Webinar Instructions

Welcome to the Gabriella Miller Kids First RFA-RM-21-011 Pre-Application Webinar!

- Every participant is muted upon entry.
- To ask public questions, use the Q&A bar (right side of your screen). We encourage you to save these for the question periods.
- You can ask also use the "chat" service to send private messages to the host or presenters throughout the webinar.
- After the webinar, additional questions can be emailed to: valerie.cotton@nih.gov

This webinar will be recorded. We will start at 12pm (EDT)



Gabriella Miller Kids First Pediatric Research Program Expert-Driven Small Projects to Strengthen Gabriella Miller Kids First Discovery, RFA-RM-21-011

March 29, 2021 12:00 pm EDT



Public Webinar: April 13th!

Register here:

https://nih.webex.com/nih/onstage/g.php?MTID=e7dcd35de768586aa8c80352b1f544601

4:00PM Introduction; NIH Kids First Staff

4:05PM Detection of novel genetic bases for congenital cranial dysinnervation disorders (CCDDs) by whole genome sequencing:

Elizabeth Engle, MD

4:35PM: Kids First Data Resource Center

- New Portal Updates
- Getting Started with Kids First

5:05PM: Proteogenomic Analysis: Breakthroughs for pediatric cancer through cross-platform collaboration; Adam Resnick, PhD, Pei Wang,

PhD, Francesca Petralia, PhD

- 5:25PM: Questions & Answers

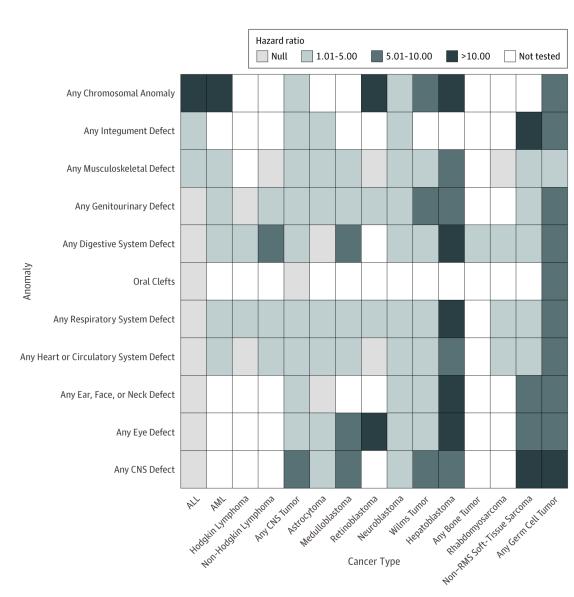
5:35PM: NIH Program Updates

5:50PM: Questions & Answers

Gabriella Miller Kids First Pediatric Research Program: childhood cancer & structural birth defects

Birth defects are associated with increased risk of cancer among children... suggesting shared genetic pathways

From: Association Between Birth Defects and Cancer Risk Among Children and Adolescents in a Population-Based Assessment of 10 Million Live Births



Vision



Alleviate suffering from childhood cancer and structural birth defects by fostering collaborative research to uncover the etiology of these diseases and supporting data sharing within the pediatric research community.



Kids First: Phase 1



Kids First Major Initiatives

- 1. Identify & sequence cohorts of children with **childhood cancer and/or structural birth defects**.
- 2. Build the Gabriella Miller Kids First Data Resource to empower discovery







Kids First Sequencing Cohorts 2015-2020

40 projects | 40,000 genomes | 16,000 cases | 19 released datasets







- Disorders of Sex Development
- Congenital Diaphragmatic Hernia
- Ewing Sarcoma
- Structural Heart & Other Defects
- Syndromic Cranial Dysinnervation Disorders
- Cancer Susceptibility
- Adolescent Idiopathic Scoliosis
- Neuroblastomas
- Enchondromatoses
- Orofacial Clefts in Caucasian, Latin American, Asian & African, Filipino populations
- Osteosarcoma
- Familial Leukemia
- Craniofacial Microsomia
- Intersection of childhood cancer & birth defects
- Microtia
- Esophageal Atresia and Tracheoesophageal Fistulas
- Kidney and Urinary Tract Defects

- Nonsyndromic Craniosynostosis
- Hemangiomas, Vascular Anomalies & Overgrowth
- Bladder Exstrophy
- Hearing Loss
- Cornelia de Lange Syndrome
- Intracranial & Extracranial Germ Cell Tumors
- Fetal Alcohol Spectrum Disorders
- Myeloid Malignancies + overlap with Down syndrome
- Congenital Heart Defects & Acute Lymphoblastic Leukemia in Children with Down Syndrome
- Structural Brain Defects
- Structural Defects of the Neural Tube (Spina Bifida: Myelomeningocele)
- CHARGE Syndrome
- Laterality Birth Defects
- T-cell Acute Lymphoblastic Leukemia
- Pediatric Rhabdomyosarcoma
- Valvar Pulmonary Stenosis



