

# FAIRness and Usability for Open-access Omics Data Systems

**S50: User-centered Design** 

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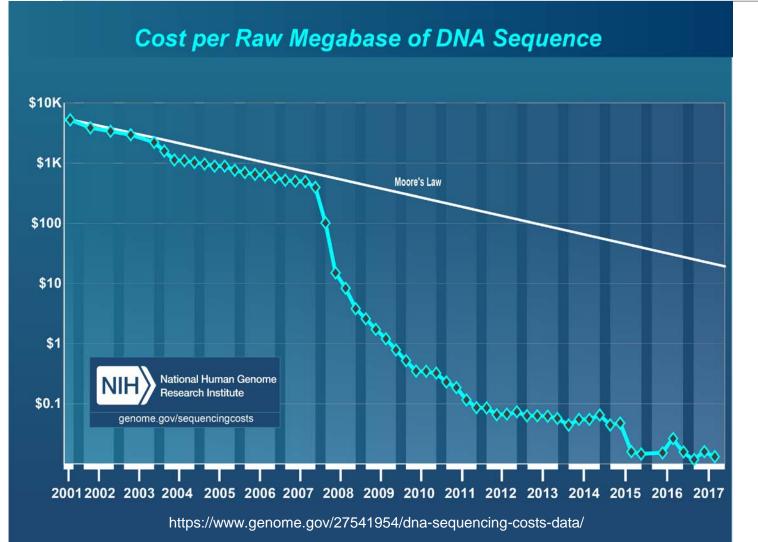




- Introduction: Omics Data & Data Systems, FAIRness
- Methods: Metrics, Raters, Systems Rated
- Results
  - Findability
  - Accessibility
  - Interoperability
  - Reusability
- Conclusions
- \* No relevant financial disclosures

# **Trajectory of Sequence Data Generation**





Cost of sequencing data acquisition falling precipitously

Continued development of even more high-throughput sequencing applications and techniques

- Single-cell omics (e.g., scRNA-Seq)
- Spatial transcriptomics
- Epigenetic applications: Epigenomics, Epitranscriptomics, Proteogenomics

Inundation of the biomedical community by omics data unlikely to abate

Developers are increasingly focused on the needs of users to discover, annotate, share, and analyze omics

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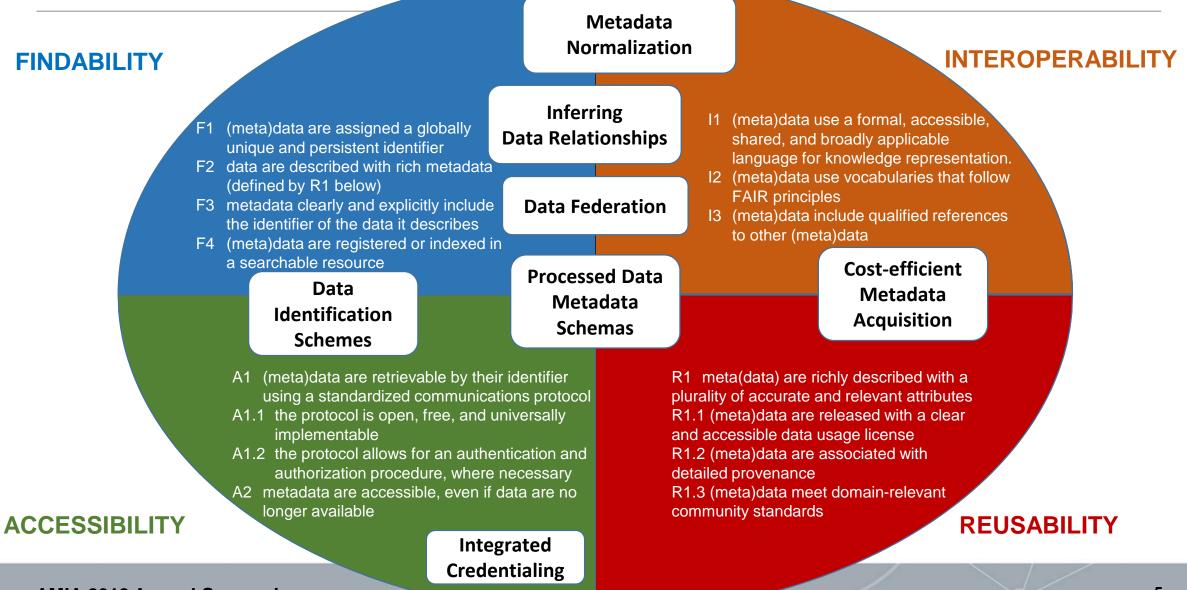
## **Omics Data Systems Multiplying**



BaseSpace Arvados GenomeSpace INSDC Databases MG-RAST Metabolights BlueBee Many, many, more...

