

# DATA REUSE IN AGRICULTURAL GENOMICS RESEARCH: Challenges, solutions, and a case study

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AgBioData Data Reuse WG

# MOTIVATION FOR DATA REUSE WG



Sequence-based datasets + WWW + Open Science movement  
□ a lot of data out there



No dataset is perfect



Data are often underutilized due to insufficient metadata and other challenges related to the FAIR data standards



**Objective for WG: to identify bottlenecks in data reuse and critical needs to propose solutions for agricultural genomics community**



**Personal objective: understand the lack of reusability of methylome data**



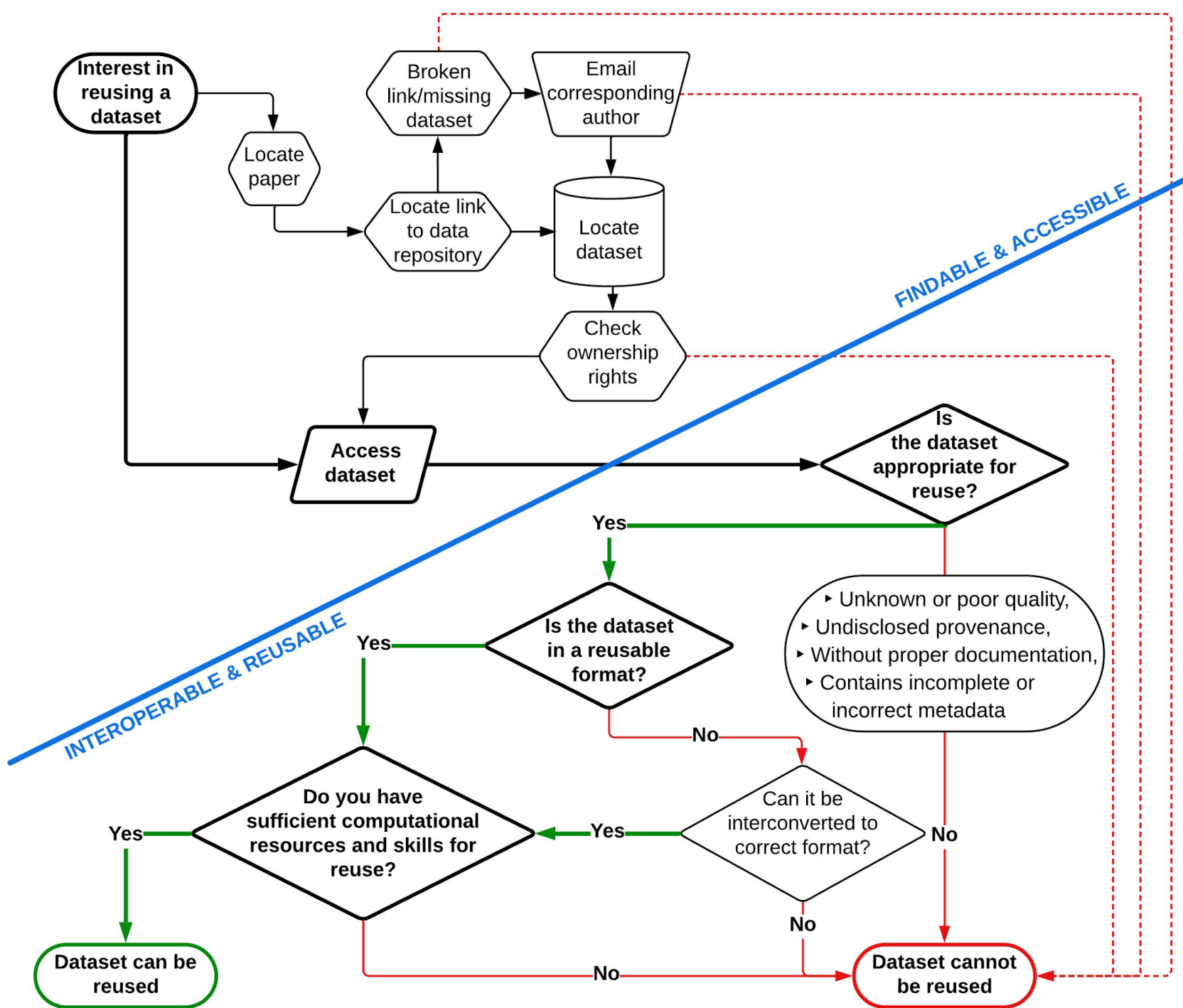
Barriers to  
data reuse and  
recommendations to  
overcome them

