Data Deposit for Health Sciences Research

January 21, 2025

UNIVERSITY OF TORONTO | Centre for Research & Innovation Support

Turning ‘live captions’ on and off

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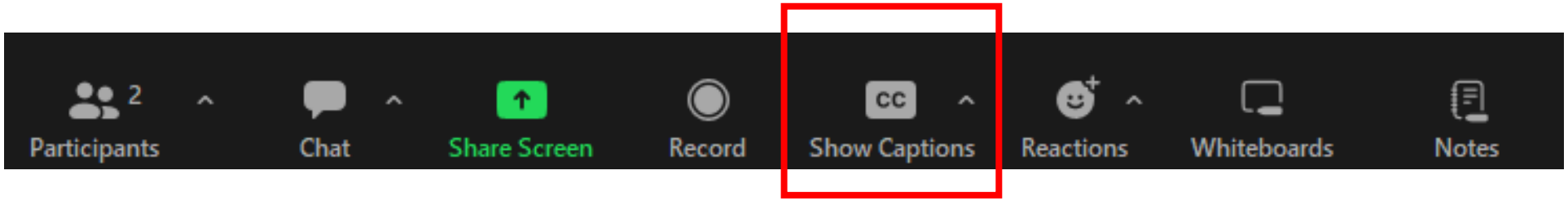


Land Acknowledgement

We wish to acknowledge this land on which the University of Toronto operates.

For thousands of years it has been the traditional land of the Huron-Wendat, the Seneca, and the Mississaugas of the Credit.

Today, this meeting place is still the home to many Indigenous people from across Turtle Island and we are grateful to have the opportunity to work on this land.

Housekeeping

- This webinar is being recorded and transcribed
- A link to the recording and presenter slides will be sent to all participants after the session
- Please put questions into the chat, we will hold all questions until the end of the presentations

Purpose & Agenda

Bring together the University of Toronto tri-campus and TAHSN health sciences research community for facilitated conversations about research data management.

Learning Objectives:

- Preparing data for deposit
- Considerations for selecting a repository and managing access
- Finding and using secondary data sets

1. **Data deposit basics**
2. **Panelist presentations**
3. **Panel discussion and Q&A**

Data Deposit – The Basics

What

Transferring research data to a data repository for secure storage and preservation

Researchers control data accessibility

Includes:
- Collected data
- Accompanying documentation
- Source code
- Software
- Metadata
- Other supplementary materials

Why

Purpose: Ensure that data are securely preserved and accessible to researchers after project completion

Can support reuse, validation, replication and links with other research

Requirements & considerations
- Funders (e.g., Tri-Agency Research Data Management Policy)
- Publication
- Disciplinary norms
- Ethical, cultural, legal, and commercial requirements

How

Factors
- FAIR Principles
- Indigenous data sovereignty
- Data sensitivity & confidentiality

Types of repositories
- Disciplinary
- Multidisciplinary/generalist
- Institutional

Resources:
- University of Toronto Libraries – Data Repositories

Panelists

Dr. Rachel Harding
Assistant Professor, Department of Pharmacology and Toxicology & Principal Investigator, Structural Genomics Consortium

Conrad Pow
Senior Lead for Digital Health at Diabetes Action Canada

Dr. Daniel Roth
Associate Professor, Department of Paediatrics & Clinician-Scientist, Division of Paediatric Medicine at SickKids

Dr. Michael M. Hoffman
Associate Professor, Department of Medical Biophysics & Senior Scientist, Princess Margaret Cancer Centre

The SGC is a global public-private partnership focused on open drug discovery

SGC

SGC

neuro
Montreal Neurological Institute-Hospital

Karolinska Institutet

University of Toronto

University of North Carolina at Chapel Hill

Goethe Universität Frankfurt am Main

UCL

Impact of SGC protein structures

RCSB PDB PROTEIN DATA BANK

4,000+

DEPOSITED STRUCTURES

addgene

4,450+

PLASMIDS DISTRIBUTED

SGC www.theSGC.org

1,500+

DETAILED PURIFICATION PROTOCOLS

PubMed.gov

1,100+

PEER REVIEWED PUBLICATIONS OF STRUCTURES

Evolving science and partners to address pressing global needs

SGC

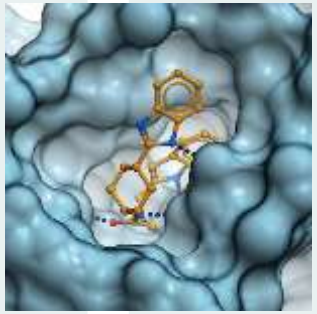
2004 | 2007 | 2011 | 2015 | 2020 | 2025

Phase I | **Phase II** | **Phase III** | **Phase IV** | **Phase V**

Scientific Focus

Structural Genomics

Human Protein Families



Chemical Genomics

TARGET 2035

Bio-active Chemical Tools

Data driven Drug Discovery

Machine Learning

Patient-derived tissue disease assays

Industry Partners

Phase I: GlaxoSmithKline

Phase II: GlaxoSmithKline, Pfizer, MERCK, NOVARTIS

Phase III: GlaxoSmithKline, Takeda, Pfizer, janssen, Lilly, abbvie, Boehringer Ingelheim, BAYER, NOVARTIS

Phase IV: Takeda, Boehringer Ingelheim, janssen, MERCK, Pfizer, abbvie, BAYER, MSD, NOVARTIS

Phase V: Genentech, janssen, MERCK, Pfizer, Boehringer Ingelheim, Takeda, BAYER, Bristol Myers Squibb

SGC chemical probe development

Chemical probe = a drug-like small molecule that selectively modulates the activity of a specific protein in cells

Probe Criteria

Potent: KD/IC_{50} < 100 nM *in vitro*

Selective: **>** 30x over related proteins

Cell activity: at 1 µM or less

Low/No off-target cellular toxicity

Ideally, a negative control molecule

HIGHLY ENABLING RESEARCH TOOLS

Bibliometric analysis shows that chemical probes were the most impactful reagent/tool to enable researchers to work on new targets


COMMENT

Too many roads not taken

- Used to interrogate protein function in cells
- Chemical counterpart to genetic knock-out/knockdown methods
- Enables development of novel disease target hypotheses
- The first step in a drug discovery program
- All shared in public domain

www.theSGC.org/chemical-probes/

Impact of SGC chemical probes

SGC CHEMICAL PROBES BY THE NUMBERS

DISCOVERED

200+

Novel chemical probes developed in collaboration with industry and academic partners

DISTRIBUTED

50,000+

Samples of chemical probes distributed globally by SGC and trusted vendors

CITATIONS

13,000+

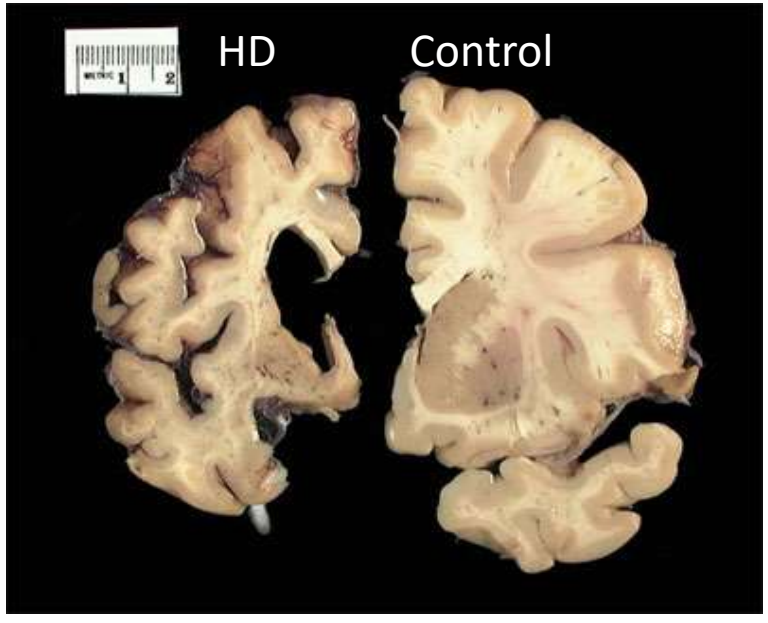
SGC chemical probes used by scientists around the world

CLINICAL TRIALS

85+

Clinical trials and late-stage preclinical programs based on therapeutic hypotheses generated with SGC chemical probes

Huntington's disease research at the SGC – open in practise

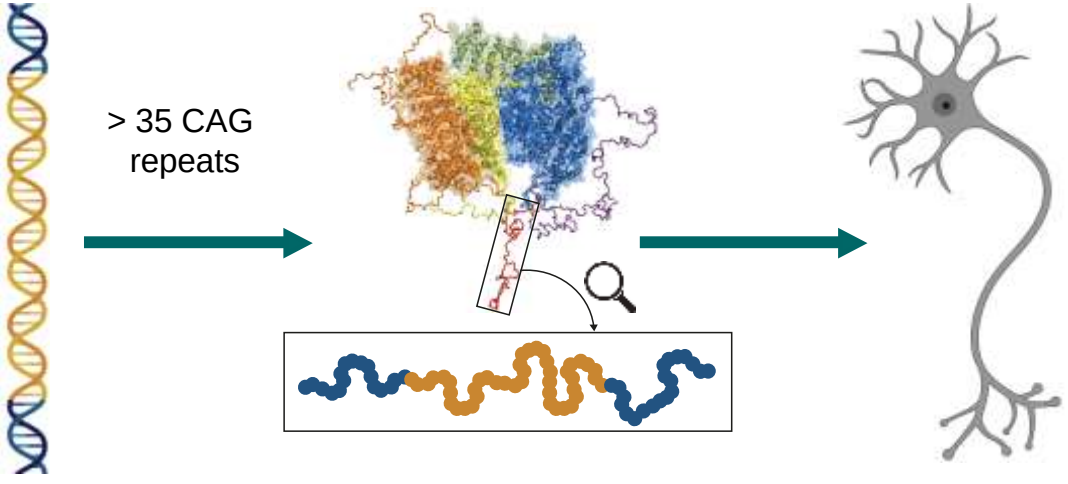


Patient population huntingtin gene

> 35 CAG repeats

Aberrant huntingtin protein

Neurodegeneration



Outstanding Questions:

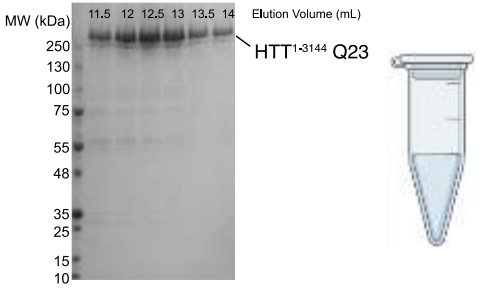
Why is there a mutation threshold for disease?