### **The "FAIR" Principles**



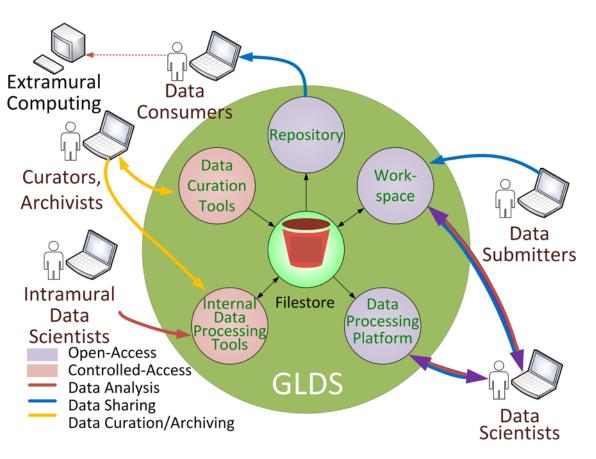


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## NASA GeneLab Data Systems (GLDS)

- Single platform for Omics data archiving, sharing, and analysis
  - Diversity of users: citizen scientists, students, educators, NASA-funded PIs, other investigators
  - Diversity of usage: data browsing to data analysis, data submission, data set curation
  - Open access, with private data option (for prepublication)
- Seeking best practices for complying with FAIR principles
  - Identify costs of implementing, particularly "trailblazing" system features
  - Identify widely vs. rarely compliant principles









- Assess the "FAIRness" of 4 systems in the research omics data domain
- Compare FAIRness with that of the GLDS
- Gather knowledge of technical and cost challenges for FAIR compliance
- Incorporate this knowledge in GLDS designs

### **Methods**

### 5 Omics Data Systems, similar to GLDS

- Data archiving capabilities
- Open access
- Government-operated or government-funded, research lab-developed

### 14 candidate FAIRness metrics

- 5 Findability, 3 Accessibility, 3 Interoperability, 3 Reusability
- Developed by the FAIR Metrics Group (<u>http://fairmetrics.org/</u>)



#### NCBI GEO

**MG-RAST** 

ENA European Nucleotide Archive





### Methods Cont'd

#### 3 Raters

- PASS (1): No evidence of failure of any test, for any input
- PARTIAL PASS (0.5): Failure of some, but not all tests, or test steps/components
- FAIL (0): No evidence of compliance to the principle, for any inputs tested

### Consensus

 Individually-assessed ratings combined through dialogue among the raters until consensus reached





