AgBio Databases & FAIR Principles

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* With slides by Lisa Harper, Leonore Reiser & members of the AgBioData Consortium

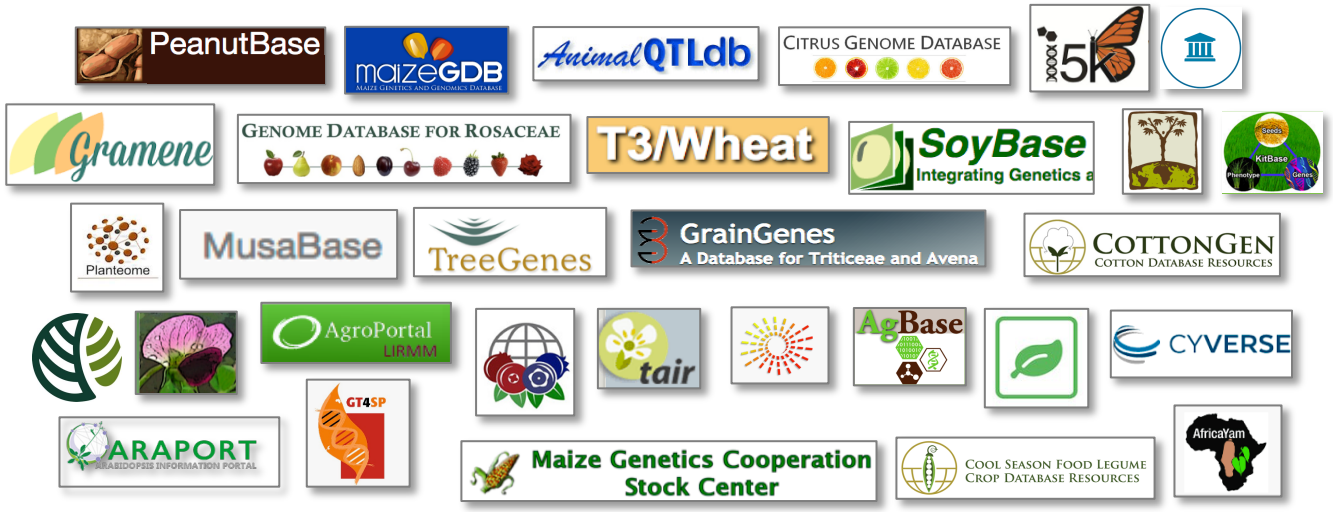
Data & Databases

- Proper **data management** is critical for scientific discovery and reproducibility
  - Acquiring, validating, storing, protecting, and processing *data* to ensure the accessibility, reliability, and timeliness of the *data* for its users
- **Databases** are physical entities to store and organize these data so that it can be easily accessed, *managed* & shared
- What are the **FAIR data principles** & why should you care?
- **Bioinformatics** resources for cereal crops

The AgBioData Consortium

=> Improve handling of data in AgBio databases via collaboration, communication, and developing recommendations & standards.

Comprised of > 100 members from >30 databases



https://www.agbiodata.org/databases

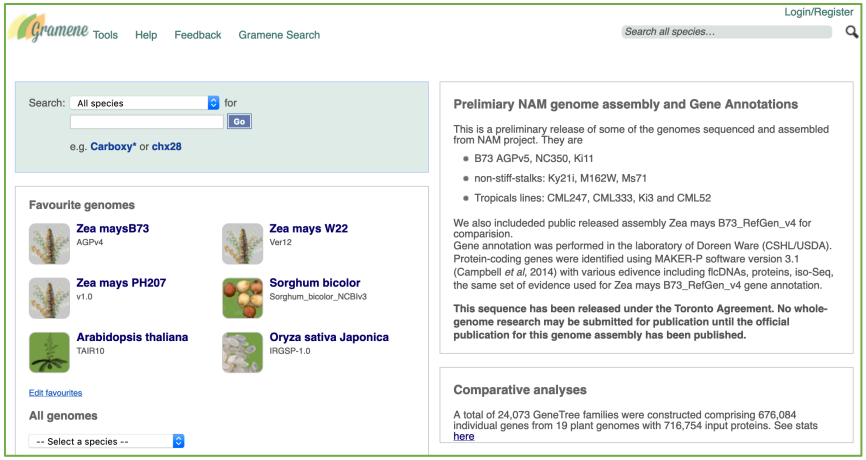
Structural & functional annotation via GO, SO (maize, rice) → **AgBase***
Ag ontologies → **AgroPortal***
Alfalfa Breeder's Toolbox
Arabidopsis Biological Resource Center
Animal QTLdb
AraPort
Bovine Genome Database
CassavaBase
Citrus Genome Database
Cool Season Food Legume Database
CottonGen
CyVerse*
Genome Database for Rosaceae
Genome Database for Vaccinium
Wheat, barley, oat → **GrainGenes**
Comparative genomics & pathways → **Gramene**
Germplasm resources → USDA-ARS **GRIN***
Hardwood Genomics
Hymenoptera Genome Database
i5K National Ag Library
Rice mutants → **KitBase**
Legume Information System
MaizeGDB
Maize Stock Center
MusaBase
National Animal Disease Center
PeanutBase
Plant ontologies → **Planteome***
PulseCrop
Solanaceae Genomics Network
SoyBase
SweetPotatoBase
Triticeae (wheat, barley) & oat → **T3**
TAIR
TreeGenes
WheatIS
YamBase