How does this (relatively) small change to the huntingtin protein initiate neurodegeneration?

New Approaches to Seek Answers:

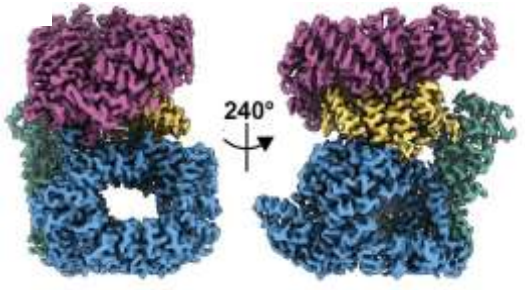
Robust protein biochemistry

Samples shared freely with community



Structure-function analysis

Data deposited prior to publication



Novel modalities for chemical biology

Develop unencumbered tools

Diabetes Research Connect

Conrad Pow
Sr. Lead, Digital Health
Diabetes Action Canada

Diabetes Action Canada
Preventing complications. Transforming lives.

CPCSSN RCSSSP
Canadian Primary Care Sentinel Surveillance Network
Réseau canadien de surveillance sentinelle en soins primaires

Strategy for Patient-Oriented Research SPOR
Putting Patients First
Stratégie de recherche axée sur le patient SRAP
Le patient d'abord

Action diabète Canada
Prévenir les complications. Transformer les vies.

Diabetes Action Canada

- Pan-Canadian Diabetes Research Network with **120 researchers**, and over **400 Patient Partners**
- Funded by the **Canadian Institutes for Health Research (CIHR), funding partners** (i.e. Diabetes Canada) and through **philanthropic support**
- Strengthening healthcare systems through multi-disciplinary collaboration among experts in primary and specialist care, **health data management**, analytics and policy
- Advancing Patient-oriented research by fostering collaborations between **people living with diabetes** and research teams dedicated to preventing complications
- Primary focus on addressing the needs of **equity denied communities**

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Diabetes Research Connect

- **Secure Virtual Platform**
- **Largest National Primary Care Data Repository**
- **Over 1,200 primary care providers**
- **Over 1.8 million patient data**
- **Approval from DAC's Digital Health Governing Committee**
- **All projects co-designed with Patient Partners**

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Data Collection

Data is collected through an **REB approved, systematic process** involving the extraction of **de-identified** patient information from electronic medical records (EMRs) used by primary care providers across Canada.

Data Collection Process:

1. Data Extraction
2. Data De-identification
3. Data Standardization
4. Data Storage
5. Data Quality Assurance

Data Sources

- De-identified National EMR data
- Agreements from 8 Provinces and 1 Territory

EMR Vendors (and products):

Telus: (Kinlogix, Med Access, Medesync, Nightingale, Practice Solutions, Telin, Wolf)

QHR: (Accuro, Jonoke, Healthscreen, xwave)

OSCAR

Da Vinci

Healthquest

InputHealth

IntraHealth

Purkinje

P&P

- Inclusion of Ontario Community Health Centres (BIRT)

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Data

Data Extraction:
- CPCSSN does **not** extract all patient data
- Focuses mainly on **structured data**
- Does **not** extract notes or PDFs

Data De-identification:
- No identifiable information is extracted, and only **de-identified** **data** is processed

Extracted Data Fields:
- Includes billing, health conditions, reasons for visits, lab results, family history, medications ICD-9, referrals, vital stats…

Extraction Schedule:
- Data extractions occur biannually (June 30 and December 31)

Research Environment

Researchers are provided with a suite of analytical and development tools to conduct their studies. Software provided includes:

- SAS
- R/R Studio
- Stata
- Anaconda
- Jupyter Notebook
- Sublime Text

Researchers may request additional software applications be installed in their environments

*Researchers must provide their own licenses for software not already present in the SRE.

** Software that utilizes concurrent licensing (i.e. SPSS) cannot be used due to disabled internet access.

Role of DRC in Health Research

Impact of government-funded insulin pump programs on insulin pump use in Canada: a cross-sectional study design using the National Diabetes Repository. **Weisman, A. et al.**

Increased Accessibility: Government funding has made insulin pumps more accessible, confirming the positive impact of financial support on technology uptake.

Persistent Disparities: Despite funding, disparities persist, with lower-income individuals less likely to use insulin pumps, indicating that financial support alone is insufficient.

Non-Financial Barriers: Other factors, including healthcare provider biases and limited access to specialized care, contribute to the underutilization of insulin pumps among certain populations.

Need for Comprehensive Strategies: To achieve equitable access, it's crucial to address both financial and non-financial barriers through comprehensive approaches that include education, support, and systemic changes.

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Role of DRC in Health Research

Achievement of treatment targets among patients with type 2 diabetes in 2015 and 2020 in Canadian primary care. ***Lau, D. et al.***

Medication Usage: The study found suboptimal use of statins and ACE inhibitors or ARBs, especially among women, suggesting potential gaps in adherence to clinical guidelines or prescribing practices.

Trends Over Time: Between 2015 and 2020, there was an increase in HbA1c target achievement, stability in LDL-C target rates, but a decline in blood pressure target achievement and the use of recommended medications, indicating areas needing quality improvement.

Implications for Practice: The findings underscore the necessity for targeted interventions to enhance the comprehensive management of type 2 diabetes, with particular attention to gender disparities and the declining trends in blood pressure control and medication usage.

This study emphasizes the critical role of primary care in managing type 2 diabetes and the ongoing need for quality improvement initiatives to ensure patients achieve comprehensive treatment targets.

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Thank You!

Questions?

Image: DALL-E

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Preparing and depositing health research data for public access: SEPSiS project experience

Daniel Roth

January 21, 2025

SEPSiS Project in Dhaka, Bangladesh

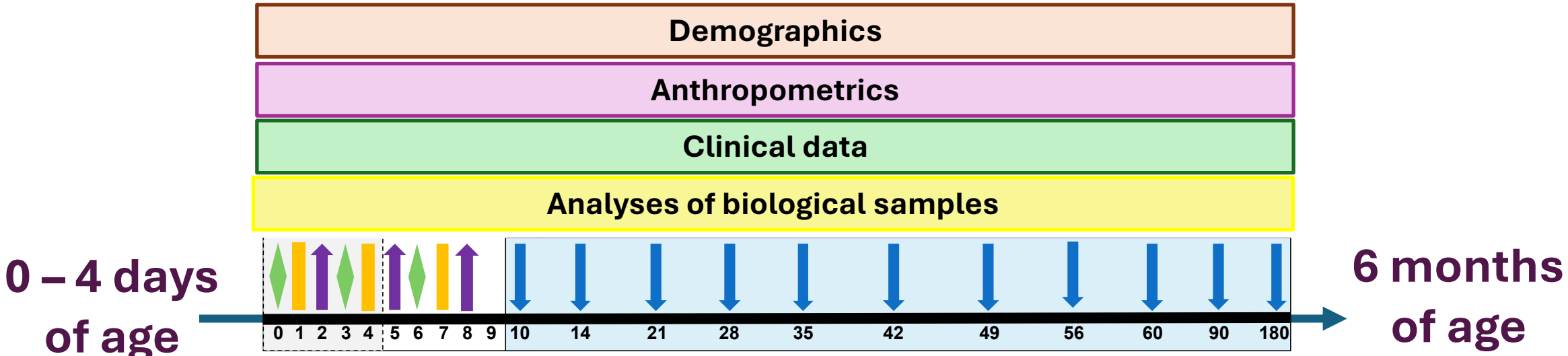
icddr,b
KNOWLEDGE FOR GLOBAL LIFESAVING SOLUTIONS