**MG-RAST** 

ENA European Nucleotide Archive



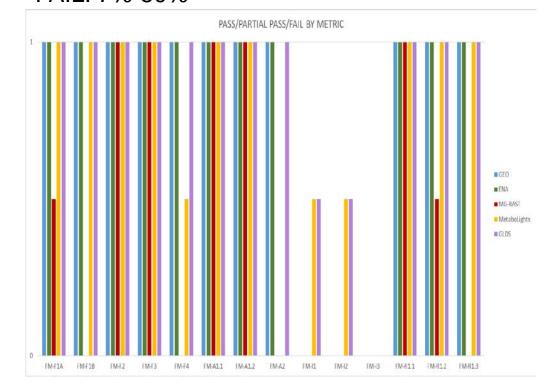






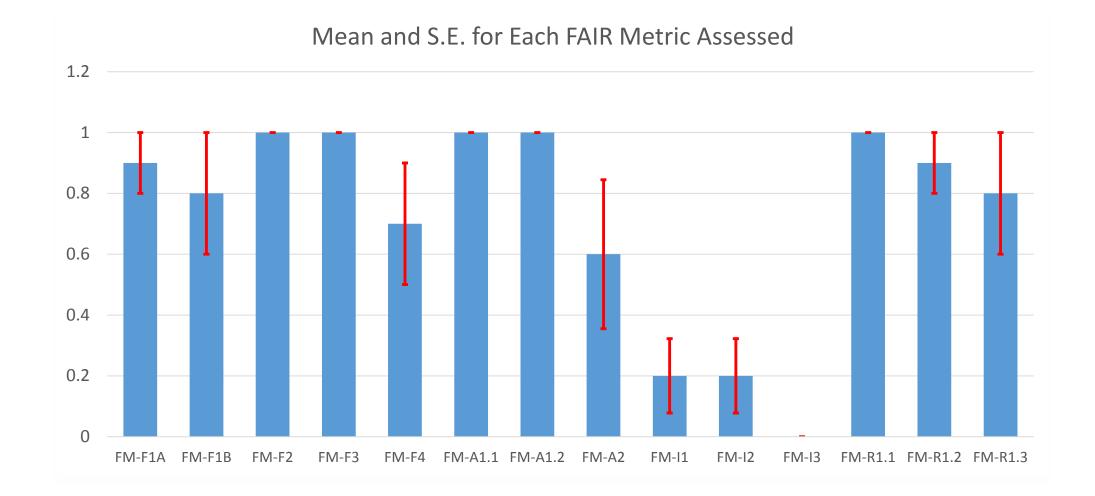
<ul> <li>Pass</li> <li>Partial pass</li> <li>Fail</li> </ul>	Metric	GEO <sup>4</sup>	ENA <sup>7</sup>	MG-RAST <sup>6</sup>	Metabolights <sup>8</sup>	GLDS
F1. (meta)data are assigned globally unique and persistent identifier	FM-F1A			0	$\bullet$	
F1. (meta)data are assigned globally unique and persistent identifier	FM-F1B			0	•	
F2. data are described with rich metadata (defined by R1 below)	FM-F2					
F3. metadata clearly/explicitly include identifier of data it describes	FM-F3				•	
F4. (meta)data are registered or indexed in a searchable resource	FM-F4			0	0	
A1. (meta)data are retrievable by identifier using a standardized communications protocol	N/A					
A1.1 the protocol is open, free, and universally implementable	FM-A1.1				•	
A1.2 the protocol allows for an authentication and authorization procedure, where necessary	FM-A1.2	•	•	•	•	•
A2. metadata are accessible, even when data are no longer available	FM-A2			0	0	•
<ol> <li>(meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.</li> </ol>	FM-I1	0	0	0	0	•
I2. (meta)data use vocabularies that follow FAIR principles	FM-I2	0	0	0	0	0
I3. (meta)data include qualified references to other (meta)data	FM-I3	0	0	0	0	0
R1. meta(data) are richly described with a plurality of accurate and relevant attributes	N/A					
R1.1. (meta)data released with clear, accessible data usage license	FM-R1.1					
R1.2. (meta)data are associated with detailed provenance	FM-R1.2	•	•	0		•
R1.3. (meta)data meet domain-relevant community standards	FM-R1.3			0		
Overall FAIRness Score		11	11	6	10.5	12

Range of FAIRness Scores (all systems) PASS: 29-79% PARTIAL PASS: 0-21% FAIL: 7%-50%



### **Results**





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FM-F1A: Data identifier uniqueness

#### FM-F1B: Data identifier persistence

- URIs/IRIs were not designed to be persistent, but are being used as if they were
- DOIs were, yet as still not widely used for Data Citation
- GeneLab Data Systems will employ DOIs using in-house DOI services

FM-F4: Submit metadata to data search engines

# ACCESSIBILITY



- Integrated credentialing and authentication ("single sign-on") are valuable for users, yet not common
- GeneLab Data Systems employing Google or Agency credentials for logins





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#### Data transport is frequently required by omics data analysis systems

- Can require minutes to hours to move data into analysis environment
- Would be of value to have a FAIR principles for data location/transport

A1.2.1	Authentication protocols should support multiple credential providers
A3	Data transport should be minimized



All systems lacking interoperable metadata (and data)

- Lack of metadata schemes grounded in formal semantics (DL languages like RDF/OWL/etc.)
- Some use ISA-Tab, which has at least been modeled in RDF, although they do not represent metadata in RDF
- Community-derived, controlled vocabularies usage uncommon
- Semantic linkage of data through metadata also uncommon





- All the omics systems assessed had some FAIRness shortcomings
- Un-FAIRness in areas that support data interoperability is common
  - Lack of metadata representations with formalized semantics
  - Lack of use of FAIR vocabularies
  - Low prevalence of semantic normalization, perhaps due in part to
    - High costs of manual semantic normalization
    - Lack of automated semantic normalization resources
  - Impedes the development of functions relying on system-system interoperability

## **Acknowledgements**



#### NASA GeneLab Team

Jon Galazka Sigrid Reinsch Homer Fogle Sam Gebre

To see a system demonstration of NASA GeneLab:

NASA's GeneLab: An Integrated Omics Data Commons and Workbench S64: Ontology Driven Health Information Systems Architectures Tuesday, November 6, 2018 9:00 AM Yosemite A/B

**FAIR Metrics Group**