A case study of  
methyloome  
data reuse

The future of  
data reuse

**DATA REUSE =**

*the practice of utilizing existing data for  
a novel scientific purpose beyond their original scope*



# 1. BARRIERS TO DATA REUSE & RECOMMENDATIONS TO OVERCOME THEM



Data quality



Metadata



Data availability



Interoperability



Data ownership



User skill and  
resources



## DATA QUALITY: STANDARDS AS A SOLUTION

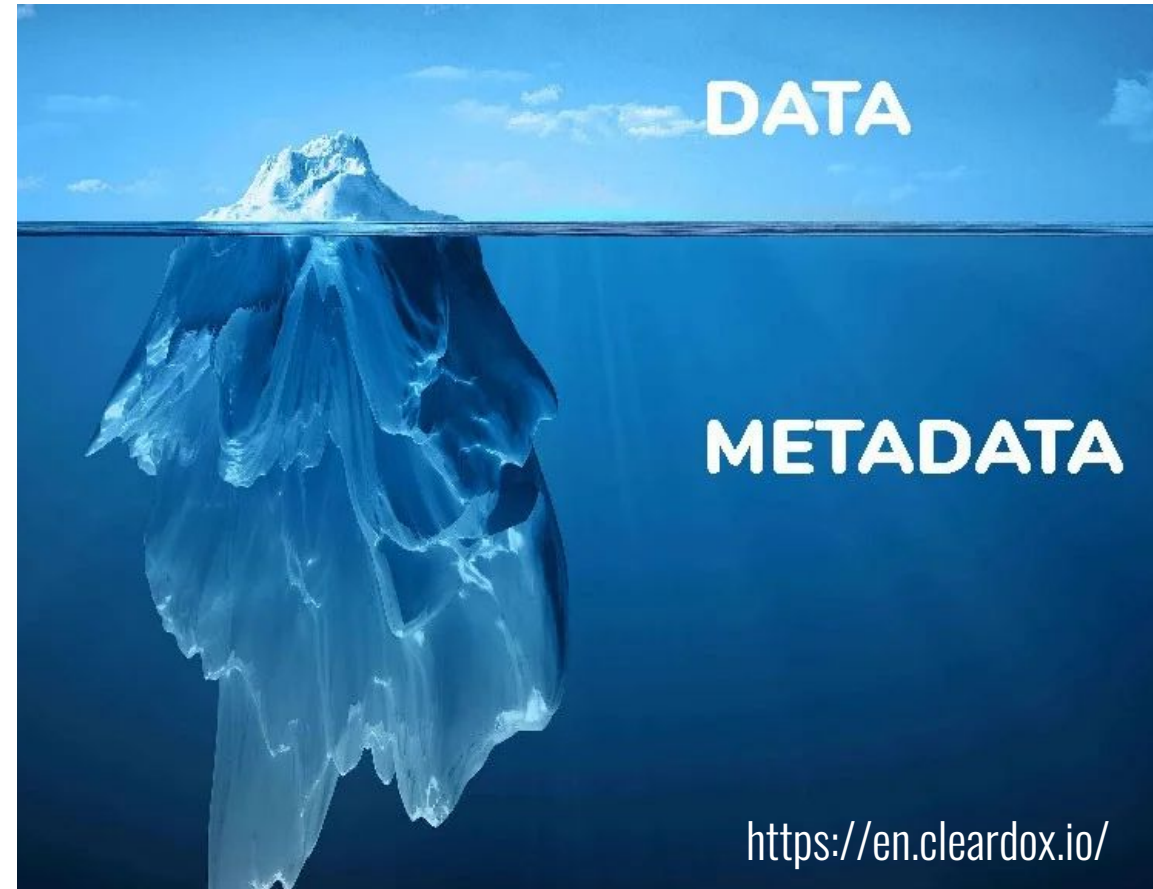
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- Data made publicly available regardless of quality  a (subjective) decision on suitability for reuse
- Factors to assess:
  - coverage,
  - depth,
  - technical and biological replication,
  - tissue type,
  - sample collection method,
- Limited scope of existing standards (even for common data types and organisms)
  - extraction method and library preparation,
  - sequencing technology,
- difficult to obtain experimental and computational protocols for informed reuse & meta-analyses
  - other dataset properties
- **More protocol, pipeline, and statistical standards needed in agricultural genomics field**



