The NIH Genomic Data Sharing Policy: Applicability to the Intramural Research Program

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Objectives

- Describe the critical elements of National Institutes of Health (NIH)
 Genomic Data Sharing Policy.
- Recognize when the NIH Genomic Data Sharing Policy has applicability to intramural investigators generating genomic data (human and non-human).
- Discuss the critical components of adherence to the NIH Genomic Data Sharing Policy.
- Identify the protocol and consent specific content required by the NIH Genomic Data Sharing Policy.
- Illustrate how to identify your NIH Genomic Data Sharing Policy Genomic Program Administrator (GPA).

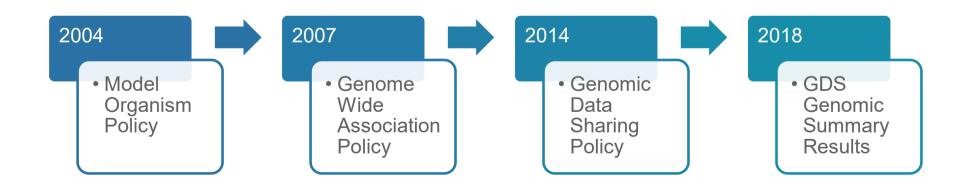


Critical Elements of the NIH Genomic

Data Sharing Policy and
Applicability to Intramural Investigators

Background

- NIH supports a culture of sharing
- Track record of continued support for data sharing policies that facilitate research that can improve human health since 1999
- Some examples include:



Benefits of Data Sharing

- Increases the capacity to answer research questions in the context of rare diseases
- Maximizes the utility of genomic data to explore additional research questions
- Enables higher statistical power as data from multiple studies can be combined to answer important questions
- Facilitates reproducibility
- Facilitates innovation of methods and tools for research.

Genomic Data Sharing Policy Effective Dates

- The GDS Policy takes effect for competing grant applications and contract proposals submitted to NIH on or after January 25, 2015
- The Intramural Research Programs were directed to comply with the GDS policy on data generated on or after August 31, 2015
- On November 1, 2018, the GDS Policy was updated to allow unrestricted access to Genomic Summary Results

NIH Intramural Investigator Responsibilities Under the NIH GDS Policy https://osp.od.nih.gov/wp-content/uploads/NIH_Intramural_Investigator_Responsibilities_under_the_GDS_Policy.pdf



Genomic Summary Results

- Permits unrestricted access to genomic summary results
 - Aggregate genomic data
 - Genomic summary statistics
 - Genotype counts and frequencies; allele counts and frequencies; effect size estimates and standard errors; likelihoods; and p-values
- Useful to investigators seeking to determine which genomic variants may contribute to a disease or condition
 - These data are typically published in peer reviewed scientific literature

Green E., Wollinetz, C. (2018). Protecting Participants, Empowering Researchers: Providing Access .gov/news/news-release/Protecting-Participants

-Empowering-Researchers-Providing-Access-to-Genomic-Summary-Results https://grants.nih.gov/grants/guide/notice-files/NOT-OD-19-023.html



Genomic Summary Results, cont.

- Excludes public release of genomic summary results in sensitive populations
 - Isolated geographic regions
 - With rare or potentially stigmatizing traits
 - i.e. HIV
 - Populations with data restrictions
 - i.e. Native American/Alaska Native or other indigenous populations
 - Study population small enough that participants privacy could be at risk

Green E., Wollinetz, C. (2018). Protecting Participants, Empowering Researchers: Providing Access to Genomic Summary Results https://www.genome.gov/news/news-release/Protecting-Participants -Empowering-Researchers-Providing-Access-to-Genomic-Summary-Results https://grants.nih.gov/grants/guide/notice-files/NOT-OD-19-023.html



Intramural GDS Policy Applicability

- All intramural NIH-funded research that generates large-scale genomic data
 - Human or non-human genomic data
 - Non-human consists of Model organisms, Microbes, Microbiome
 - Genome-Wide Association Studies (GWAS)
 - Single Nucleotide Polymorphisms (SNP) arrays
 - Genome Sequence
 - Transcriptomic
 - Metagenomic
 - Epigenomic
 - Gene Expression