The Kids First Data Resource for Collaborative Discovery

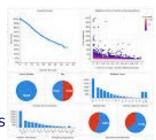
Data Resource Portal

Entry point. Query, search, discover, build & visualize synthetic cohorts



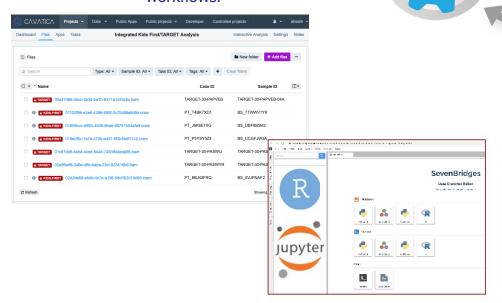
Knowledge Base Integrations (PedcBioPortal)

Integrations with existing curated/published data visualizations



Cavatica

Pull data from multiple sources into one workspace.
Use notebooks, bring-your-own or use available
workflows.





Data Services

Model clinical data in FHIR-based data services and API for sharing layers of harmonized data





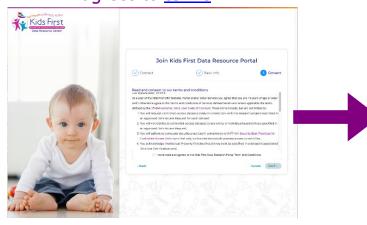
STRIDES

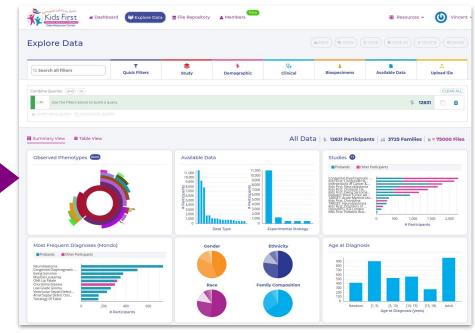
Index and point to files in the cloud

ndex and point to files in the cloud (for approved users)

Use Case: Compare genetic variants of congenital heart defects & neuroblastoma

Anyone can <u>register & login</u> to the portal (via ORCID, Google). User agrees to <u>terms</u>





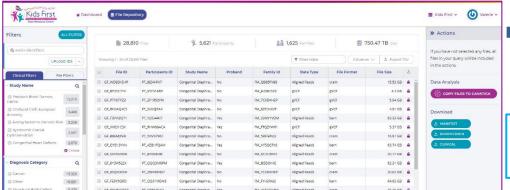
In *Explore Data*, user searches the terms "heart" and "neuroblastoma". Discovers data from children with congenital heart disease (KF) & neuroblastoma (KF & NCI TARGET)





User builds a synthetic cohort based on these criteria and can view summary & deidentified individual-level clinical, demographic, and phenotypic information.

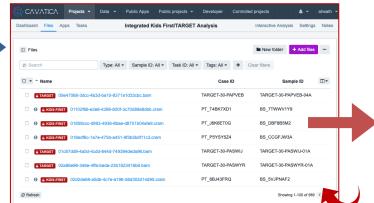
Synthetic cohort is ported to the *File Repository* where user selects which **genomic** and **histology image** files they want to analyze.



User has or applies for dbGaP access for genomic data



User pushes genomic, clinical, and image data into Cavatica for analysis & visualization



User runs statistical analyses in notebooks



User iterates through genomic workflows

Kids First: Phase 2



Phase 2 Strategic Planning: 7 Consensus Recommendation Themes

1. Innovation: Resource, infrastructure, or tool development.

Activities: Data Visualization tools; other tools for clinical/phenotypic data



2. Clinical/phenotypic data extraction, harmonization, & curation.Activities: Collect, extract, organize, curate, harmonize, and submit deep clinical and phenotypic data; annotate variants with pathogenicity, ClinGen scores.



3. Collaborative validation and discovery.

Activities: Building synthetic cohorts; identify structural variants; test pipelines.

*Engage trainees in data analysis projects**Bring users to the platform*



4. Integration and interoperability of external pediatric datasets.

Activities: Using DRC workflow and best practices to harmonize external pediatric datasets; Building tools that can operate across multiple spaces



5. Consent and data sharing.

Activities: Re-consenting cohorts in line with our data sharing expectations



6. Validation with model organisms.

Activities: validating KF findings/variants, deep phenotyping of animal models



7. Continue WGS & data generation, invest in long-read, consider other – omics. Reissues of: https://grants.nih.gov/grants/guide/pa-files/PAR-19-104.html



NIH Council of Councils September 11, 2020

Common Fund Concept Clearance: Gabriella Miller Kids First Pediatric Research Program: Plans for FY22-24 (Phase 2) James Coulombe, Ph.D. Chief, Developmental Biology and Structural Variation Branch Eunice Kennedy Shriver National Institute of Child Health and Human Development

Goal of Phase 2 Initiatives: Enhance the value and impact of the Kids First Data Resource to accelerate pediatric research to improve preventative measures, diagnostics, and therapeutic interventions.

The archived videocast of the Council of Councils meeting is publicly available and can be viewed here (Kids First discussion begins at 4:48:00).

The presentation materials are available here.