## ON THE ROAD TO COMPLETE METADATA: INCENTIVES

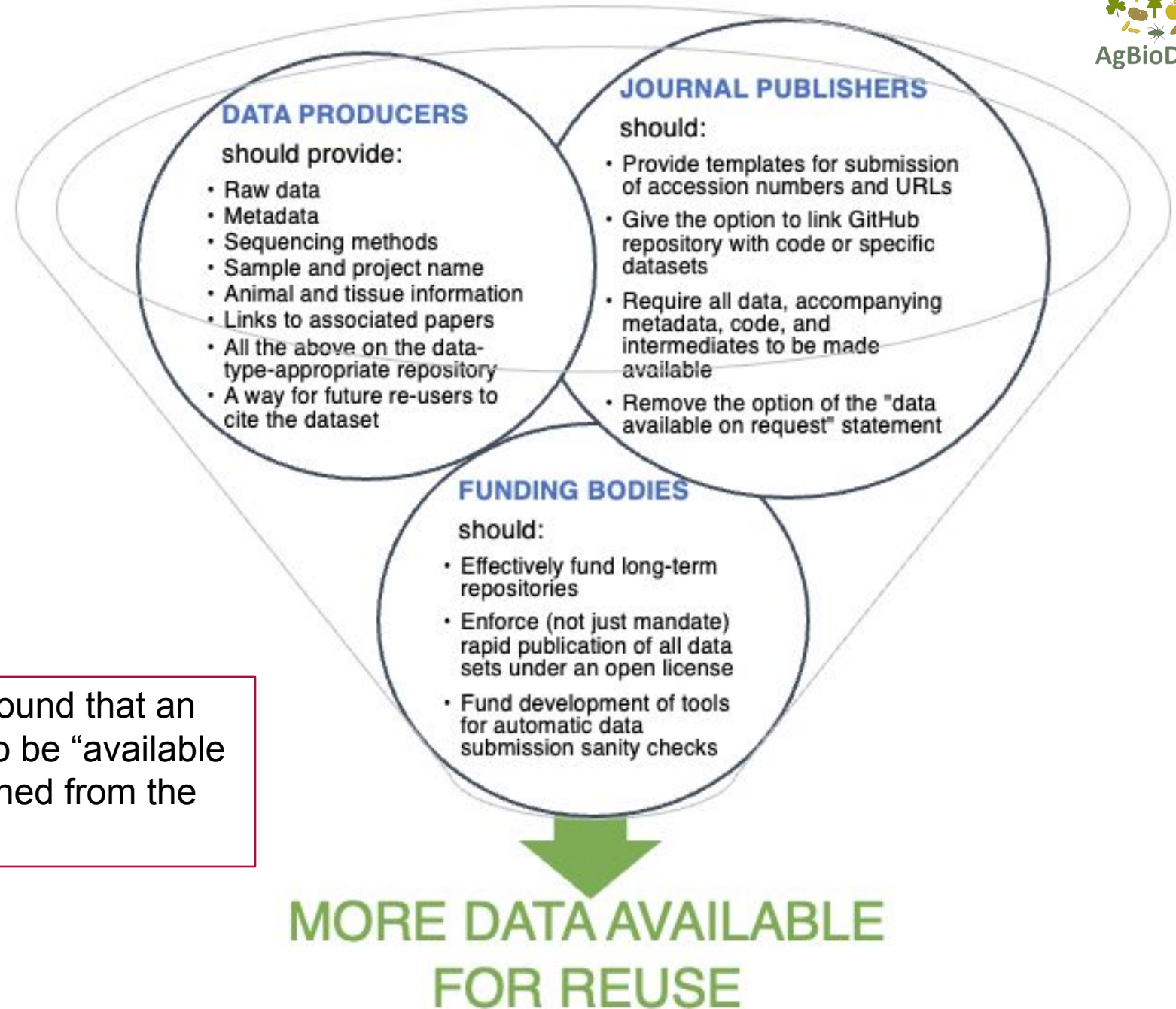
- Limited/incomplete/missing metadata submission templates
- Submission requires work  Trade-off between collecting all some metadata via a lenient submission system and mandating comprehensive metadata
- **Incentives are needed! E.g., data citations...**