CHRF

November 2020

↓

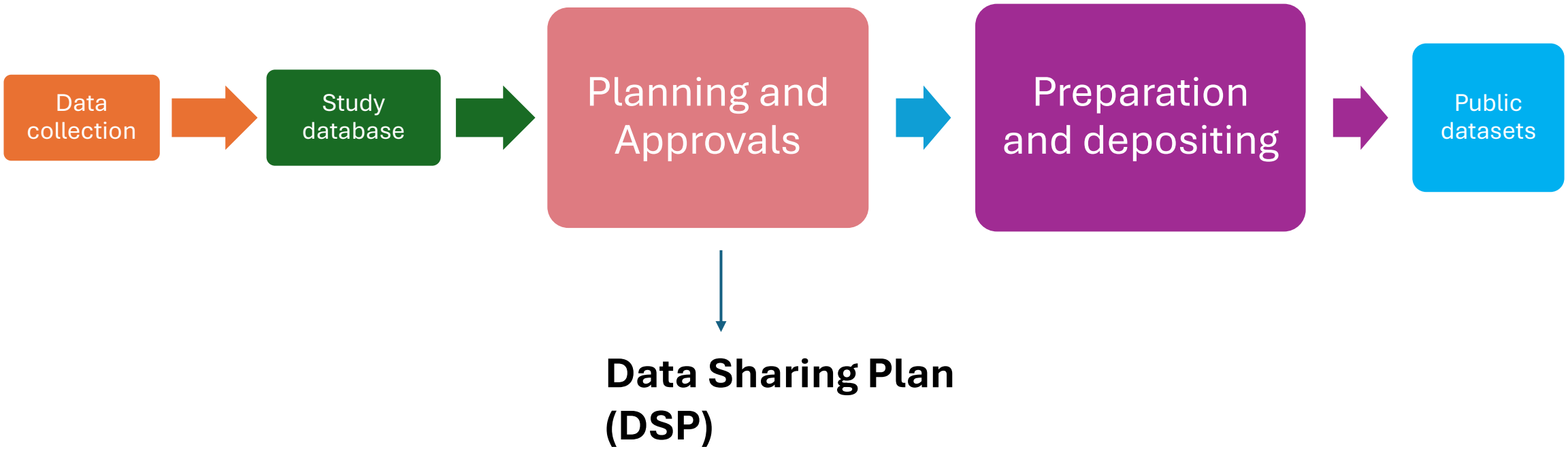
November 2022



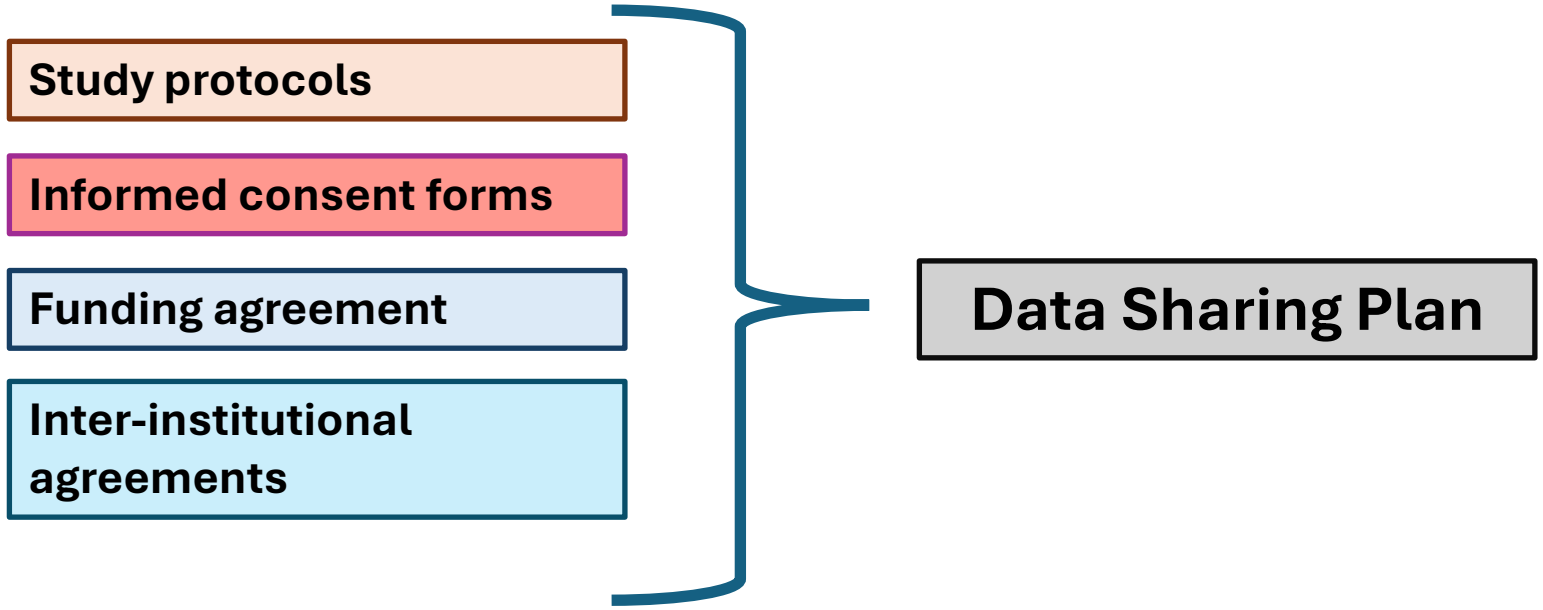
N = 2,458 infants

Research Data Sharing – initial assumption

Research Data Sharing – reality

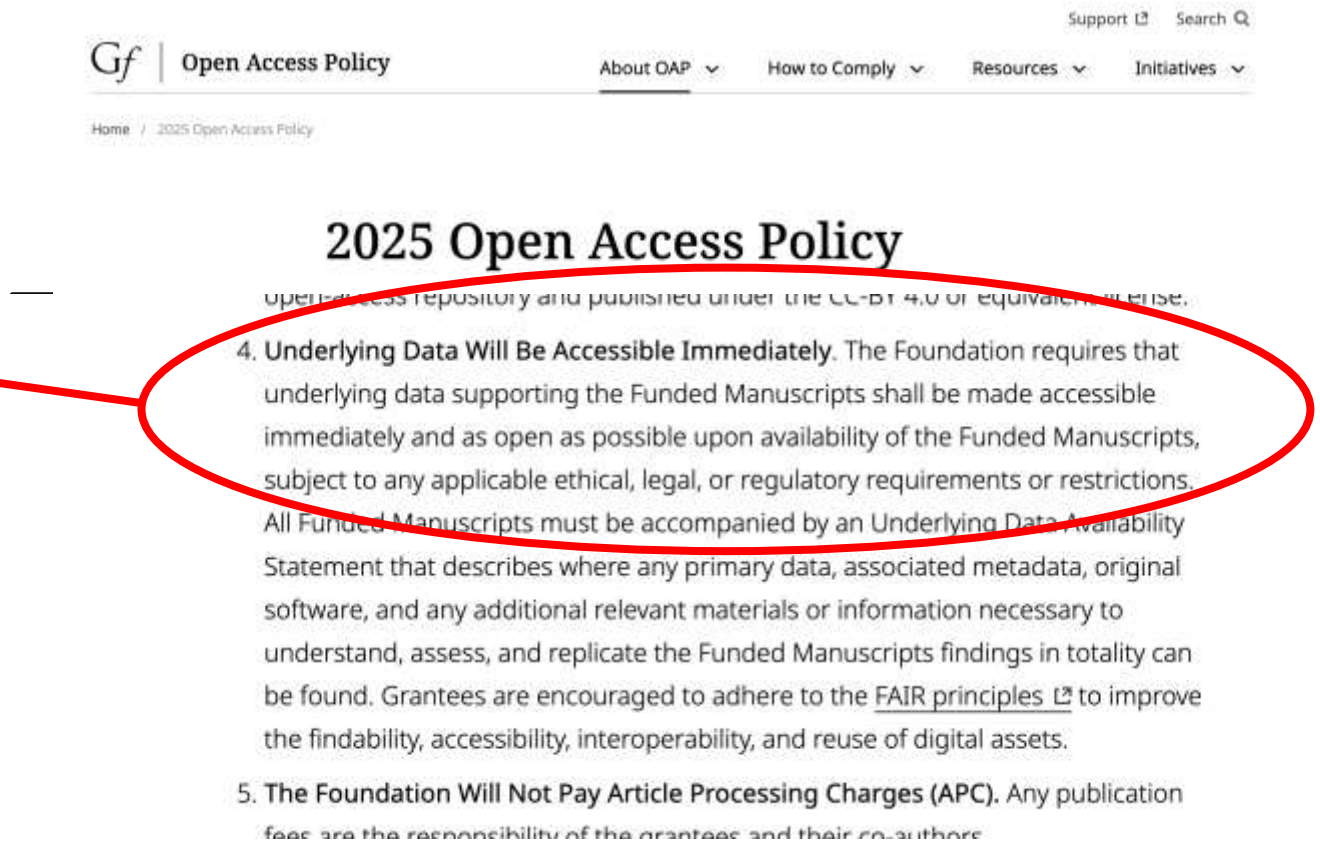


Data Sharing Plan (DSP)



Data Sharing Plan (DSP)

- **Study protocols**
- **Informed consent forms**
- **Funding agreement**
- **Inter-institutional agreements**



Support Search

Gf | Open Access Policy

About OAP | How to Comply | Resources | Initiatives

Home / 2025 Open Access Policy

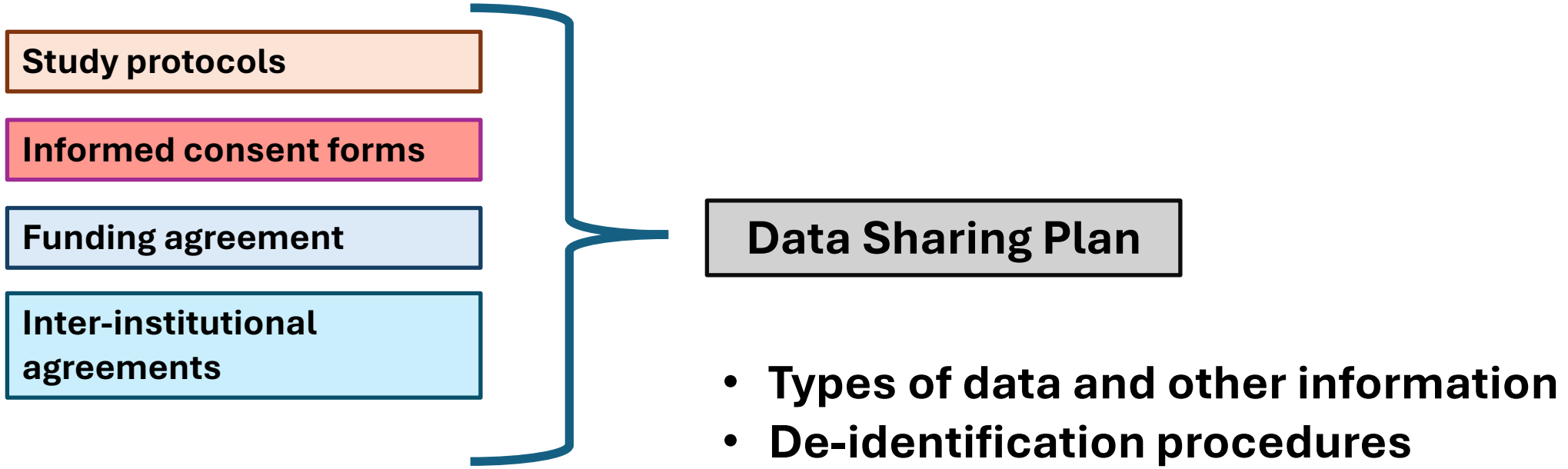
2025 Open Access Policy

open-access repository and published under the CC-BY 4.0 or equivalent license.