Phase 2 Initiatives Approved \$12.6M/year (FY22-24)

1) Additional generation of childhood cancer and structural birth defects-related -omics data



➤ Add epigenomic and proteomic assays





➤ Plan for sustaining the Data Resource beyond FY24

3) Expert-driven activities to increase the value of Kids First data



➤ Engage Kids First & community experts in activities such as integration, curation, and/or harmonization of rich clinical and phenotypic data



RFA-RM-21-011

Expert-Driven Small Projects to Strengthen Gabriella Miller Kids First Discovery (R03 Clinical Trial Not Allowed)



Purpose

Engage experts in a variety of activities that will enhance the utility of childhood cancer and/or structural birth defects datasets generated by the Kids First program and associated resources.

These activities should strengthen <u>future</u> analyses with the **ultimate** goal of improving diagnostic capabilities and therapies for children and their families affected by these conditions.



Goals

Build on and improve Kids First:

These projects must use Kids
 First data, standards,
 infrastructure, and resources,
 as much as possible ...

Share data & resources

Address challenges or gaps

Collaborate & coordinate:

- Incorporate a diversity of complementary expertise
- Coordinate with X01s, DRC, etc, to build on, but <u>not</u> duplicate, existing efforts
- Create a profile in the portal



Collaborate & Coordinate

Kids First X01 investigators:

- https://kidsfirstdrc.org/partners/partnersinvestigators/
- https://commonfund.nih.gov/kidsfirst/x01projects

Kids First DRC members:

https://kidsfirstdrc.org/about/

Kids First Sequencing Centers:

https://kidsfirstdrc.org/partners/portal-sequence-data/



Sharon Plon
Baylor College of Medicine
Research Focus: Identifying novel cancer susceptibility mutations



Jonathan Rios

UT Southwestern Medical Center

Research Focus: Genomics of orthopaedic disease program

VIEW PROFILE >



Jun Shen
Brigham and Women's Hospital
Research Focus: Hearing loss
VIEW PROFILE >

VIEW PROFILE >



Azeez Butali
University of Iowa
Research Focus: Craniofacial genetics

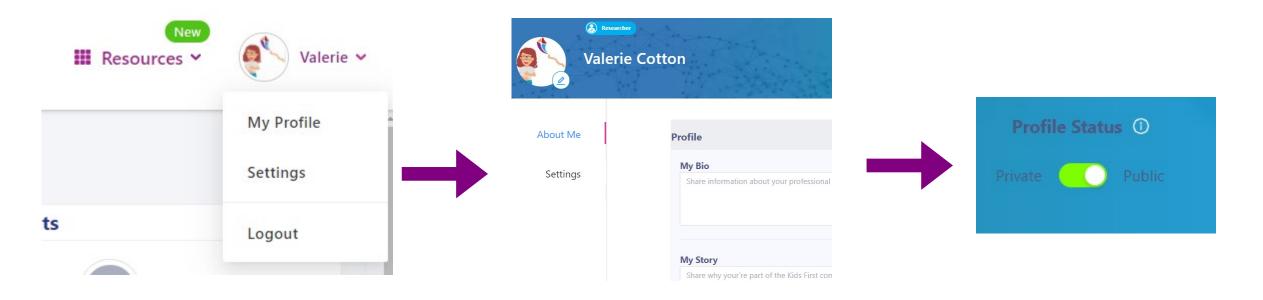
VIEW PROFILE >

Collaborate & Coordinate

Create & Share a Portal Profile

New to the Kids First Data Resource Portal? JOIN NOW >

PORTAL LOGIN





Search other members

https://portal.kidsfirstdrc.org/memberPage

Data & Resource Sharing Expectations

- It is expected that any data (including resultant raw, derived, aggregated, and summary data), tools, workflows, and/or pipelines created or used with support from this FOA will be provided to the Kids First Data Resource Center to be shared with the wider scientific community, if not already part of the Data Resource, in a timely manner that would enable other researchers to use and build on for future research efforts.
 - Example: If you create a new survey instrument to collect deeper data, or a tool to extract data from EHRs, the questions, code, and other documentation must be shared.
 - Example data sharing plans: https://commonfund.nih.gov/kidsfirst/FAQ



Examples: Improve Discovery by...

- Collecting, extracting, submitting deeper data or new data types associated with Kids First datasets
- 2. Harmonizing or processing data to promote cross-disease or cross-species (or cross-dataset analysis)
- 3. Portal analysis workflows to deploy withing the Kids First Data Resource (e.g., CAVATICA)
- 4. Creating or integrating, a new or separate tool to federate with the Kids First Data Resource
- 5. Consenting for broader data sharing



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FHIR for Electronic Health Record Extractions

HL7 FHIR® (Fast Healthcare Interoperability Resources)

Why FHIR?

