

Data Use Certification Agreement

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson PI.

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 NIDA 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 NIDA, 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.

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.

Specific Terms:

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

Three Methods for Accessing deCODE data for Genetics of Nicotine Dependence:

There are three methods for gaining access:

- I) Predefined summary data is distributed to dbGAP. These summary data can be subsequently combined with other summary data.
- II) Ad-hoc capability for scientists to define new summary statistics through the deCODE secure remote Disease Miner interface. These data can be combined with dbGAP primary data by uploading dbGAP data to the deCODE server to generate new summary statistics.
- III) Full access to the project data within the data enclave in Iceland, with the support of deCODE staff. Under this circumstance project data can be analyzed together with dbGAP data by uploading dbGAP data to the deCODE server.

Timelines for Data Sharing

Data will be made accessible by deCODE once they have been generated and cleaned, or immediately upon publication of a paper that utilizes the data. Data generated for the project from the current funding period for 2R01DA17932-06A1 (7/01/2011-6/30/2016) shall be made accessible as soon as possible after they have been cleaned, and no later than 1 year after generation. After the exclusionary period investigators approved by the dbGAP Joint Addiction, Aging, and Mental Health Data Access committee (JAAMH-DAC) will have direct access to sequencing and genotyping and phenotype data generated with the support of 1R01DA17932 and 2R01DA17932, "Genes contributing to nicotine dependence in humans" as described below under **Process for Data Access**.

Investigators approved by the dbGAP Joint Addiction, Aging, and Mental Health Data Access committee (JAAMH-DAC) will have immediate access to the descriptive and summary data for GWAS results in dbGAP from the previously funded by 1R01DA17932-01A1. Remote access to individual genotype and phenotype data generated by 1R01DA17932-01A1 through a secure password protected web interface (through a secure VPN connection) through the internet will be made accessible as soon as the site is ready but no later than June 30, 2012. Researchers approved by the JAAMH-DAC may also gain immediate access to genotype and phenotype data generated by 1R01DA17932-01A1 through the data enclave model, where interested researchers will be able to analyze data on the deCODE site in Reykjavik, Iceland, starting July 1, 2011.

Process for Data Access

An investigator wishing access to deCODE data shall request access to the deCODE data through NIH dbGAP Joint Addiction, Aging, and Mental Health Data Access committee (JAAMH-DAC). Once granted access by the JAAMH-DAC, investigators may retrieve the summary data directly from dbGAP, or they could go to a stand-alone firewalled deCODE server and request an analysis of the data to create an unidentifiable summary statistic data set to be downloaded from the deCODE server. No individual level data from Icelandic research participants shall be deposited outside deCODE as specified by Icelandic law and all handling of personal data and use of samples shall adhere to Icelandic laws. Researchers approved by the JAAMH-DAC will have access to data on the data described above through a secure password protected web interface (through a secure VPN connection) through the internet on servers located at deCODE headquarters in Iceland. The following informatics and statistical algorithms will be made available based on deCODE's Disease Miner Professional package without licensing fees.

- Clinical data – phenotypes: Import, manage, and query large datasets (including the phenotypeSDL query algorithm for defining phenotype datasets).

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

- Family data: Import data, cluster subfamilies and analyse pedigrees for extended families
- Genetic Analysis: Genome-wide association (Fishers-Exact, TDT, S-TDT, CNV, LD, Clark's inference algorithm)
- Genome browser: High speed visualization and browsing with multiple analyses results in one view
- Marker and gene data base: Database of over 30,000 known genes and 9 million SNPs.

This interface will be flexible and allow inclusion of other algorithms upon request that may implemented by deCODE's statistics and informatics departments. The remote Disease Miner web interface does however not provide unrestricted access to primary data during the analysis stage and prevents data inference by applying a dynamic k-anonymization approach. The main principle is to defer modification of the personal primary data until statistical results are delivered to the end-user.

The dynamic k-anonymization approach differs from regular k-anonymization approaches that are used to protect privacy, by preventing data inference, typically bin data values into buckets or perturb then in some other way. This is because these approaches work on the entire data set that is to be released at any given time. Under the dynamic k-anonymization approach scientists can define patient sets (or control sets or inputs for QTL analysis) based on all the variables that are captured for each subject in the Disease Miner database. Behind the scenes (on deCODE's servers), these patient sets will be evaluated based on the actual primary data. However, if a scientist wants for instance to see the distribution of BMI in his patient set, the system ensures that no BMI value (range) is returned unless it applies to at least k-individuals. (The size and cardinality of the data set will be taken into consideration when determining the size of k, but it will be no larger than 10,) Similarly, when the deCODE servers calculate summary statistics such as odds-ratios (per marker or haplotype) or perform regression in QTL, deCODE servers use the actual primary data, while the actual data table for the primary data (or a subset of it) is never returned. The main benefit of this approach is that it applies to any data sets, regardless of their cardinality, while the conventional approaches would limit the number of data attributes one can capture or work with per subject.

Thus, investigators given remote access will not be able to modify the algorithms used to analyze the data. Nor will the user be able to see any of the typical primary data tables. The investigator will however have an easy way of exploring the entire data set, e.g. define patient sets and analyze the distribution of one or more variables within these sets. This should provide scientists with an easy way, and full capacity, to define the statistical analysis remotely without any support or intervention from deCODE staff, which results files they will be able to download or view in the deCODE built-in genome browser.

Full access to primary data (with all its flexibility to modify algorithms) is only possible within the data enclave in Iceland.

