH GWAS datasets) please be sure to indicate any new questions that have arisen that you propose to address using the currently approved datasets.

- If proposed research plans include revised or new research questions and/or the inclusion of additional NIH GWAS datasets, please submit a revised Data Access Request through dbGaP for review by the DAC.
- List of all completed or accepted scientific presentations that include (or will include) findings made with the individual-level NIH GWAS data that was accessed through dbGaP. Please include title, authors, bibliographic citation (if any), and meeting/abstract submission date.
- List of publications and manuscripts submitted that include findings made with the NIH GWAS individual-level data. Please include PubMed ID, title, authors, and bibliographic citation.
- Description of other data sources that have been linked to the NIH GWAS individual-level data covered under current data access approval.
- Description of any intellectual property generated as a result of using the NIH GWAS individual-level data.
- Summary information on any inappropriate data release incidents or other data security issues, including the date that the DAC was first notified. Inappropriate data release incidents should have been reported to the DAC as they occurred. If an incident was not reported at the time it occurred, please do so immediately, noting what was done to remedy the situation and what steps were taken to prevent future occurrences.
- General comments regarding the effectiveness of the dbGaP data portal, such as ease of access and use, appropriateness of data format, and challenges in complying with NIH GWAS policies.
- Suggestions for improving NIH GWAS, study-specific data access, or NIH GWAS policy or procedures in general.

10. Non-Endorsement, Indemnification

The Requester and Approved Users acknowledge that although all reasonable efforts have been taken to ensure the accuracy and reliability of NIH genomic data, the NIH, the NIMH, and JAAMH Data Access Committee, and Contributing Investigators do not and cannot warrant the results that may be obtained by using any data included therein. The NIH, the NIMH, the JAAMH Data Access Committee, and all contributors to these datasets disclaim all warranties as to performance or fitness of the data for any particular purpose.

No indemnification for any loss, claim, damage or liability is intended or provided by any party under this agreement. Each party shall be liable for any loss, claim, damage, or liability that said party incurs as a result of its activities under this agreement, except that the NIH, as an agency of the United States, may be liable only to the extent provided under the Federal Tort Claims Act, 28 U.S.C. 2671 et seq.

11. Termination and Violations

This Data Use Certification will be in effect for a period of one (1) year from the date the dataset(s) are made accessible to the Approved User ("Approved Access Date"). At the end of the access period, Approved Users agree to destroy all copies of the requested dataset(s), except as required by publication practices or law to retain them.

Consideration will be given to a renewal of this agreement upon submission of a new DAR. Copies of NIH genomic dataset(s) may not need to be destroyed if, with advance notice and approval by the JAAMH Data Access Committee, the project has been transferred to another Approved User. In this case, documentation must be provided that other Approved Users are using the dataset(s) under an active DAC approved research project at the same institution.

The Requester and Approved User acknowledge that the NIH or the NIMH may terminate this agreement and immediately revoke access to all NIH genomic datasets at any time if the Requester is found to be no longer in agreement with the policies, principles and procedures of the NIH and the NIMH.

By submission of the attached Data Access Request, the Requester through the Institutional Signing Official attests to the Approved Users' qualifications for access to and use of NIH genomic dataset(s) and certifies their agreement to the NIH principles, policies and procedures for the use of the requested datasets as articulated in this document and as summarized in the dbGaP Approved User Code of Conduct, including the potential termination of access should a violation of any of these agreement terms be identified.

Requesters and the Principal Investigator further acknowledge that they have shared this document, the dbGaP Approved User Code of Conduct, and the NIH GWAS data sharing policies and procedures for access and use of genomic datasets with any Approved Users, appropriate research staff, and all other Key Personnel identified in the DAR.

Institutional Signing Officials acknowledge that they have considered the relevant NIH GWAS policies and procedures, that they have shared this document and the relevant policies and procedures with appropriate institutional organizations, and have assured compliance with local institutional policies related to technology transfer, information technology, privacy, and human subjects research.