4. **Underlying Data Will Be Accessible Immediately**. The Foundation requires that underlying data supporting the Funded Manuscripts shall be made accessible immediately and as open as possible upon availability of the Funded Manuscripts, subject to any applicable ethical, legal, or regulatory requirements or restrictions. All Funded Manuscripts must be accompanied by an Underlying Data Availability Statement that describes where any primary data, associated metadata, original software, and any additional relevant materials or information necessary to understand, assess, and replicate the Funded Manuscripts findings in totality can be found. Grantees are encouraged to adhere to the FAIR principles to improve the findability, accessibility, interoperability, and reuse of digital assets.
5. **The Foundation Will Not Pay Article Processing Charges (APC).** Any publication fees are the responsibility of the grantees and their co-authors

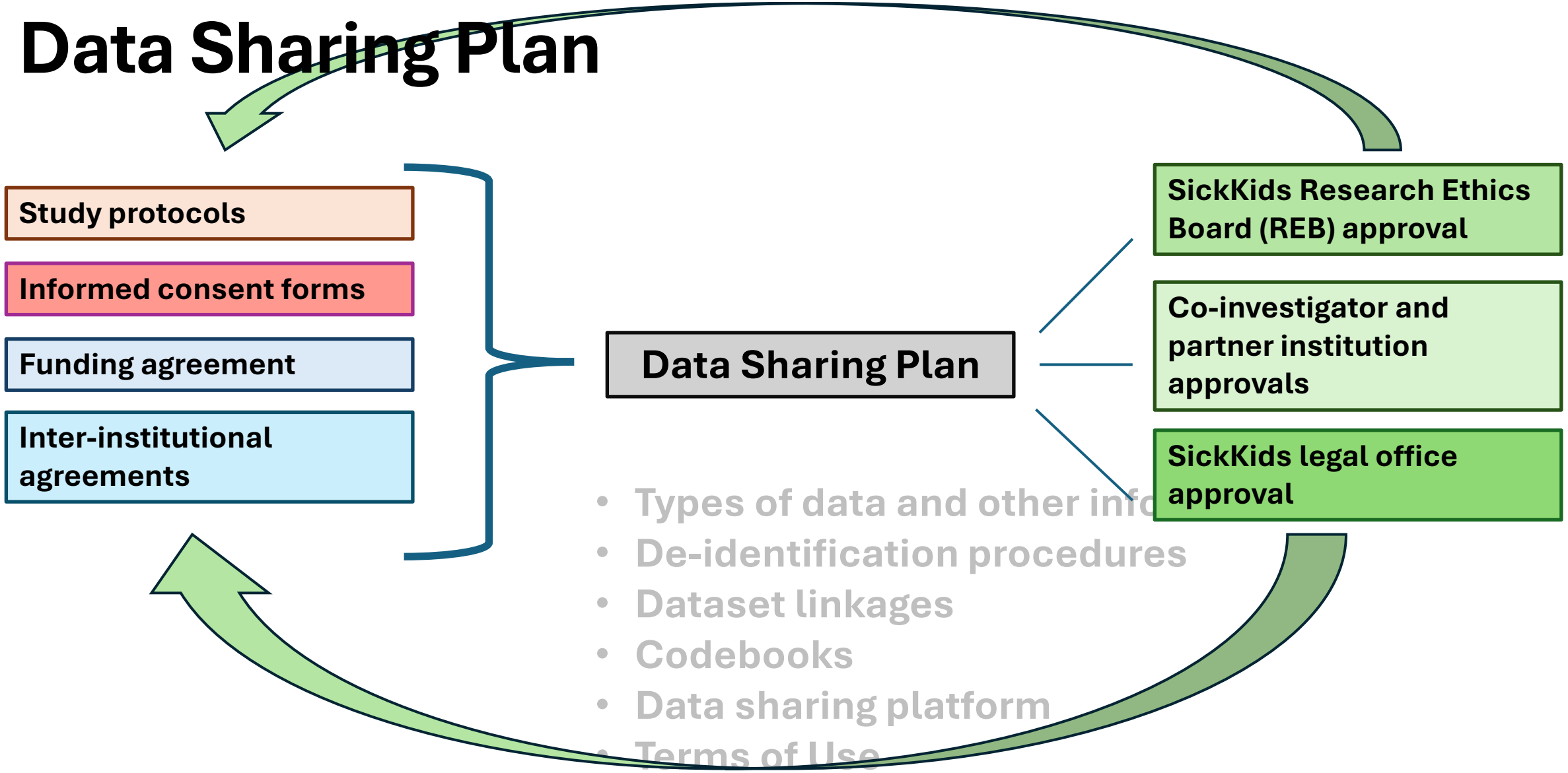
https://openaccess.gatesfoundation.org/open-access-policy/

Data Sharing Plan

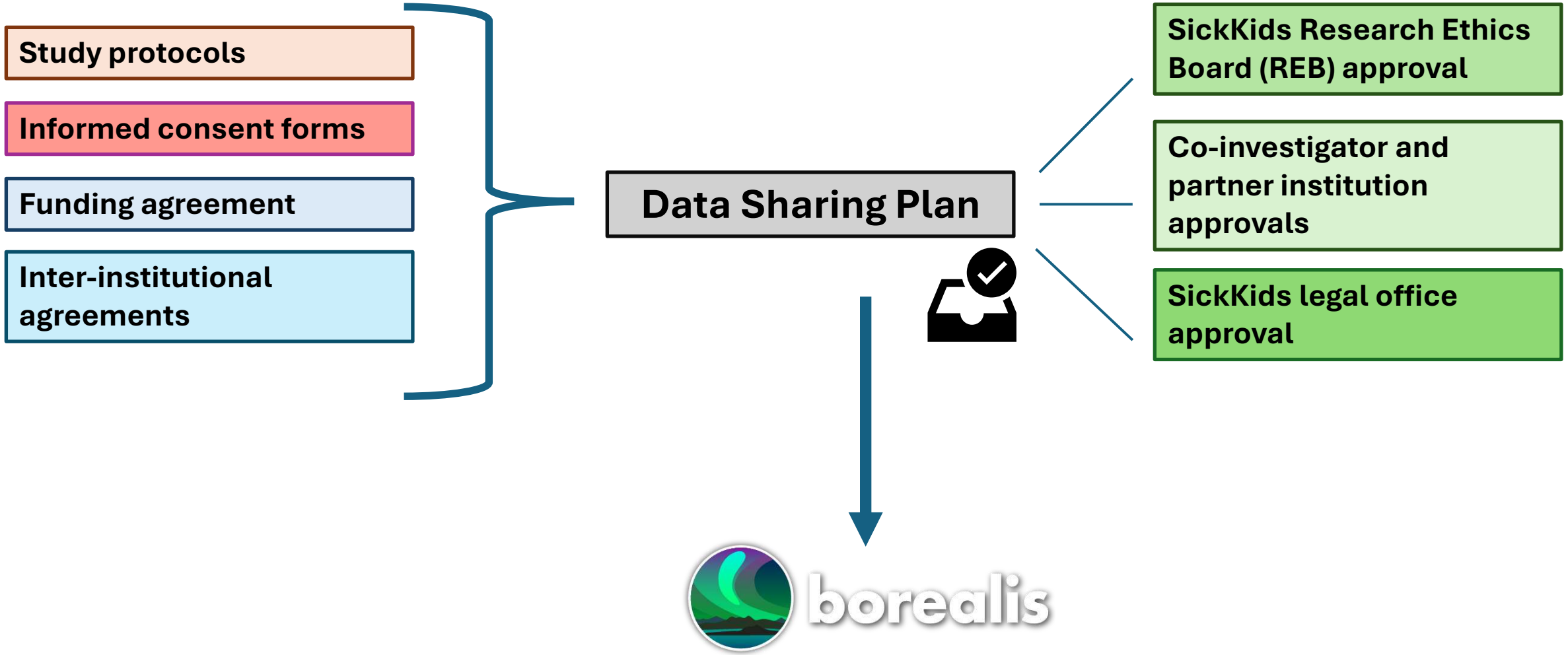


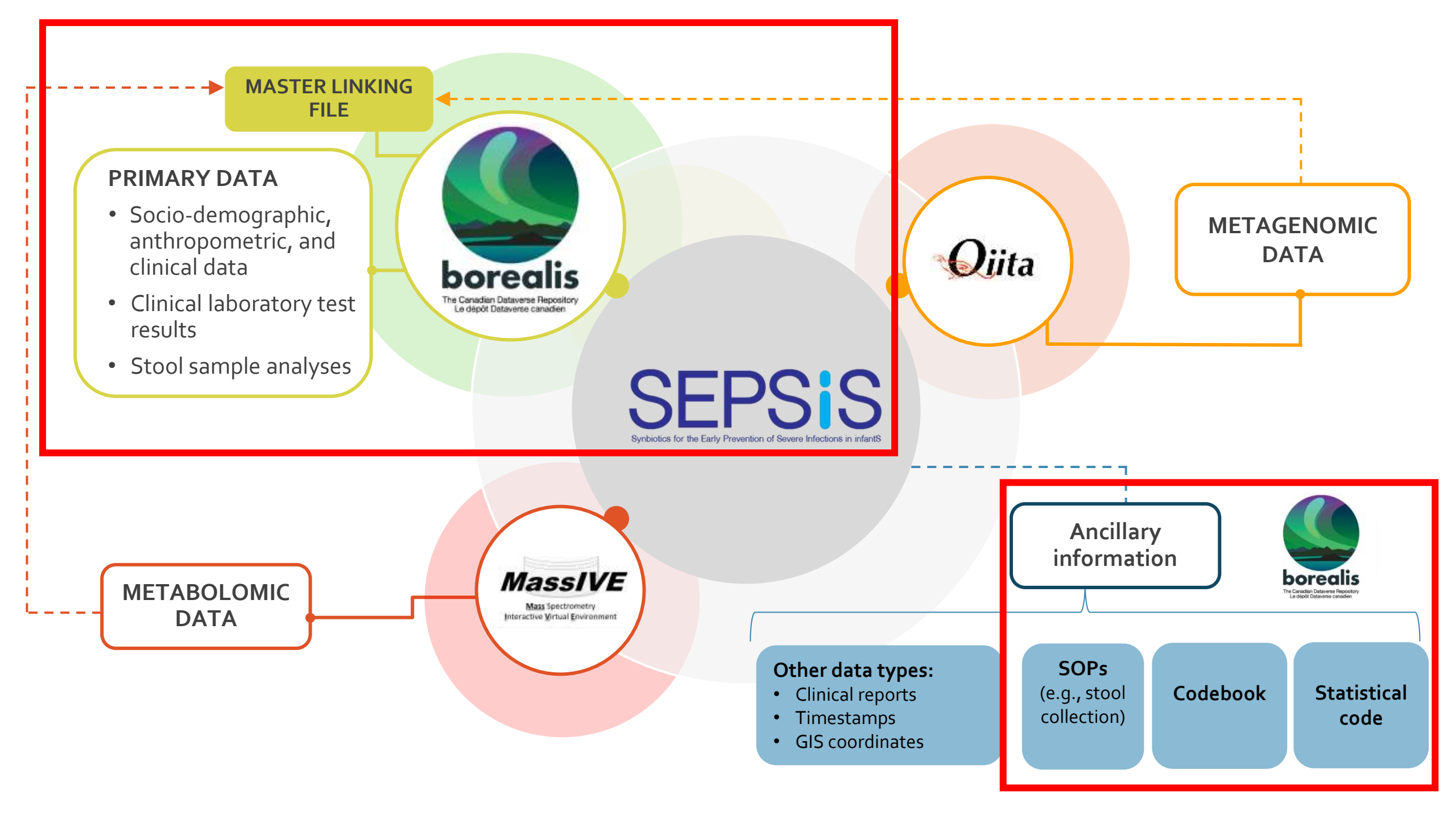
- Types of data and other information
- De-identification procedures
- Dataset linkages
- Codebooks
- Data sharing platform
- Terms of Use