- FHIR is the bridge from hospital-based data to research
- Enough structure for computational approaches/tools
 - Immediate structure for EHR-based data
 - Transformations to existing data models (e.g., OMOP)
 - Facilitate ingest >> populate into tools & search portals
 - Facilitate analysis across multiple/different datasets
- But enough **flexibility** to capture rich/complex data elements that may get lost in datasets "harmonized" to Common Data Models
 - Ability to expand data models beyond EHR and/or Common Data Models (e.g., research surveys, case report forms)

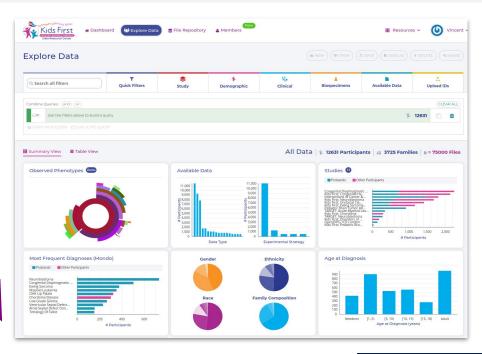




Got Images?

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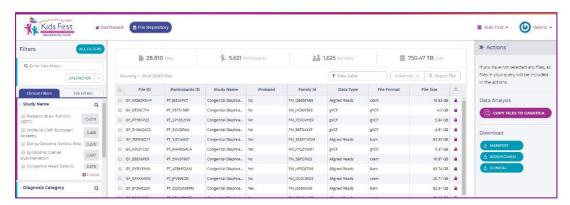


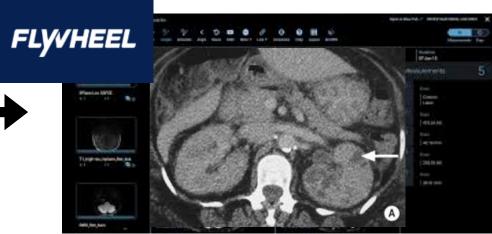


In *Explore Data*, user searches the term "kidney" and discovers data from children with congenital kidney defects (KF data) & COVID-related kidney complications (MIS-C).

User builds a synthetic cohort based on these criteria and can view summary & deidentified individual-level clinical, demographic, and phenotypic information.

Synthetic cohort is ported to the *File Repository* where user selects which **imaging** files they want to analyze (e.g. DICOM).



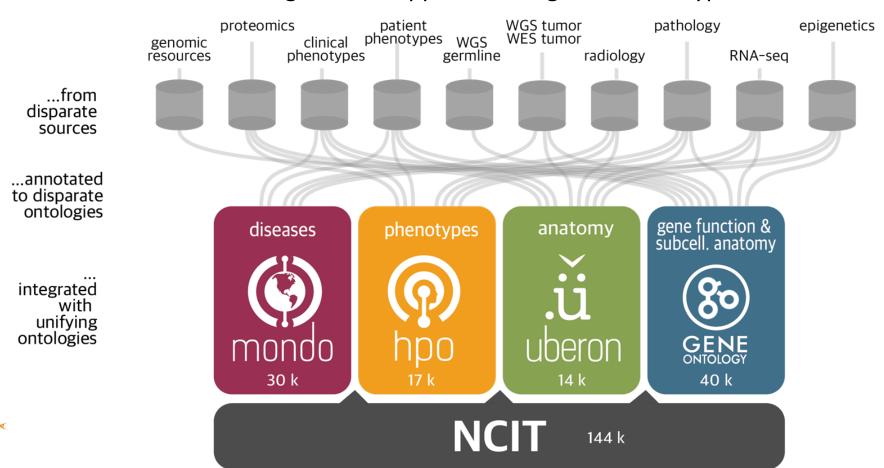


User pushes imaging files into FlyWheel for analysis

Innovation across the Phenotypic Translational Divide Webinar Series

Information: https://monarch-initiative.github.io/phenomics/pages/clin-phen-webinar.html

Curation with ontologies that support heterogenous data types in Kids First



Innovation across the Phenotypic Translational Divide Webinar Series

Part 1

Pediatric Neuropsycho-**Down Syndrome** Cardiac **logical Data** -Congenital Genomics Harmonization **Heart Disease** Consortium (PCGC) Stephanie Joaquin Espinosa Sherman **Betsy Goldmuntz** Enchondroma-Down toses and Syndrome-ALL Related & Rhabdomyo-Malignant sarcoma **Tumors** Phillip Lupo Nara Sobreira Adolescent Cornelia de Idiopathic **Orofacial Clefts** Lange Scoliosis Syndrome **Mary Marazita Carole Wise** Sarah Raible