Researchers approved by the JAAMH-DAC may also access data through the data enclave model, where interested researchers will be able to analyze data on site in Iceland. This Data Enclave would be a secure database associated with power processors but with no connections to the outside, therefore requiring access locally rather than remotely. Office space and efficient informatics assistance would be available to researchers visiting Iceland. Certain types of analysis may not be possible through remote access in a timely fashion, or would in some case require modification of software that need to be approved by the Data Protection Authority and the Scientific Ethics Board of Iceland.

Research access to the requested deCODE dataset is granted for a period of one (1) year.

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

An Investigator wishing to combine dbGAP data with summary deCODE data shall request access to the deCODE data through dbGAP. Once granted access by JAAMH-DAC, investigators may retrieve the summary data from dbGAP directly, or go to the deCODE server directly (see above) and request an analysis of the data to create an unidentifiable summary statistics dataset to be downloaded from the deCODE server to their own servers and combine with dbGAP data and any other data (as is typical of most meta-analyses through large consortia); or

An investigator wishing to combine primary sequence or genotype data from dbGAP with primary data from deCODE shall apply for access to download dbGAP data. At the same time, deCODE will apply for access to the same requested datasets as the investigator so that those data sets can be downloaded directly to the deCODE server without going through the 3rd party (investigator). The analysis will be done on the deCODE server. The dbGAP data will only temporarily reside on deCODE's server, for the limited time to conduct analyses approved by the access committee, and this period will be typically no longer than 3 months unless specifically approved by the access committee. While on deCODE's data servers, dbGAP data shall be safeguarded to the same extent as the data being shared by deCODE. Summary data will be returned to the investigator.

An Investigator wishing to work and view directly deCODE primary sequence or genotype data generated with the support of R01DA17932 and combine with dbGAP data shall request access to dbGAP. In this case the investigator must travel to deCODE. Once granted access by the JAAMH-DAC, the investigator may travel to deCODE to work inside the deCODE data enclave. At the same time, deCODE will also need to apply for access to the same requested datasets as the investigator so those data sets can be download directly to the deCODE server without going through the 3rd party (investigator). The analysis will be done on the deCODE server. The dbGAP data will only temporarily reside on deCODE servers, for the limited time required to conduct the analyses approved by the access committee, and this period will typically be no longer than 3 months unless specifically approved by the access committee. While on deCODE's servers, dbGAP data would be safeguarded to the same extent as the data being shared by deCODE.

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 Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

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.

All handling of personal data and use of personal data shall adhere to Icelandic laws, including but not limited to the The Act on Patients rights No. 74/1997 and Government Regulation No. 286/2008 on Medical Research, The Data Protection Act No. 77/2000 based on the European Data Protective Directive, and various rules and government regulations promulgated there under the Minister of Justice and the Icelandic Data Protection authority. These include "Rules on the Obligation to Notify and Processing which Requires a Permit" No. 698/2004, and the The Act on biobanks, No. 110/2000 and Government Regulation No. 134/2001. For English translations contact the NIH dbGAP Joint Addiction, Aging, and Mental Health Data Access committee.

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 [dbGAP Security Best Practices](#) 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-DAC 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

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

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 [dbGaP Security Best Practices](#), including its detailed description of requirements for security and encryption. These include, but are not limited to:

- 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);
- 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;
- 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;
- 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;
 - NIDA or the JAAMH-DAC 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-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 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-DAC notification, the Requester, through the Approved User and the Institutional Signing Official, agree to submit to the JAAMH-DAC 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-DAC Data Access Committee
URGENT Email

The JAAMH-DAC, 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 JAAMH-DAC 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:

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

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 pre-competitive, 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's Best Practices for the Licensing of Genomic Inventions](#) and 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 [NIH GWAS Policy for Data Sharing](#), and as expressed through the submission of the DAR, Approved Users acknowledge the NIH's expectation **that they will not *submit findings using the Genes Contributing to Nicotine Dependence in Humans 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 [dbGaP](#) 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 **Genes Contributing to Nicotine Dependence in Humans** dataset(s) follows:

"The authors acknowledge the contribution of data from Genes Contributing to Nicotine Dependence in Humans supported by R01DA17932 and accessed through dbGAP to the analysis presented in this communication, i.e. publication, presentation, or grant application."

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-DAC 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-DAC 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

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

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:

Jonathan D. Pollock, Ph.D.
Chief
Genetics and Molecular Neurobiology Research Branch
National Institute on Drug Abuse
6001 Executive Blvd, Rm 4103
Bethesda, MD 20892
Tel. 301-435-1309
Fax. 301-594-6043
Email. jpollock@mail.nih.gov

Note that any inadvertent or inappropriate data release incidents should be reported to the JAAMH-DAC Data Access Committee according to the agreements and instructions under Term 6.

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 [JAAMH-DAC 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 [I/C or DAC Name] JAAMH-DAC 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-DAC 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 NIDA 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

Genes contributing to nicotine dependence in humans, R01DA17932, Kari Stefansson, PI

agreement with the policies, principles and procedures of the NIH and the NIDA.

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 JAAMH 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 JAAMH DAC notification, the Requester, through the PI and the Institutional Signing Official, agree to submit to the JAAMH 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:

JAAMH Data Access Committee URGENT: URGENTJAAMHDAC@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 JAAMH and NIH to assure that plans and procedures that are developed to address identified problems are mutually acceptable and consistent with applicable law.

Addendum to the Data Use Certification

Effective for all dbGaP study datasets registered prior to July 31, 2013

- Annual Data Use Reports will no longer be submitted by email to the relevant Data Access Committee(s) (DACs), as stated in the Data Use Certification(s) associated with the datasets you are requesting.
- Principal Investigators are now expected to submit online research progress updates through the dbGaP system, as part of the annual renewal process or close-out process.