Data Sharing Plan



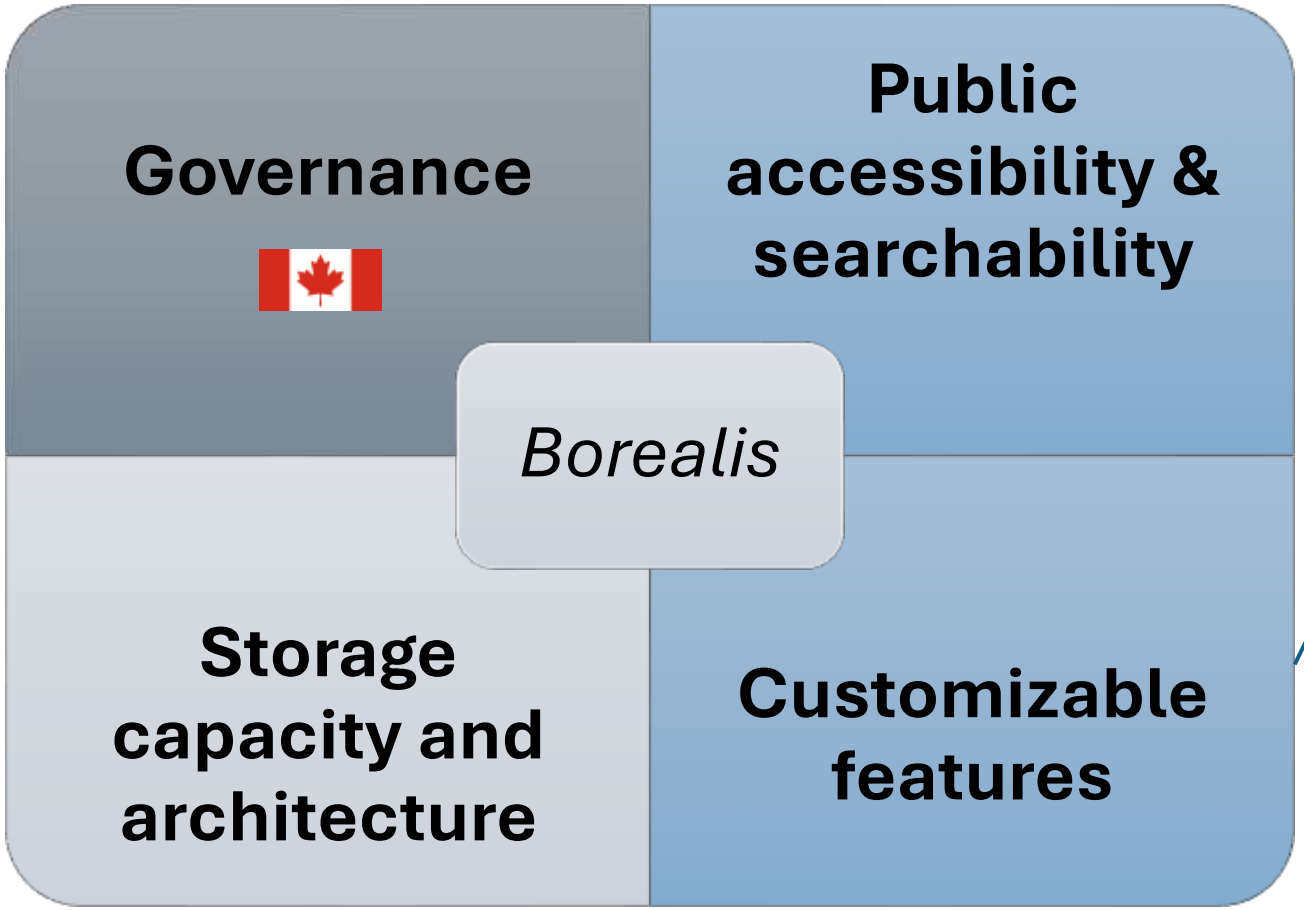
Data Sharing Plan




MASTER LINKING FILE
PRIMARY DATA
• Socio-demographic, anthropometric, and clinical data
• Clinical laboratory test results
• Stool sample analyses
borealis
The Canadian Dataverse Repository
Le dépôt Dataverse canadien
SEPSiS
Synbiotics for the Early Prevention of Severe Infections in infantS
Qiita
METAGENOMIC DATA
METABOLOMIC DATA
MassIVE
Mass Spectrometry Interactive Virtual Environment
Ancillary information
borealis
Other data types:
• Clinical reports
• Timestamps
• GIS coordinates
SOPs (e.g., stool collection)
Codebook
Statistical code

Borealis – Canadian Dataverse Repository

https://borealisdata.ca



a. ***Custom Terms of Use***

b. **Guestbook** - user data (i.e., name, email, institution, and position)

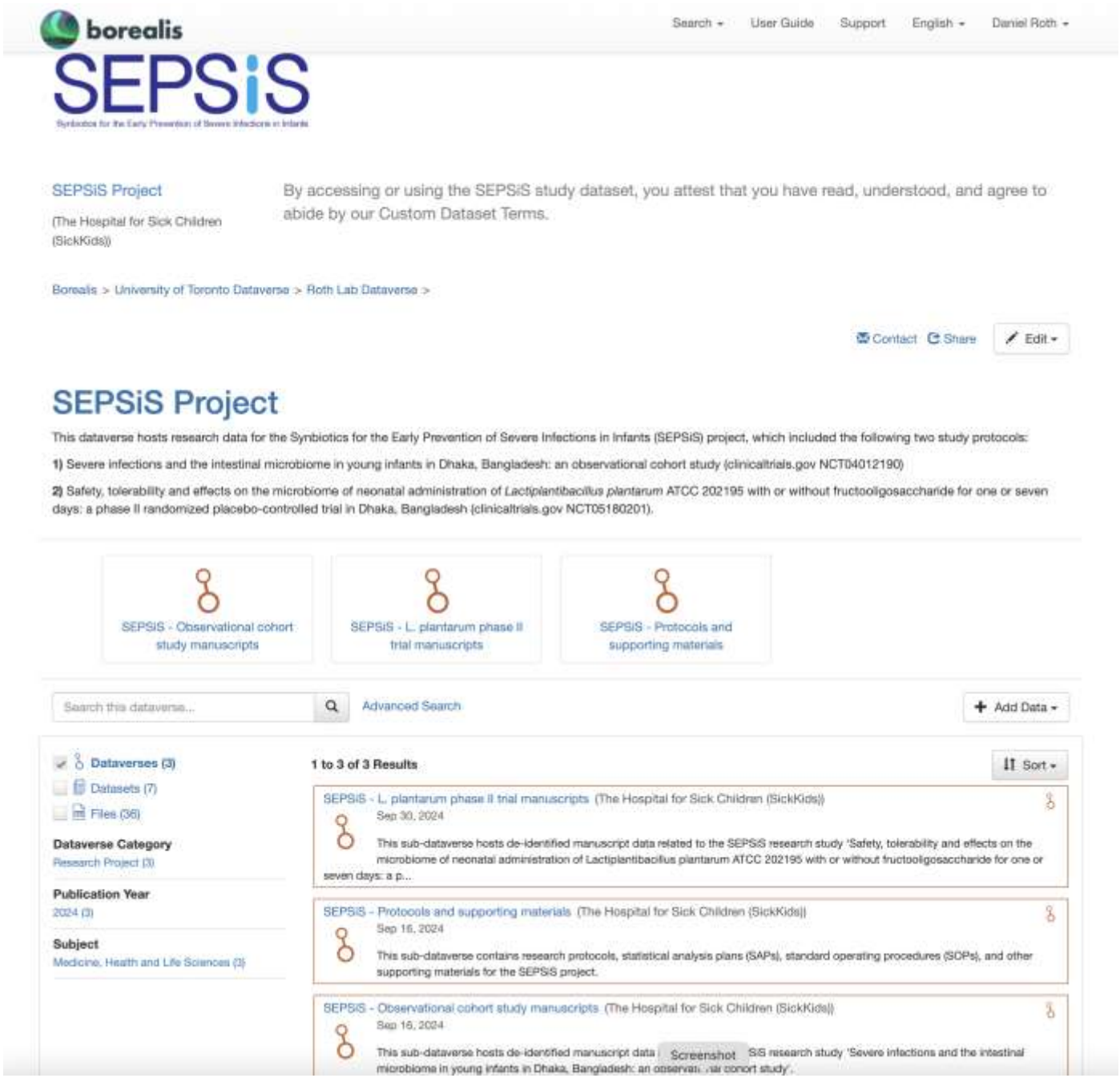
borealis

https://borealisdata.ca

Dataverse:

Sub-dataverses:

https://borealisdata.ca/dataverse/SEPSiS_Project



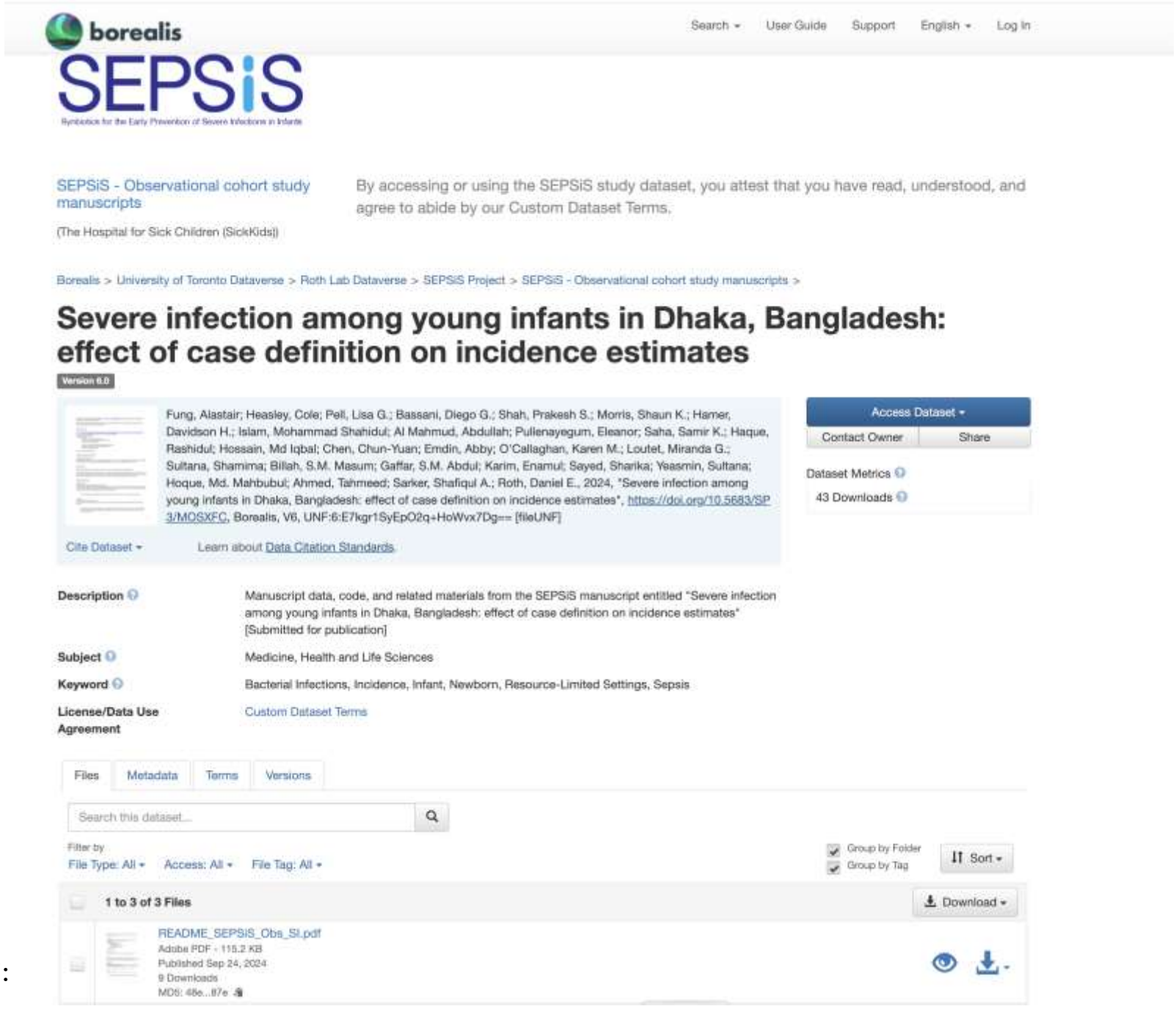
borealis

https://borealisdata.ca

Dataset:

Files:

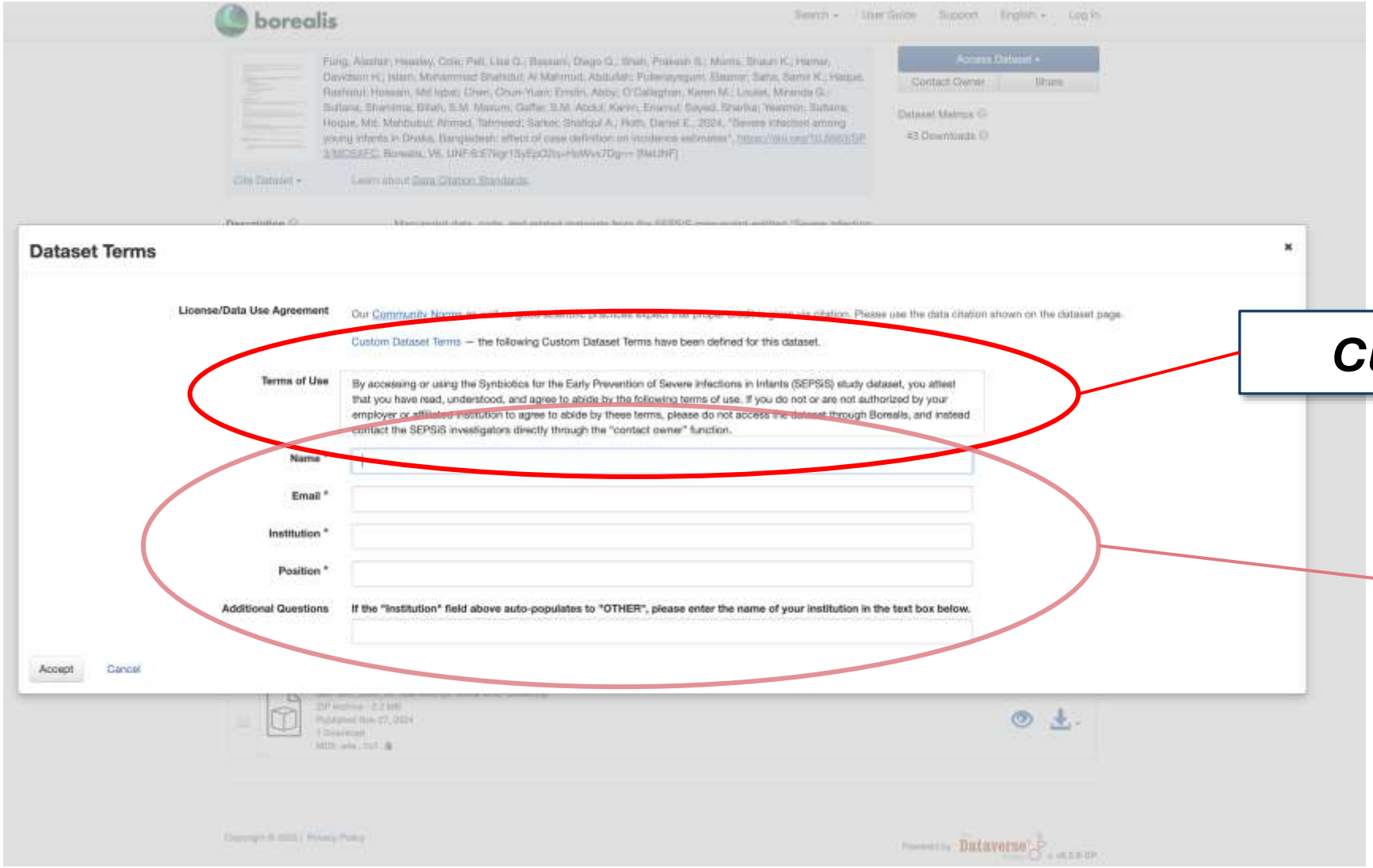
https://borealisdata.ca/dataset.xhtml?persistentId=doi:10.5683/SP3/MOSXFC