Species-specific:

MaizeGDB https://www.maizegdb.org

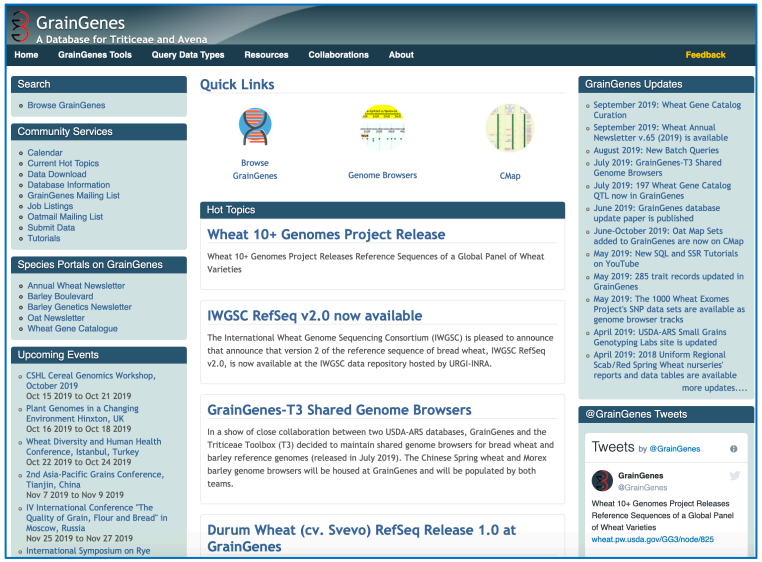
Pan-species:

PanMaize
http://maize-pangenome-ensembl.gramene.org



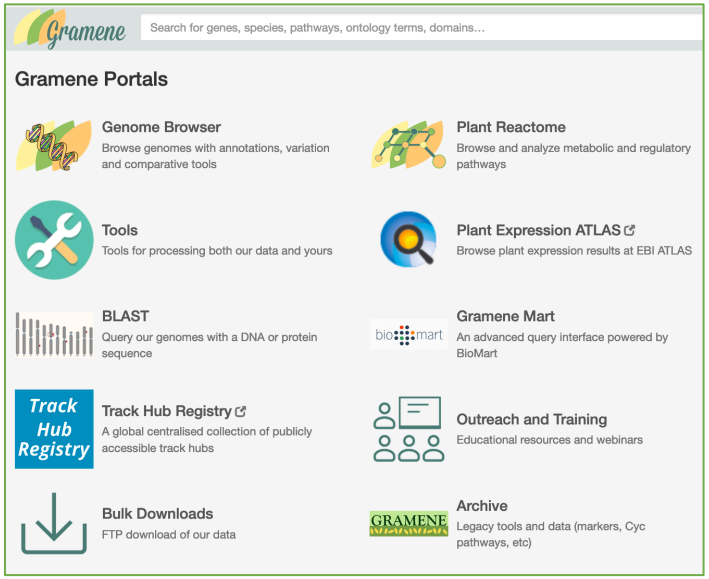
Clade-specific:

GrainGenes https://wheat.pw.usda.gov/GG3



Comparative multi-species:

Gramene http://www.gramene.org



Maize
Sorghum
Rice (12)
Wheat (4)
Barley
Fox millet

agbiodata.org

AgBioData

Toward enhanced genomics, genetics, and breeding research outcomes through standardization of practices and protocols across agricultural databases

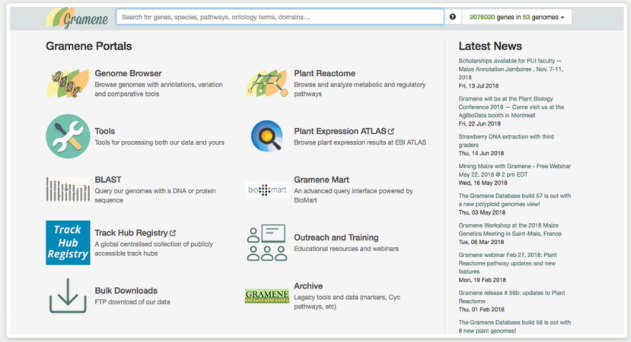
Home | About Us | Databases | Working Groups | Meetings | Forums | Contact us | Search

To cite AgBioData, please use: Harper, L. et al. (2018) AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database, 2018 1-32.