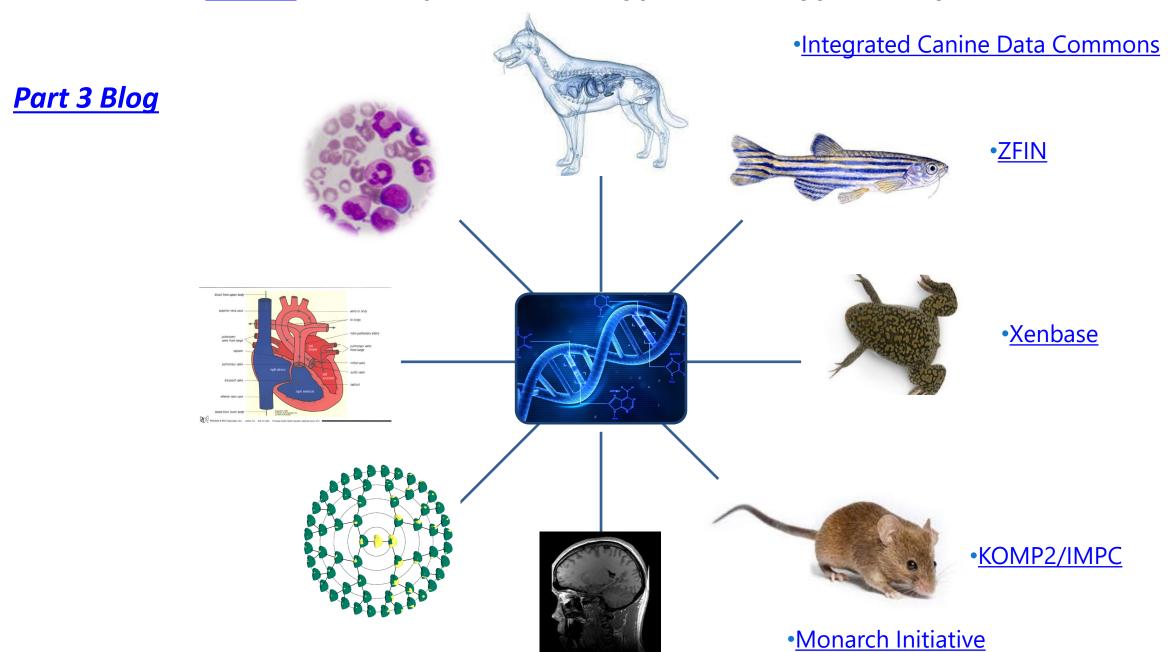
Part 2



Webinar Information:

https://monarch-initiative.github.io/phenomics/pages/clin-phen-webinar.html

Part 3: Cross-Species Genotype-Phenotype Analysis



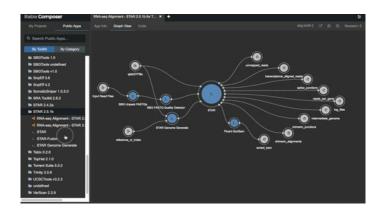
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Seven Bridges CAVATICA: Use or Create Workflows

Build, use, optimize, share new or existing workflows



Tailor a workflow with a Workflow Editor



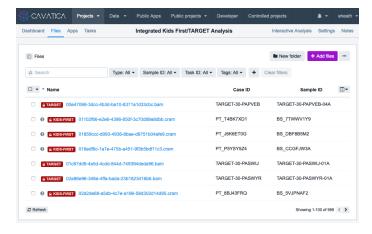




SevenBridges: https://docs.sevenbridges.com/

CWL: https://www.commonwl.org/

Researchers bring multiple datasets together and run workflows over the data in secure private workspaces



Federate a new (or existing) tool with the Data Resource!

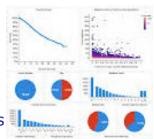
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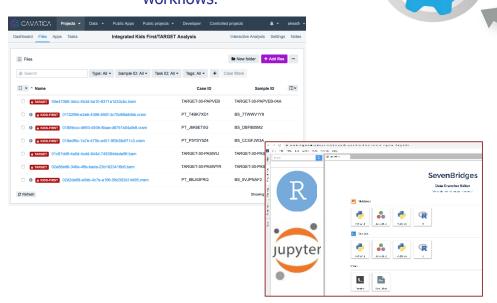
Knowledge Base Integrations (PedcBioPortal)

Integrations with existing curated/published data visualizations



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Data Services

Model clinical data in FHIR-based data services and API for sharing layers of harmonized data





STRIDES

Kids First



Framework Services

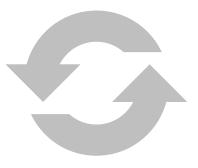
Index and point to files in the cloud (for approved users)

NIH Cloud Based Platforms Interoperability (NCPI)

Goal: Empower end-user analyses across platforms through federation & interoperability







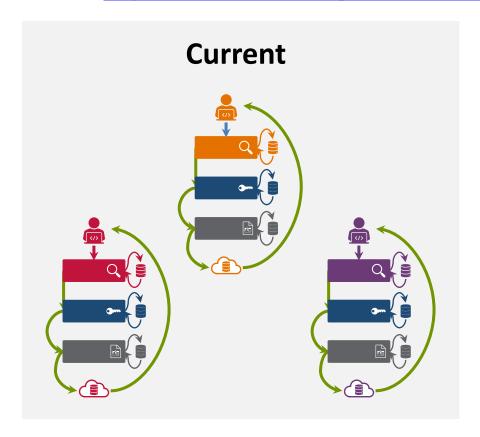




NIH Researcher Auth Services (RAS)