What is "Large Scale": Examples of Data Submission Thresholds Human Only

- Sequence data from more than one gene or region of comparable size in the genomes of >1,000 human research participants
- Sequence data from >100 genes or region of comparable size in the genomes of >100 human research participants
- Data from 300,000 or more variant sites in >1,000 human research participants
- Comparisons of differentially methylated sites genome-wide at singlebase resolution within a given sample (e.g., within the same subject over time or across cell types within the same subject).

What is "Large Scale": Examples of Data Submission Thresholds

Model Organisms, Non-Human Cell Lines, or Infectious Organisms

- Sequence data from more than 100 isolates from infectious organisms.
- Whole genome or exome sequence data of more than one model organism species or strain
- Comprehensive catalog of transcripts and non-coding RNA from one or more model organism species or strains
- Catalog of more than 100,000 single nucleotide polymorphisms (SNPs) from one or more model organism species or strains

What is "Large Scale": Examples of Data Submission Thresholds

Human and Model Organisms, Non-Human Cell Lines, or Infectious Organisms

- Sequence data from more than 100 metagenomes of human or model organism microbiomes.
- Sequence data from more than 100 metatranscriptomes of human or model organism microbiomes.
- Comparisons of genome-wide methylated sites across more than 10 cell types.

What is "Large Scale": Trans NCI Data Submission Framework

	Number of Specimens	
	Human (Including human cell lines)	Model Organisms, Non-Human Cell Lines, Infectious Organisms
SNP array data from >500K single nucleotide polymorphisms (SNPs) (e.g., GWAS data)	1,000	500
DNA sequence data from < 100 genes or regions of interest (e.g. targeted sequencing)	1,000	500
DNA sequence data from ≥ 100 genes or regions of interest (e.g., targeted sequencing, whole exome sequencing, whole genome sequencing)	100	50
Genome-wide RNA sequencing (RNA-seq) data (e.g., transcriptomic data)	100	50
Genome-wide DNA methylation data (e.g., bisulfite sequencing data)	100	50
Genome-wide chromatin immunoprecipitation sequencing (ChIP-seq) data (e.g. transcription factor ChIP-seq, histone modification ChIP-seq)	100	50
Metagenome (or microbiome) sequencing data (e.g., 16S rRNA sequencing, shotgun metagenomics, whole-genome microbial sequencing)	100	50
Metatranscriptome sequencing data (e.g., microbial/microbiome transcriptomics)	100	50

Genomic Data Sharing Applicability

- If you are unsure whether your research falls into Genomic Data Sharing Policy required sharing, contact your Genomic Program Administrator (GPA)
- NIH Institutes or Centers may choose on a case-by-case basis to apply the Policy to projects generating data on a smaller scale depending on the state of the science, the needs of the research community, and the programmatic priorities of the IC
 - For example, the Scientific Director of the Center for Cancer Research, issued guidance on sharing of genomic data for projects examining rare diseases and rare cancers with no minimum thresholds
 - Definition of rare disease a disease that affects less than 200,000 persons in the United States (U.S Food and Drug Administration (FDA)).

Components Necessary to Adhere to the NIH Genomic Data Sharing Policy



Genomic Data Sharing Plan

- "All investigators doing research covered by GDS Policy must develop and have in place an approved data sharing plan PRIOR to start of the research."
 - What data will be shared
 - How and where data will be shared
 - All human studies must be registered in dbGaP regardless of where the data will ultimately be shared
 - Timeframe for sharing

https://osp.od.nih.gov/wp-content/uploads/NIH_Intramural_Investigator_Responsibilities_under_the_GDS_Policy.pdf



Institutional Certification

Confirms that data submission is:

- Consistent with national, tribal, and state laws and regulations as well as relevant institutional policies
- Consistent with the informed consent
- Consideration was given to the to the study participants from whom the data were obtained, including access to genomic summary results
- Any limitations on the research use of the data as specified in the informed consent are reflected on the Institutional Certification (Table 3)
- The investigators plan for de-identifying datasets is consistent with the GDS policy
 - Assigned random unique codes by investigator(s)

Institutional Certification

- For Studies Using Data Generated from Cell Lines Created or Clinical Specimens Collected AFTER August 31, 2015
 - Consent is required
- For Studies Using Data Generated from Cell Lines Created or Clinical Specimens Collected BEFORE August 31,2015
 - Lack Consent
 - Have Consent
- The Institutional Certification is required PRIOR to the start of the research
 - OSP-Scientific Review
 - Study Initiation



Institutional Certification-Multi-Site Studies

- Provided for all institutions contributing samples
- Two options
 - Primary study site may submit one* Multi-Center Institutional Certification indicating that it is providing certification on behalf of all collaborating sites
 - *Documentation of consent and data use limitations from all collaborating sites
 - Each site providing samples may provide their own Single-Site Institutional Certification.

Data Use Limitations

What are Data Use Limitations?

- Description of limitations, if any, on the distribution and use of human data submitted to controlled-access NIH designated data repositories
- Based on the terms included in the informed consent
- Stipulated by the submitting institution
- Many Data Use Limitations are General Research Use
 - Data would generally be made available to any qualified investigator, irrespective of the specific research purpose

Exceptions

- When Institutional Certification criteria cannot be met
 - Provide a justification for any data submission exceptions
 - Investigator expected to develop an alternate plan to share data through other mechanisms
 - IF an exceptions is granted, the study must still be registered in dbGaP
 - The reason for the exception will be included
 - A reference will be provided to an alternative data-sharing plan or resource

Study Registration

Human Data

- All human genomic data studies covered by the GDS Policy must be registered in dbGaP
- This is regardless of which NIH-designated data repository (e.g., dbGaP, GEO, SRA, etc.) will ultimately house and distribute the data

https://osp.od.nih.gov/wp-content/uploads/NIH_Intramural_Investigator_Responsibilities_under_the_GDS_Policy.pdf

Level	General Description of Data Processing	Example Data Types	Data Submission Expectation	
			Human	Non-Human
0	Raw data generated directly from the instrument platform	Instrument image data	Not expected	Not expected
1	Initial sequence reads, the most fundamental form of the data after the basic translation of raw input	DNA sequencing reads, ChIP-Seq reads, RNA-Seq reads, SNP arrays, Array CGH	Not expected	Not expected except for de novo sequence data

Level	General Description of Data Processing	Example Data Types	Data Submission Expectation		
			Human	Non-Human	
2	Data after an initial round of analysis or computation to clean the data and assess basic quality measures	DNA sequence alignments to a reference sequence or de novo assembly, RNA expression profiling	Project specific; after data cleaning and quality control, which is generally within 3 months after data have been generated	Data submission is expected no later than the time of initial publication; an earlier submission date may be designated for certain data types or NIH projects	

Level	General Description of Data Processing	Example Data Types	Data Submission Expectation		
			Human	Non-Human	
3	Analysis to identify genetic variants, gene expression patterns, or other features of the dataset	SNP or structural variant calls, expression peaks, epigenomic features	Project specific; after cleaning and quality control, which is generally within 3 months after data have been generated	Data submission is expected no later than the time of initial publication; an earlier release date may be designated for certain data types or NIH projects	

Level	General Description of Data Processing	Example Data Types	Data Submission Expectation		
			Human	Non-Human	
4	Final analysis that relates the genomic data to phenotype or other biological states	Genotype- phenotype relationships, relationships of RNA expression or epigenomic patterns to biological state	Data submitted as analyses are completed	Data submission is expected no later than the time of initial publication	