# BRIDGING THE DATA AVAILABILITY GAP: A ROLE FOR ALL STAKEHOLDERS

Survey of *Science* and *Nature* in 2021 found that an alarming less than 50% of data stated to be “available upon request” could be effectively obtained from the original authors (Tedersoo et al., 2021)







## TOWARDS INTEROPERABILITY: DATA FORMATTING

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- Our community has converged on (meta)data standards for data file types:  
FASTQ, SAM/BAM, VCF, GTF, GFF3, BED, ...
- Issue: ~~lack of standards~~  consistency of use
- Reference genome mapping can be an issue down the line
- “Backwards compatibility”: outdated lab and sequencing methodology can be combated through extensive metadata (<https://www.protocols.io>)



## DATA OWNERSHIP & SHARING REQUIREMENTS

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- Challenge: Having access to relevant, affordable study populations from breeding companies that can also be shared publicly as sequence or genotype data
- **Already many sharing requirements + 2026 mandate to make research funded by the USA government publicly available**



## USER SKILL LEVEL & RESOURCE AVAILABILITY

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- A recent study (LaFlamme et al., 2022) shows **that skill or perceived ability** was identified by many participants as a **major factor** influencing reuse behavior.
- 2017-2018 global survey: most scientists exhibited “**high and mediocre risk data practices**” (Tenopir et al., 2020).
- US-based institutions: computational resources likely not the limiting factor  it's skill level
- **Education programs** for awareness-raising and good practice training needed
- **Incentives (!):**DataWorks! Prize (<https://www.herox.com/dataworks>)

## 2. A CASE STUDY OF METHYLOME DATA REUSE

- Sample provenance
- Type of replicate

- Consistency of formats
- .pdf

- Computational resources
- Barrier of entry

Data quality

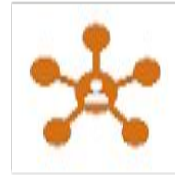
Metadata

Data availability

Interoperability

Data ownership

User skill and resources



- Depth of sequencing
- Experimental design
- Tissue type
- **REPLICATES!**

- Pipeline intermediates
- Code
- "Available on request"
- .pdf

- Crops?

Hafner, A., Mackenzie, S. Re-analysis of publicly available methylomes using signal detection yields new information. *Sci Rep* **13**, 3307 (2023).

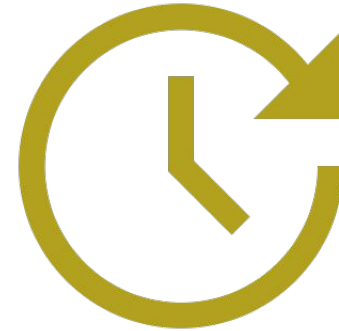
<https://doi.org/10.1038/s41598-023-30422-4>