Appendix

Definitions of Terminology

Annual Data Use Report: A report submitted to the DAC on the anniversary of access approval summarizing the analysis of NIH genomic datasets obtained through the Data Access Request and any significant findings derived from the work.

Approved User: Post-DAC approval will include the PI, collaborators at the home institution who are named in the "Senior/Key Person Profile" portion of the DAR, the IT Director or designee named in the "Senior/Key Person Profile" portion of the DAR, and trainees or staff to these investigators.

Contributing Investigator: The researcher who submitted the genomic dataset to dbGaP.

Data Access Request: SF 424 (R&R) cover pages and requested attachments, if any.

Data Derivative: any data including individual-level data or aggregate genomic data that stems from the original dataset obtained through dbGaP. Excepted from this term is summary information that is expected to be shared through community publication practices.

dbGaP Approved User Code of Conduct: A short summary highlighting key principals and practices agreed to by all research investigators requesting access to NIH genomic data from dbGaP. The elements within the Code of Conduct reflect the Terms of Access in this Data Use Certification (DUC) agreement. Failure to abide by the Code of Conduct as agreed to at the time a dbGaP Project Request is submitted may result in revocation of access to any and all approved data sets.

Final Data Use Report: A final report submitted to the DAC at the conclusion of the approved access period when no additional access is sought, or when leaving an institution. This report should summarize the analysis of genomic study datasets obtained through the Data Access Request and any significant findings derived from the work.

Information Technology Director: Someone with the authority to vouch for the IT capacities at an institution, or higher-level division of an institution (e.g., the School of Medicine).

Institutional Signing Official: Someone with the authority to sign on behalf of the Requester and credentialed through the eRA system as such.

Requester: The home institution/organization for the Primary Investigator (PI) that will use the requested data.

Senior/Key Persons: Collaborators at the home institution, and the IT Director or designee.

Addendum to the Data Use Certification Agreement Modification of Data Security Terms and Best Practices

Effective for all dbGaP Data Access Requests submitted on or after March 23, 2015, Section 6 of the Data Use Certification Agreement is replaced in its entirety by the following:

6. Data Security and Data Release Reporting

The Requester and Approved Users, including the institutional IT Director, acknowledge NIH's expectation that they have reviewed and agree to manage the requested dataset(s) according to the current NIH Security Best Practices for Controlled-Access Data Subject to the GDS Policy and the institutional IT security requirements and policies, and that the institution's IT security requirements and policies are sufficient to protect the confidentiality and integrity of the NIH controlled-access data entrusted to the Requester.

If approved by NIH to use cloud computing for the proposed research project, as outlined in the Research and Cloud Computing Use Statements of the Data Access Request, the Requester acknowledges that the IT Director has reviewed and understands the cloud computing guidelines in the NIH Security Best Practices for Controlled-Access Data Subject to the GDS Policy.

Requesters and PIs agree to notify the NDAR DAC of any unauthorized data sharing, breaches of data security, or inadvertent data releases that may compromise data confidentiality within 24 hours of when the incident is identified. As permitted by law, notifications should include any known information regarding the incident and a general description of the activities or process in place to define and remediate the situation fully. Within 3 business days of the NDAR DAC notification, the Requester, through the PI and the Institutional Signing Official, agree to submit to the NDAR Data Access Committee a detailed written report including the date and nature of the event, actions taken or to be taken to remediate the issue(s), and plans or processes developed to prevent further problems, including specific information on timelines anticipated for action.

All notifications and written reports of data security incidents should be sent to:

NDAR Data Access Committee URGENT: ndarhelp@mail.nih.gov

GDS mailbox: gds@mail.nih.gov

NIH, or another entity designated by NIH may, as permitted by law, also investigate any data security incident. Approved Users and their associates agree to support such investigations and provide information, within the limits of applicable local, state, and federal laws and regulations. In addition, Requesters and Approved Users agree to work with the NDAR and NIH to assure that plans and procedures that are developed to address identified problems are mutually acceptable and consistent with applicable law.