Protocol and Consent Content Required by the NIH Genomic Data Sharing Policy

Consent, the GDS Policy and the revised Common Rule

- The revised Common Rule (effective January 19, 2018) does not require informed consent for research with de-identified biospecimens or cell lines
- HOWEVER, NIH GDS Policy requires that informed consent be obtained for the future research use and broad data sharing
 - Rationale is that genomic technology and analytical methods may increase the risk for identification

Consent

- Studies using data or specimens collected after August 31, 2015
 - Consent required for genomic data sharing for future research
 - Consent data sharing template language is available in the IRBO consent templates https://irbo.nih.gov/confluence/display/ohsrp/Templates+and+Forms
 - "and even when data is from cell lines or clinical specimens if they are created or collected after August 31, 2015"
 - An Exception request should be submitted if planning to use cell lines or clinical specimens without consent
- Study population Sensitivity Determination
 - Established **BEFORE** submission to the IRB
 - Determines the consent language on Genomic Summary Results

Clinical Protocol and the GDS Policy

- Include in the Confidentiality and Privacy section of the protocol whether the population is considered Sensitive or Not Sensitive
 - Confirms the correct consent language is used for Genomic Summary Results
 - **Note-Repository studies could enroll Sensitive and Not-Sensitive populations**
- Genomic analyses should be sufficiently described in the protocol
 - A description of how samples/data will be labeled should be included
 - Will identifiers be attached to data or will samples/data be coded or unlinked
- Include whether Genomic Data Sharing is expected
 - Protocol content is NOT your Data Sharing Plan
 - A Data Sharing Plan consists of what, how, when and where data will be shared

Model Intramural Workflow: NCI/CCR Genomic Data Sharing Process



Exemplar Center for Cancer Research Genomic Data Sharing Workflow

• Sensitivity
Determination

Scientific
Review

IRB

Protocol and Consent language in place

- Data Sharing Plan
- Institutional Certification

Study Initiation Annual Report

- GDSP number
- Study updates

Infrastructure Underpinning Workflow

- CCR Wiki page
- Standard Operating Procedures
- Genomic Data Sharing Portal



Finding your NIH Genomic Data Sharing Policy Genomic Program Administrator (GPA)

Role of the Genomic Program Administrator (GPA)

- Institute specific GDS Policy implementation leaders
 - Intramural or extramural or serve in both capacities
- Answer questions about study applicability
- Answer questions about GDS Policy requirements and paperwork
 - Data Sharing Plan
 - Institutional Certification
 - Exception Requests
- Register the study in dbGaP
- Facilitate data submission processes for human NIH-designated controlled-access data repositories



Finding Your Genomic Program Administrator

Step One: Go to the NIH Office of Intramural Genomic Data Sharing Home Page





https://oir.nih.gov/sourcebook/intramural-programoversight/intramural-data-sharing/genomic-data-sharing

Finding Your Genomic Program Administrator

NIH Institutes and Centers Genomic Program Administrators

- Step Two: Find your Institute
- Each GPA listed includes
 - Name
 - Email
 - Additional details if applicable, i.e.
 Intramural or Extramural
- This list was updated Nov. 20, 2020

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Considerations



Considerations

- Genomic Data Sharing is part of the NIH mission
- Consider the Genomic Data Sharing Policy requirements when you are planning your research project
- Work with your GPA from the start of planning for your research project through data submission to help you with what is required
- For Human Studies, the GDS Policy requires consent
 - The Institutional Certification cannot be signed unless there is consent
- When your research plan evolves, how does this impact genomic data sharing? (i.e. population, accrual, types of planned analyses, etc.)

Publishers Mandating Data Sharing

- Publishers are increasingly mandating genomic data sharing regardless of whether the study meets a GDS specified threshold
 - Examples include:
 - American Association for Cancer Research Journals
 - American Journal of Human Genetics
 - Cell Press
 - Journal of the American Medical Association
 - The I ancet
 - New England Journal of Medicine
 - Science



Questions/Discussion



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Genomic Data Sharing FAQ's https://osp.od.nih.gov/scientific-sharing/genomic-data-sharing-faqs/