Welcome to AgBioData

AgBioData is a consortium of agricultural biological databases and associated resources working together to ensure standards and best practices for acquisition, display and retrieval of genomic, genetic and breeding data.

Participating Databases and Resources



News & Events

November AgBioData Conference Call
Discussion about the future of agricultural GGB databases ...
Posted: 10/02/2019

October AgBioData Conference Call
Join us for our October AgBioData conference ...
Posted: 09/12/2019

Recordings of conference calls available
Don't worry if you missed a conference call ....
Posted: 09/05/2019

September AgBioData Conference Call
Join us for our September AgBioData conference ...
Posted: 08/20/2019

August AgBioData Conference Call
Join us for our August AgBioData conference ...
Posted: 08/03/2019

June AgBioData Conference Call
Join us for our June AgBioData conference ...
Posted: 05/09/2019

May AgBioData Conference Call
Join us for our April AgBioData conference ...
Posted: 04/07/2019

More

User Login

Username or e-mail *

Password *

- Create new account
- Request new password

Log in

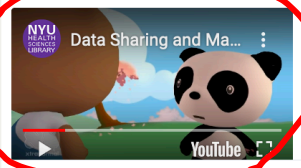
Tweets by @AgBioData

AgBioData
@AgBioData

#DataSharing and #datamanagement
Snafuyoutu.be/66oNv_DJuPc

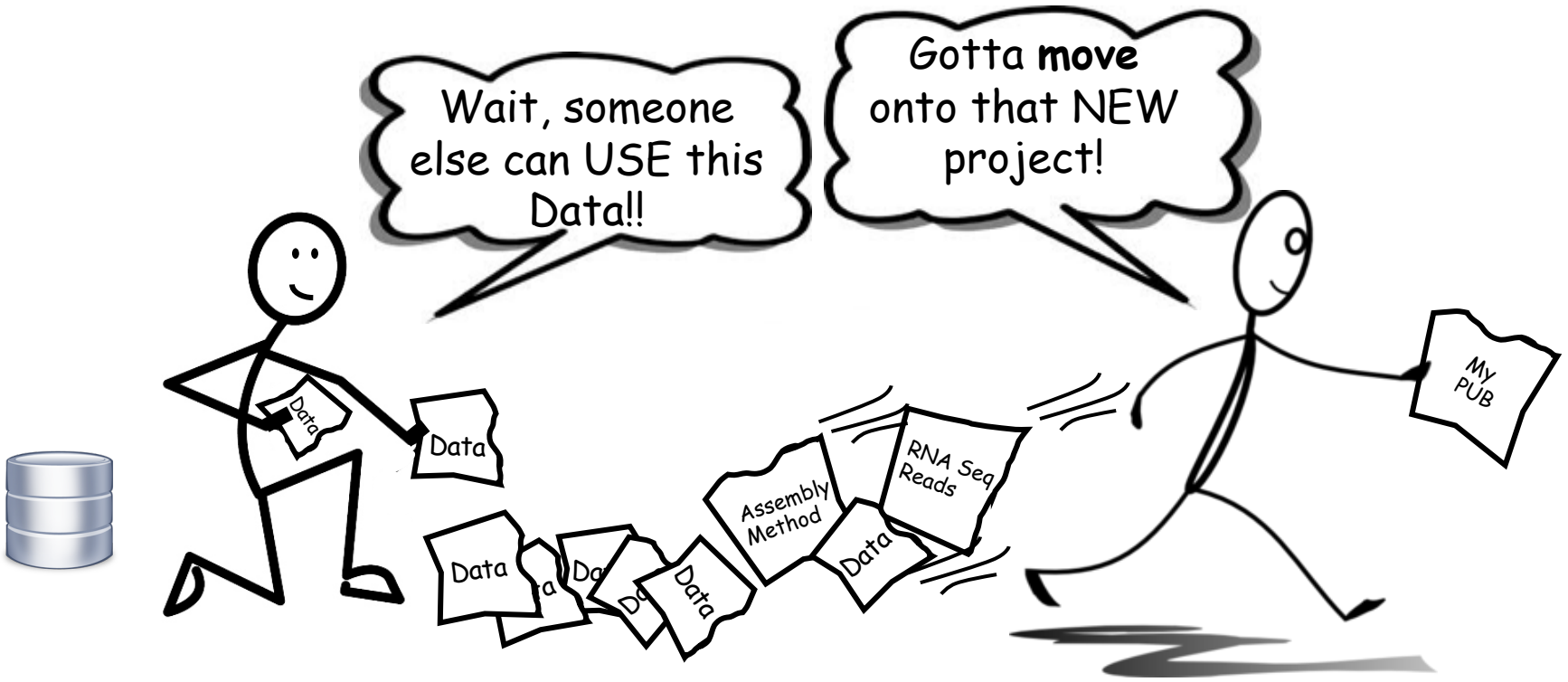
No properly described datasets whether deposited or supplemental, and the lead author may have ... returned to China ... and maybe named Sam Lee