Simplify researcher access to NIH data through federated **authentication** (linking user identity account; "passport") and **authorization** (claim to access specific studies/datasets; "visa")

https://datascience.nih.gov/data-infrastructure/researcher-auth-service







Systems Interoperation WG - Technical 1st Year Vision



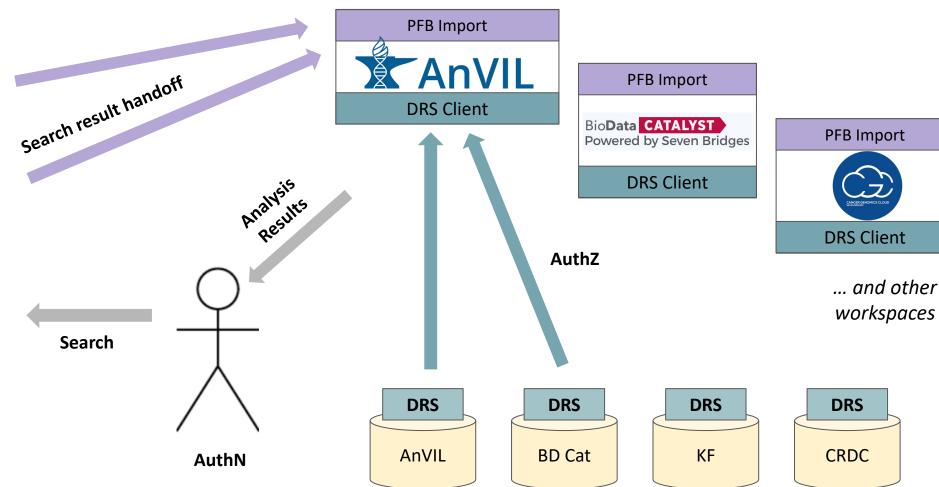
Portals











Workspaces

Data

Key NCPI Standards to Consider

NCPI: https://datascience.nih.gov/nih-cloud-platform-interoperability

- Fast Healthcare Interoperability Resources (FHIR; NOT-OD-19-122)
 - Tools that exchange or handle Kids First clinical, phenotypic, or meta-data should consider implementing FHIR standards to interact with the Kids First Data Resource's FHIR server and API
- NIH Researcher Auth Service (RAS; https://auth.nih.gov/docs/RAS/)
 - Tools accessing controlled-access data should consider implementing the ability to "consume" RAS for authentication and authorization
- Data Repository Service (DRS; https://github.com/ga4gh/data-repository-service-schemas)
 - Tools handling Kids First data (which is stored in the cloud) should consider implementing the ability to "consume" DRS for referencing data objects

Examples: Improve Discovery by...

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Standard Data Use Limitations (DULs)

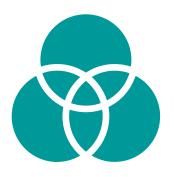
The NIH Genomic Data Sharing Policy "expects investigators generating genomic data to seek consent from participants for future research uses and the **broadest possible sharing**."

- General Research Use → Broadest
- Health/Medical/Biomedical
- Disease Specific:

When data use is restricted to a specific disease area, the data *cannot* be combined with a dataset with a different disease specific data use limitation.







Combining and crossanalyzing datasets is a primary goal of Kids First!

Institutional Certification: controlled-access data

NIH expects the submitting institution(s) to select one of the three standard <u>Data Use Limitations</u> (DULs) for appropriate secondary use, or, if necessary, create a customized DUL DULs are developed based on the original informed consent of the participant(s).

Data Use Limitations

General Research Use	GRU	Use of the data is limited only by the terms of the Data Use Certification: these data will be added to the dbGaP Collection.
Health/Medical/Biomedical	HMB	Use of the data is limited to health/medical/biomedical purposes, does not include the study of population origins or ancestry.
Disease-specific [list disease]	DS	Use of the data must be related to the specified disease.
Other		[ENTER CUSTOMIZED TEXT, IF APPLICABLE]

Additional modifiers to the standard DULs (e.g., Not-for-profit Use On basis in the informed consent from the participants or in special knowle

Data Use Limitation Modifiers (Optional)

"General Research Use" with no modifiers is expected for <u>individual-level genomic data</u>, unless specific uses are clearly prohibited in consent.

IRB Approval Required	IRB	Requestor must provide documentation CONSENT	
Publication Required	PUB	Requestor agrees to make results of studies using the data available to the larger scientific or immunity.	
Collaboration Required	COL	Requestor must provide a letter of collaboration with the primary study investigator(s).	
Not-for-profit Use Only	NPU	Use of the data is limited to not-for-profit organizations.	
Methods	MDS	Use of the data includes methods development research (e.g., development and testing of software or algorithms).	
Genetic Studies Only	GSO	Use of the data is limited to genetic studies only.	

Using the tables above, please indicate in the table below the consent group(s) for each collaborating study site. Use one row per consent group.