### 3. THE FUTURE OF DATA REUSE



The importance and benefits of equity and inclusion



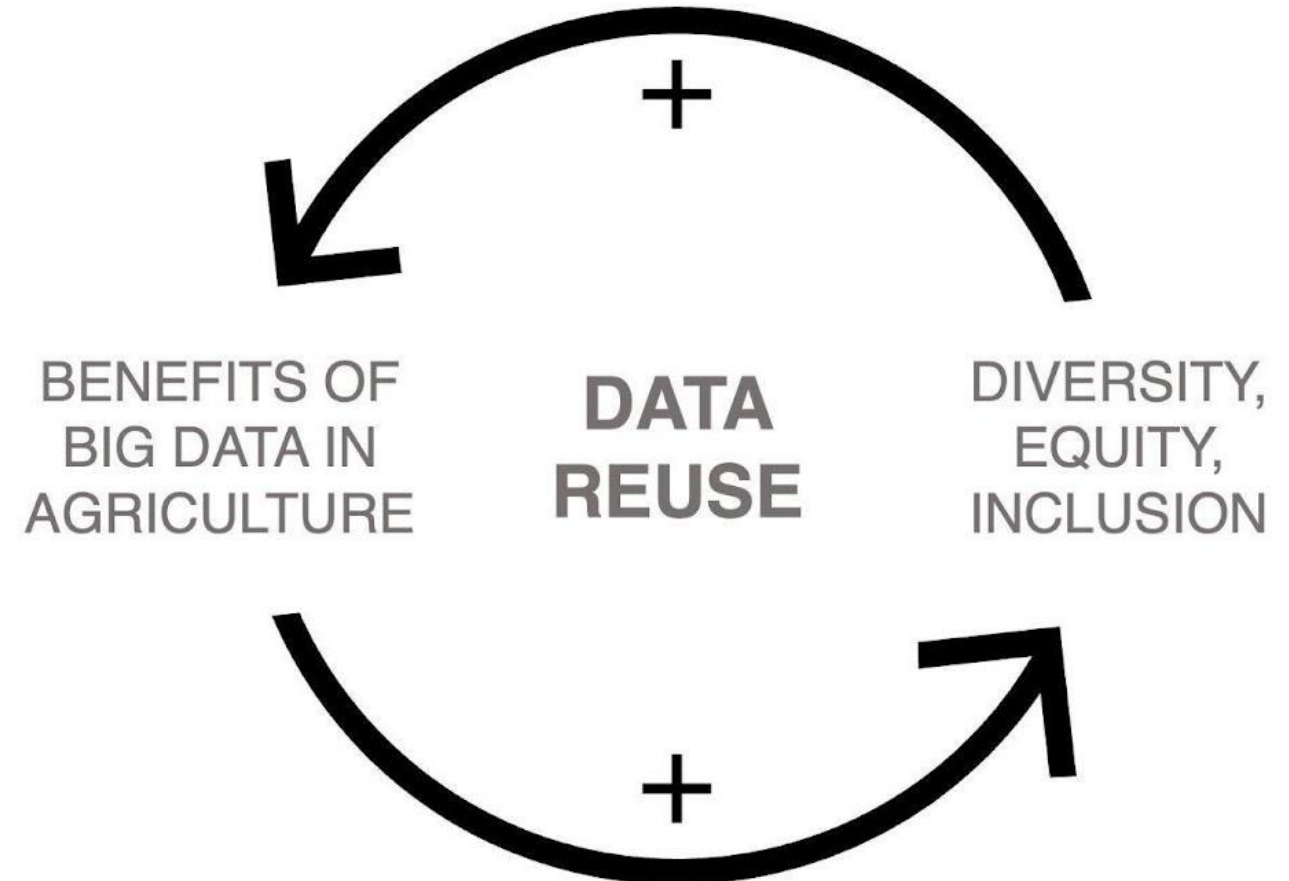
Take-aways and looking ahead



# THE IMPORTANCE AND BENEFITS OF EQUITY AND INCLUSION

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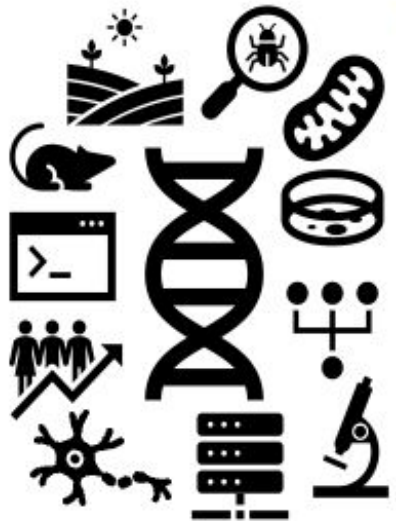
- *Diversity breeds innovation*
- Reuse requires computational capacity, internet access, digital literacy, and proficiency in dominant languages
- Data sovereignty: <https://localcontexts.org>





# TAKE-AWAYS AND LOOKING AHEAD

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## **BARRIERS & LIMITATIONS:**

- Data quality & standards
- Missing metadata
- Interoperability
- Data availability
- Ownership
- Skills & resources

***The future of data reuse  
is bright and exciting!***

- Integration of datasets
- Emerging data types:  
phenomes, metabolomes, proteomes,  
interactomes, enviromes, microbiomes,  
lipidomes, and glycomes
- AI and ML

# WG's white paper

**James Koltes**, Iowa State University (WG chair)

**Alenka Hafner**, Penn State University (WG co-chair)

**Victoria DeLeo** - Bowery Farming

**Cecilia Deng**- The New Zealand Institute

for Plant and Food Research Limited

**Christine G. Elsik** - University of Missouri

**Damarius Fleming**, USDA

**Peter W. Harrison**, European Bioinformatics Institute

**Ted Kalbfleisch**, University of Kentucky

**Bruna Petry**, Iowa State University

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<https://doi.org/10.20944/preprints202401.0780.v1>