Customizable features

borealis

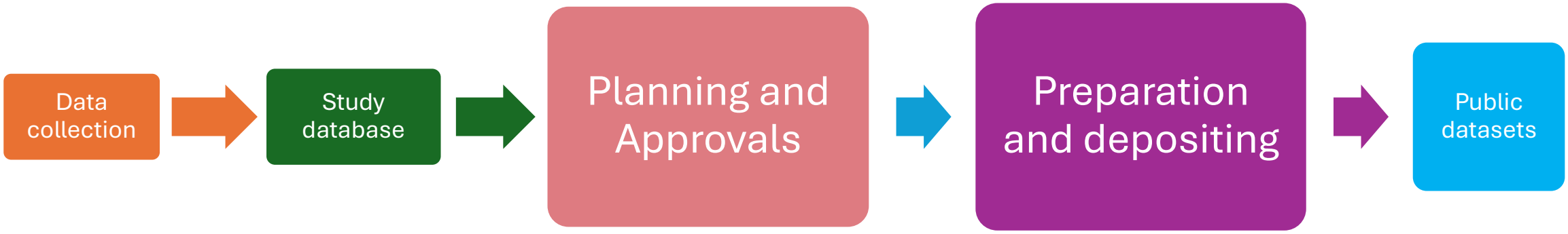
https://borealisdata.ca



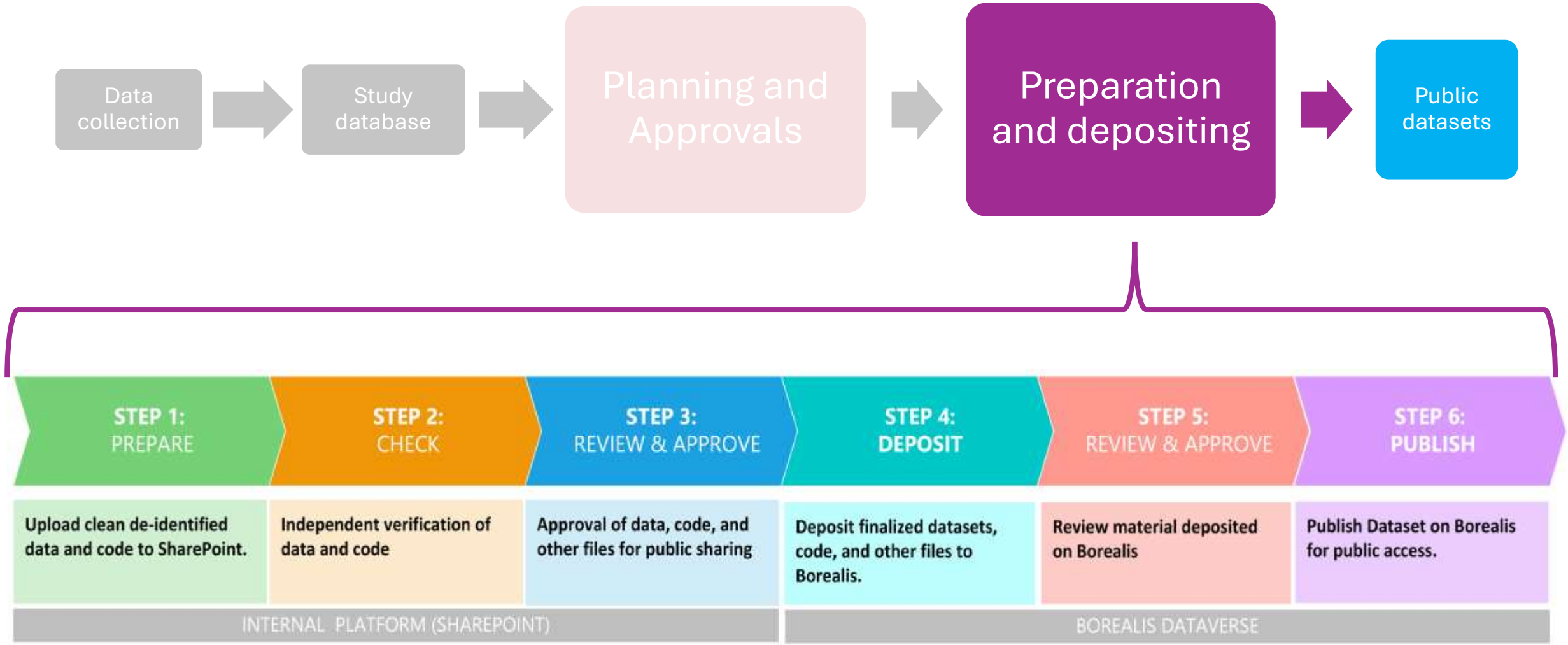
Custom Terms of Use

Guestbook entry

Step-wise process for public sharing of SEPSiS data on Borealis



Step-wise process for public sharing of SEPSiS data on Borealis



Key messages and challenges

- **Plan in advance.**
  - Needs to be addressed in protocol and consent forms.
- Requires dedicated time, personnel and expertise.
- No off-the-shelf roadmap for depositing primary data from REB-approved human subjects research
  - Engage your collaborating partners.
  - Consider requirements of funding agencies.
- Institutional approval processes
  - Institutional norms that emphasize privacy/confidentiality
- Linkages across different platforms.
- Consider the user experience (e.g., formatting files in a way to alleviate need to repeatedly sign guestbook)

Acknowlegements

- SickKids SEPSiS team
  - Veselina Stefanova
- SEPSiS project partner organizations
- Gates Foundation
- Borealis

Sharing research data: why, when, and how?

Michael M. Hoffman

Princess Margaret Cancer Centre
University Health Network

Department of Medical Biophysics
University of Toronto

Vector Institute

https://hoffmanlab.org/

Bluesky: @michaelhoffman.bsky.social

Disclosures

Competing interests:

- Patent application, licensed to Adela

Full disclosure of potential competing interests: https://github.com/michaelmhoffman/disclosure/

Why share data?

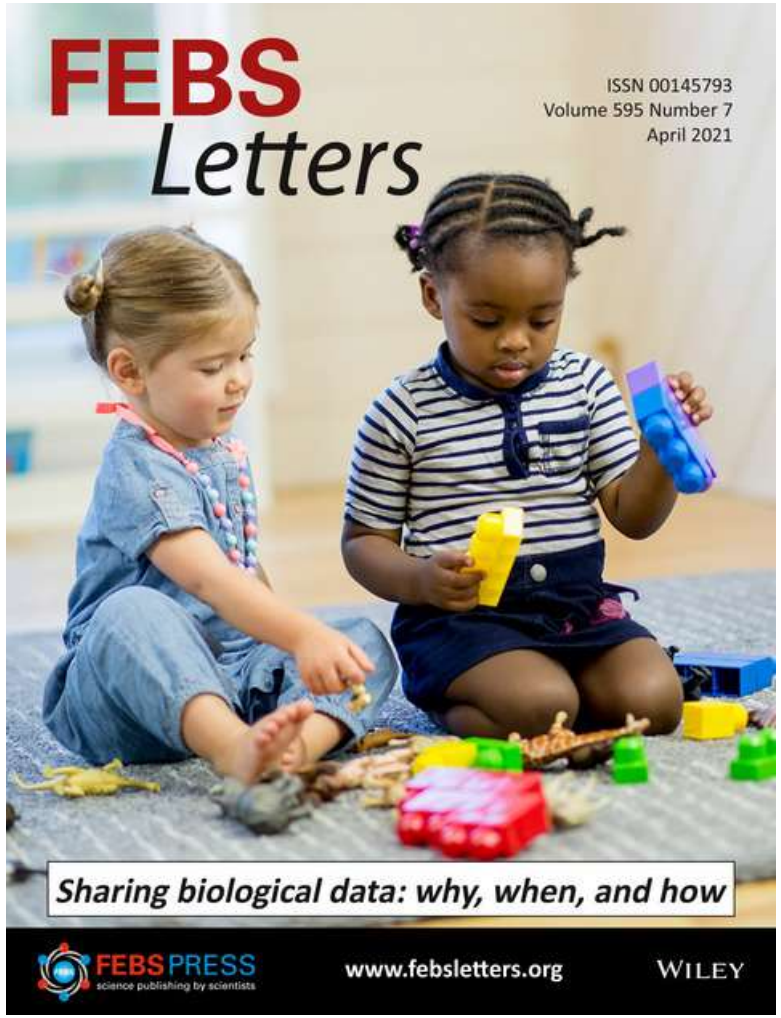
- Further progress of research and science
- Maximize the benefits provided by investment of funds, work, participation
- Best way to ensure that you can get the data later!

Wh data is needed?

- Can never reproduce without the data
- Raw data required
- Pre-existing data?
  - Include information and code required to download and pre-process data

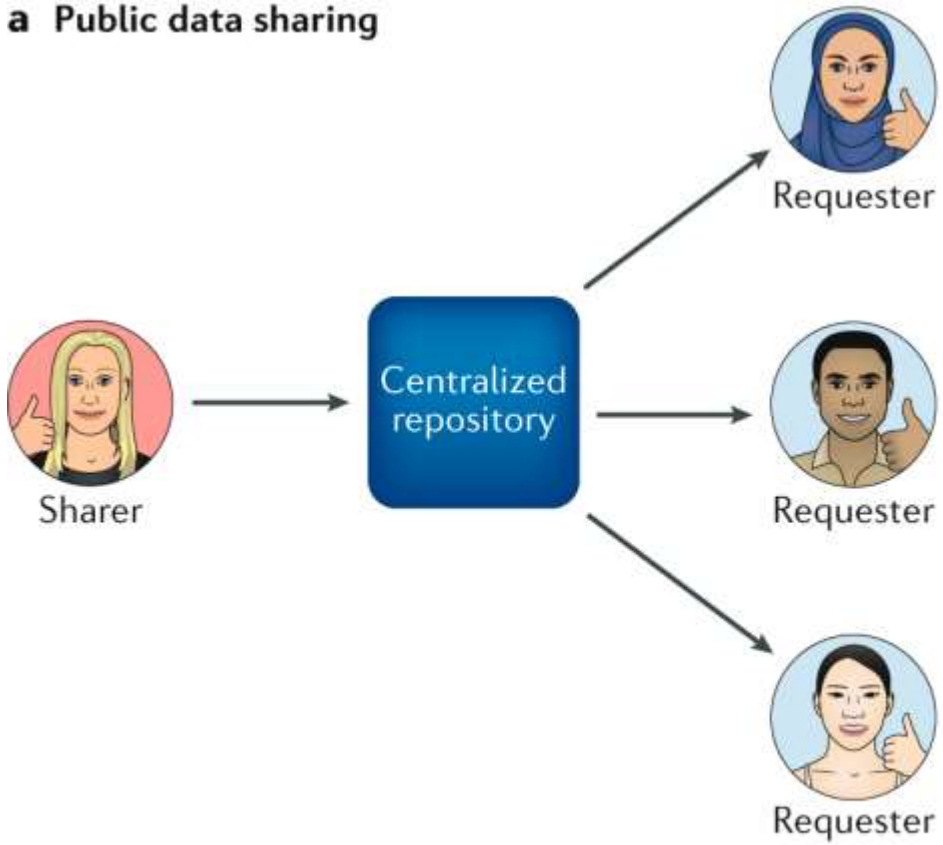
Where does the data go?

- Specialist repositories, when possible
  - Gene expression → Gene Expression Omnibus
  - Microscopy → BioImage Archive
- Generalist repositories, otherwise
  - ≤50 GB: Zenodo
  - >50 GB: Dryad
- Never under 100% author control
  - Not lab web site!
  - Not GitHub!!
  - Not an S3 bucket!!!