Collaborating Site Name	Data Use Limitation	Data vse Limitation Modifiers (optional)
Eg: Cold Cohort Study	Health/Medical/Biomedical	IRB PUB COL NPU MDS GSO
Eg: Cold Cohort Study	Disease Specific Research [Lang Cancer]	IRB □ PUB □ COL □ NPU ☑ MDS □ GSO □
	General Research Use	IRB PUB COL NPU MDS GSO
	Select consent group title	IRB PUB COL NPU MDS GSO
	Select consent group title	IRB □ PUB □ COL □ NPU □ MDS GSO 37



Consent Considerations

- The NIH Genomic Data Sharing Policy "expects investigators generating genomic data to seek consent from participants for future research uses and the broadest possible sharing."
- Example from NHGRI Informed Consent Resource (https://www.genome.gov/27565449/the-informed-consent-resource/):
 - "Your samples, genomic data and health information will be stored and shared with other researchers. The samples and information will be available for any research question, such as research to understand what causes certain diseases (for example heart disease, cancer, or psychiatric disorders), development of new scientific methods, or the study of where different groups of people may have come from."
- DUL definitions and considerations:
 - Points to Consider for Institutions and Institutional Review Boards in Submission and Secondary
 Use of Human Genomic Data under the National Institutes of Health Genomic Data Sharing
 Policy: https://osp.od.nih.gov/wp-content/uploads/GDS_Points_to_Consider_for_Institutions_and_IRBs.pdf

Other R03s and Analysis Opportunities...

These activities should strengthen Kids First X01 datasets and/or enhance the functionality of the Kids First Data Resource to improve or facilitate future analyses by the broader research community, but applications do not have to address specific analyses themselves.

For applicants seeking to analyze Kids First data, see <u>PAR-19-375</u>. For applicants seeking to analyze other Common Fund datasets see <u>RFA-RM-21-007</u>.



R03-PAR (IC funds)

Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data

- Support analyses of Kids First X01 datasets
- R03
- IC funds (NICHD, NCI, NHLBI, NIAAA, and NIDCR)
- PAR (no set asides)
- Deadline: Standard Receipt Dates, 3 per year
- Combined direct cost budget for the two-year project period may not exceed \$200,000
- Number of awards depends on IC

R03-RFA (KF funds)

Expert-Driven Small Projects to Strengthen Gabriella Miller Kids First Discovery

- Support activities that will enhance the utility of Kids First data
- R03
- Kids First funds
- RFA (set aside)
- Deadline: June 18, 2021
- Combined direct cost budget for the two-year project period may not exceed \$200,000
- 9-14 awards are anticipated from this solicitation

FOAs for Data Analyses

- "Kids First R03-PAR": https://grants.nih.gov/grants/guide/pa-files/PAR-19-375.html
- Common Fund R03: https://grants.nih.gov/grants/guide/rfa-files/RFA-RM-21-007.html
- NIH "Parent" R03: https://grants.nih.gov/grants/guide/pa-files/PA-20-200.html
- NIH "Parent" R01: https://grants.nih.gov/grants/guide/pa-files/PA-20-185.html
- NCI: Secondary Analysis and Integration of Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes (Contact: rotunnom@mail.nih.gov)
 - R01: https://grants.nih.gov/grants/guide/pa-files/PAR-20-276.html
 - R21: https://grants.nih.gov/grants/guide/pa-files/PAR-20-277.html
- NIDCR: Notice of Special Interest (NOSI) of NIDCR in Supporting Discovery, Characterization, and Mechanistic Study of Genetic Variants Underlying Dental, Oral, and Craniofacial Diseases and Conditions

 https://grants.nih.gov/grants/guide/notice-files/NOT-DE-19-016.html
- NIDCR Research Grants for Analyses of Existing Genomics Data (R01) https://grants.nih.gov/grants/guide/pa-files/PAR-20-045.html
- NIDCR Small Research Grants for Analyses of Existing Genomics Data (R03) https://grants.nih.gov/grants/guide/pa-files/PAR-20-046.html



FOAs for Variant Validation

- ORIP: Development of Animal Models and Related Biological Materials for Research (R21 Clinical Trial Not Allowed) https://grants.nih.gov/grants/guide/pa-files/PAR-19-369.html
- ORIP: Resource-Related Research Projects for Development of Animal Models and Related Materials (R24 Clinical Trials Not-Allowed) https://grants.nih.gov/grants/guide/rfa-files/RFA-OD-19-027.html
- NIDCR: Mechanistic Studies of Gene-Environment Interplay in Dental, Oral, Craniofacial, and Other Diseases and Conditions (R01 Clinical Trial Not Allowed). https://grants.nih.gov/grants/guide/pa-files/PAR-19-292.html
- NIDCR: Development of Novel and Robust Systems for Mechanistic Studies of Gene-Environment Interplay in Dental, Oral, Craniofacial, and Other Diseases and Conditions (R21 Clinical Trial Not Allowed). https://grants.nih.gov/grants/guide/pa-files/PAR-19-293.html
- NHGRI: Novel Approaches for Relating Genetic Variation to Function and Disease (R01 Clinical Trial Not Allowed) https://grants.nih.gov/grants/guide/pa-files/pa-18-868.html
- To pursue collaborations with the <u>Knockout Mouse Phenotyping Program (KOMP2)</u>, contact: <u>KidsFirstKOMP@nih.gov</u>