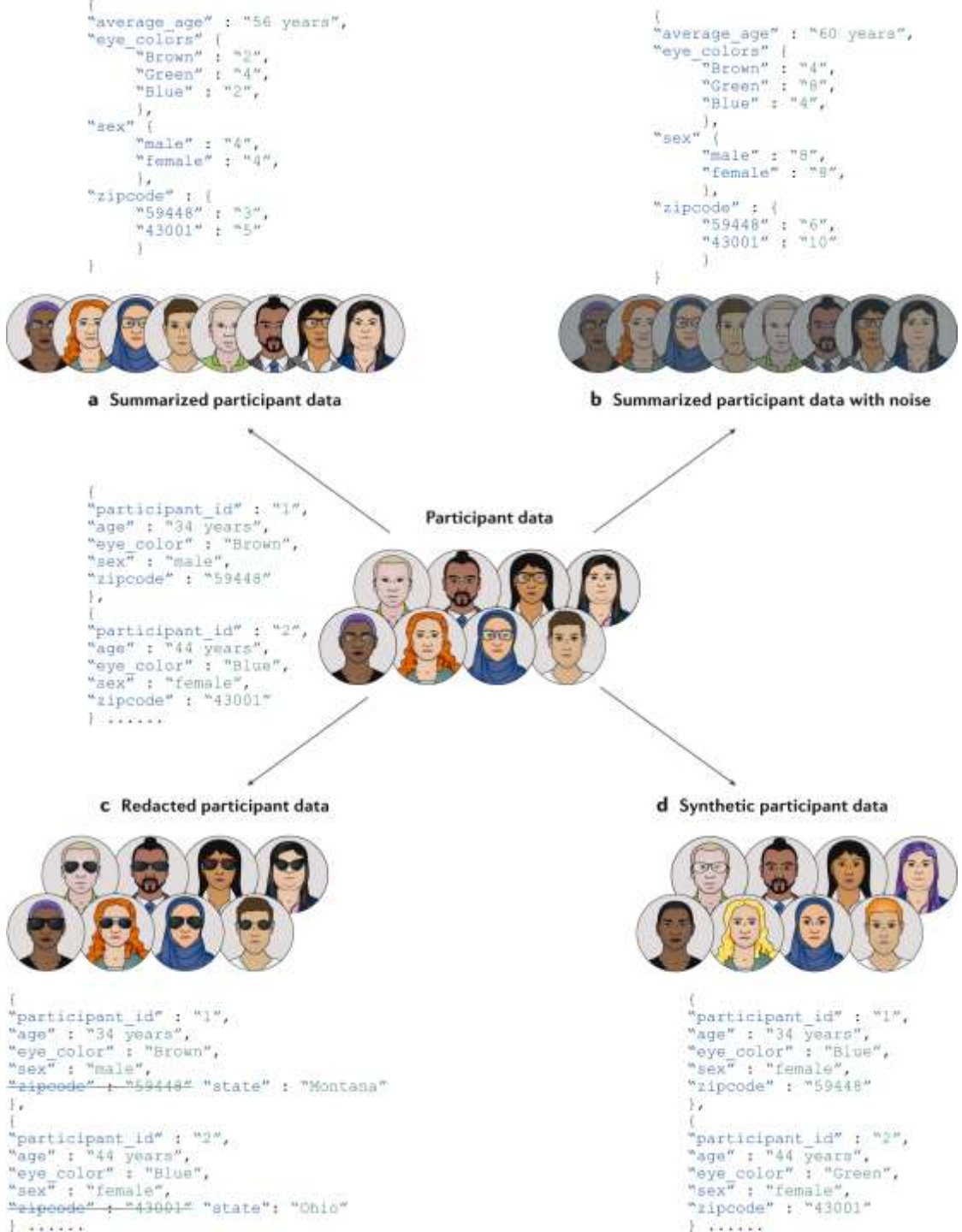


Wilson et al. 2021. *FEBS Lett* 595:845

Sharing data



Byrd et al. 2020. *Nat Rev Genet* 21:615



Byrd et al. 2020. *Nat Rev Genet* 21:615

Reproducibility standards for machine learning in the life sciences

To make machine-learning analyses in the life sciences more computationally reproducible, we propose standards based on data, model and code publication, programming best practices and workflow automation. By meeting these standards, the community of researchers applying machine-learning methods in the life sciences can ensure that their analyses are worthy of trust.

Benjamin J. Heil, Michael M. Hoffman, Florian Markowetz, Su-In Lee, Casey S. Greene and Stephanie C. Hicks

Table 1 | Proposed reproducibility standards

	Bronze	Silver	Gold
Data published and downloadable	x	x	x
Models published and downloadable	x	x	x
Source code published and downloadable	x	x	x
Dependencies set up in a single command		x	x
Key analysis details recorded		x	x
Analysis components set to deterministic		x	x
Entire analysis reproducible with a single command			x

The field of machine learning has grown tremendously within the past ten years. In the life sciences, machine-learning models are rapidly being adopted because they are well suited to cope with the scale and complexity of biological data. However, there are drawbacks to using such models. For example, machine-learning models can be harder to interpret than simpler models, and this opacity can obscure learned biases. If we are going to use such models in the life sciences, we will need to trust them. Ultimately all science requires trust[1]—no scientist can reproduce the results from every paper they read. The question, then, is how to ensure that machine-learning analyses in the life sciences can be trusted.

One attempt at creating trustworthy analyses with machine-learning models revolves around reporting analysis details such as hyperparameter values, model architectures and data-splitting procedures. Unfortunately, such reporting requirements are insufficient to make analyses trustworthy. Documenting implementation details without making data, models and code publicly available and usable by other scientists does little to help future scientists attempting the same analyses and less to uncover biases. Authors can only report on biases they already know about, and without the data, models and code, other scientists will be unable to discover issues post hoc.

For machine-learning models in the life sciences to become trusted, scientists must prioritize computational reproducibility[2]. That is to say that third parties should be able to obtain the same results as the original authors by using their published data, models and code. By doing so, researchers can ensure the accuracy of reported results and detect biases in the models.

Analyses and models that are reproducible by third parties can be examined in depth and, ultimately, become worthy of trust. To that end, we believe the life sciences community should adopt norms and standards that underlie reproducible machine learning research.

The menu

While many regard the computational reproducibility of a work as a binary property, we prefer to think of it on a sliding scale[3] that reflects the time needed to reproduce. Published works fall somewhere on this scale, which is bookended by 'forever', for a completely irreproducible work, and 'zero', for a work where one can automatically repeat the entire analysis with a single keystroke. As in many cases it is difficult to impose a single standard that divides work into 'reproducible' and 'irreproducible', we instead propose a menu of three standards with varying degrees of rigor for computational reproducibility (Table 1):

1. Bronze standard. The authors make the data, models and code used in the analysis publicly available. The bronze standard is the minimal standard for reproducibility. Without data, models and code, it is not possible to reproduce a work.
2. Silver standard. In addition to meeting the bronze standard: (1) the dependencies of the analysis can be downloaded and installed in a single command, (2) key details for reproducing the work are documented, including the order in which to run the analysis scripts, the operating system used and system resource requirements, and (3) all random components in the analysis are set to be deterministic. The silver standard is a midway point between minimal availability and full automation. Works that meet this standard will take much less time to reproduce than ones only meeting the bronze standard.
3. Gold standard. The work meets the silver standard, and the authors make the analysis reproducible with a single command. The gold standard for reproducibility is full automation. When a work meets this standard, it will take little to no effort for a scientist to reproduce it.

While reporting has become a recent area of focus[4–6], excellent reporting can look akin to a nutritional information panel. It describes information about a work, but it is insufficient for reproducing the work. In the best case scenario, it provides a summary of what the researchers who conducted

“Winner Gold, Silver, Bronze Medals” by Jernej Furman. CC BY 2.0.
https://www.flickr.com/photos/91261194@N06/51846593010/

Heil et al. 2021. *Nat Methods* 18:1132

Bronze standard 🥉

The minimum standard:

- **Data** published and downloadable
- **Models** published and downloadable
- **Code** published and downloadable

Silver standard

Bronze standard plus:

- **Dependencies** in single command+key **analysis details** recorded+**deterministic**

Gold standard

- Entire analysis reproducible with a **single command**

How do we make data sharing a priority?

Meaningful assessment improves research

- Promotes value of all scholarly outputs
  - Journal articles
  - Preprints
  - Datasets
  - Software
  - Protocols
  - Research materials
  - Well-trained researchers
  - Societal outcomes and policy changes
- Focuses on the merits of the work
  - Reduces JIF-chasing
  - Facilitates Open Science practices
  - Improves rigor and reproducibility
  - Enhances collaboration

DORA
Declaration of Research Assessment

https://sfdora.org/

Call to action

- **Your papers and grant apps:** point out your careful data sharing!
- Signal reproducibility practices important
  - **Paper reviews:** compare against standard
  - **Grant reviews:** commitment to standard
  - **Hiring:** ask for previous record

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May 30, 2017 (v2) | Dataset | Open

Mappability of the mouse and human genomes and methylomes with Umap and Bismap

Karimzadeh, Mehran; Ernst, Carl; Kundaje, Anshul; and 1 other

This dataset consists of single-read mappability (Bed files) and multi-read mappability (Wiggle files) of human and mouse genomes and methylomes (bisulfite-converted genome). We provide mappability information for the two most recent assemblies of each organism, and for four different read lengths (24 bp, 36 bp, 50 bp, and 100 bp).

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May 30, 2017 (v2) | Software | Open

Umap and Bismap: quantifying genome and methylome mappability

Karimzadeh, Mehran; Ernst, Carl; Kundaje, Anshul; and 1 other

The free Umap software package identifies uniquely mappable regions of any genome. Its Bismap extension identifies mappability of the bisulfite converted genome.

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Uploaded on May 30, 2017

1 more versions exist for this record

1464 122

October 10, 2018 (3.0.0) | Dataset | Open

Virtual ChIP-seq predictions of binding of 36 transcription factor in Roadmap Epigenomics Project tissues

Thank you!

Michael Hoffman

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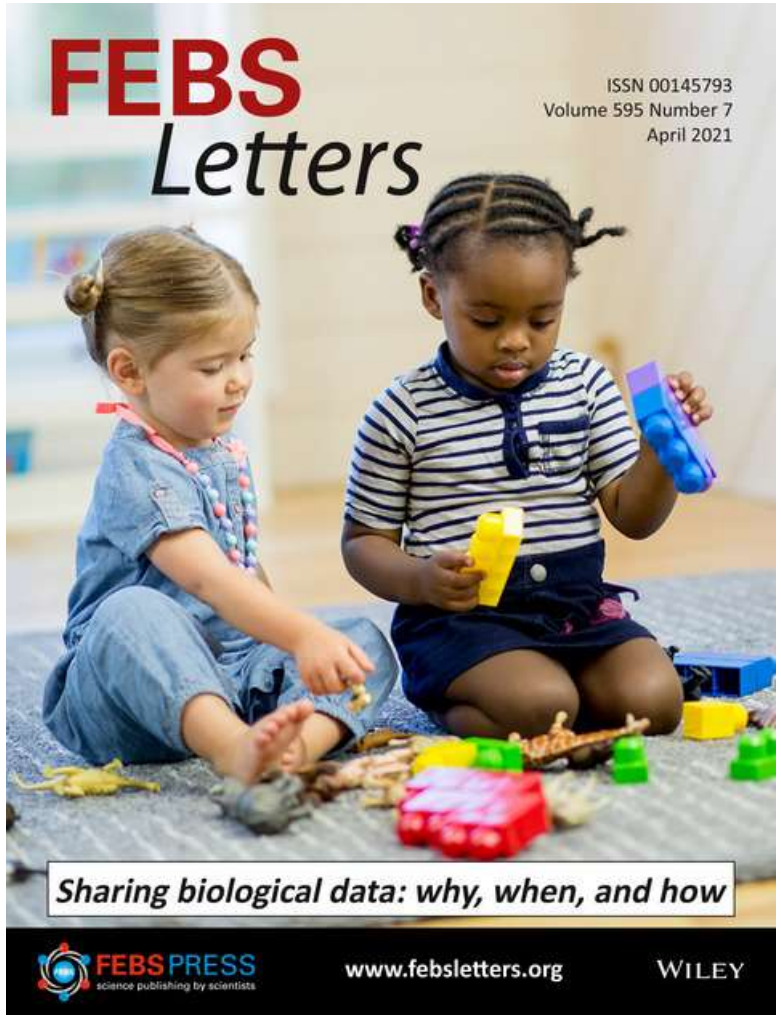

Wilson et al. 2021. *FEBS Lett* 595:845

Panel Discussion

Upcoming Event

Upcoming Event

Thank you!

- A link to the recording, presenter slides, and feedback form will be sent out after the session
- Follow-up questions can be addressed to cris@utoronto.ca