FAQ #1

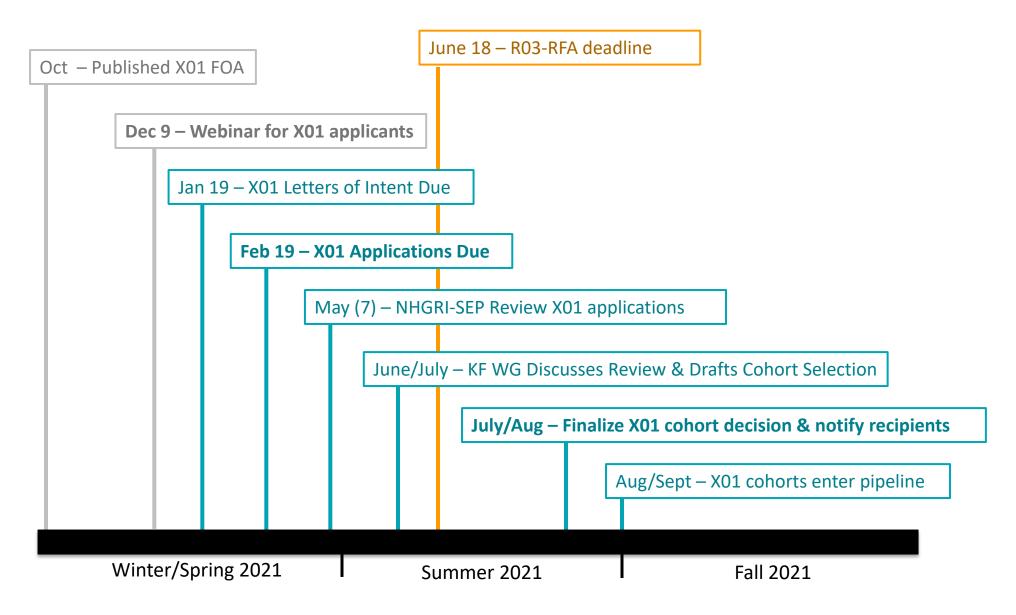
Question: I applied for the FY21 X01 sequencing opportunity, but I would like to apply for the expert-driven R03-RFA to work with colleagues to improve the associated dataset. When will X01 decisions be announced, and should I apply to RFA-RM-21-011?



Answer: Can you make a compelling argument that the activity improve Kids First regardless of the X01? Then yes, apply.



2021 X01 Timeline



FAQ #2

Question: I am planning to propose building and optimizing a workflow that can deployed in CAVATICA. Are cloud credits available for testing/running the tool?



<u>Answer</u>: Cloud credits are currently only available to X01s via a separate review process. However, there is no guarantee cloud credits will be approved for this purpose, so you should incorporate these cloud costs into your R03 budget.

→ Cost estimate resources: DRC FAQs



FAQ #3

Question: What standards have been adopted by Kids

First? What other standards might be relevant?



Answer: See attached list (will be posted on our FAQ page soon!)



Q & A

- Use the Q&A bar (lower right of your screen) to send your questions to "All Panelists". We will read your questions out loud and answer them.
- You can ask also use the "chat" service to send private messages to the host or presenters.

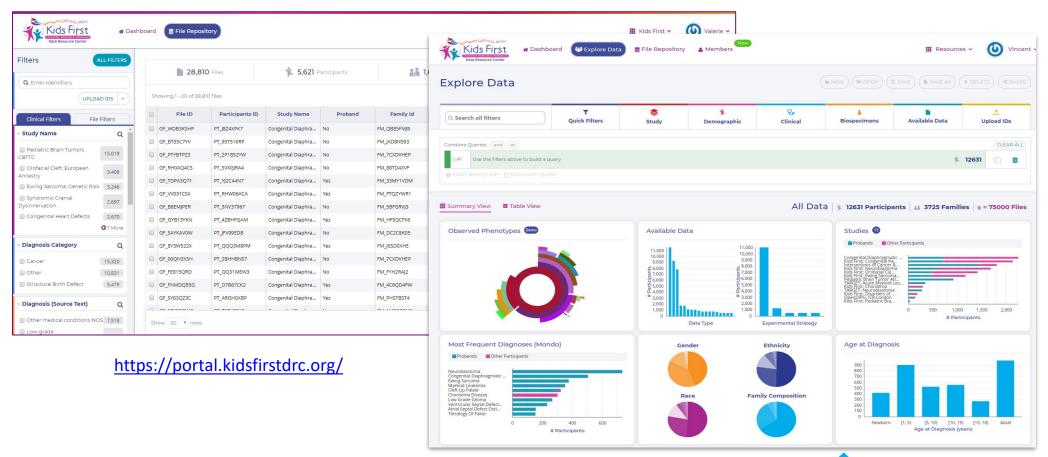




Portal demo

Anyone can register & login to the portal to filter, search, visualize datasets (build synthetic cohorts)





Submit <u>dbGaP Data Access Requests (DARs)</u> for controlled-access data