YouTube @YouTube

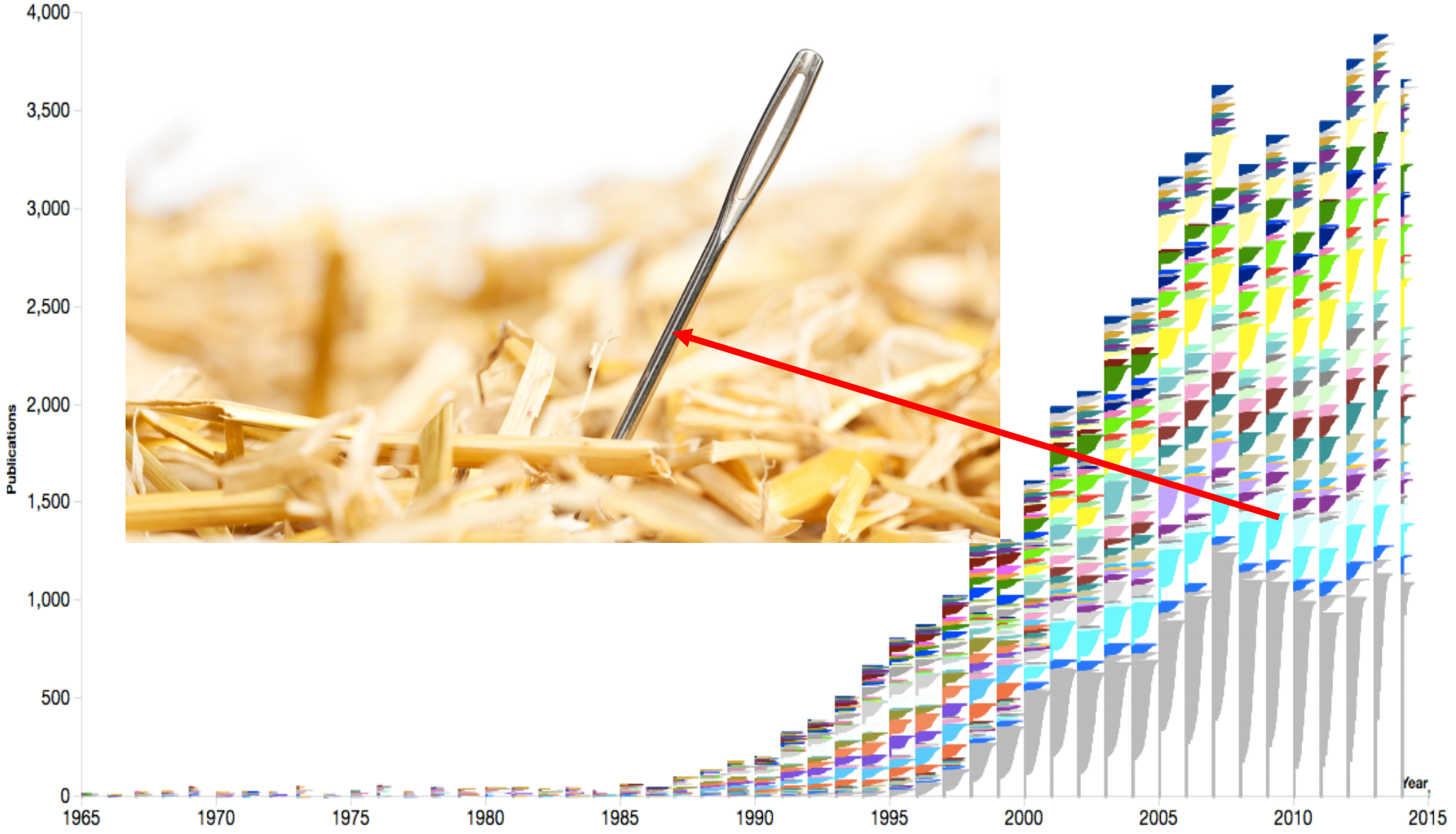


Data Sharing and Management
Snafu in 3 Short Acts

Databases TODAY…



Publications are increasing exponentially



http://bar.utoronto.ca/50YearsOfArabidopsis/

What can YOU do to make your data more visible, persistent and reusable to better support research?

Tips adapted from Lisa Harper (Maize Genetics Conference 2019)

Data LifeCycle

Making data

F indable,
A ccessible,
I nteroperable, and
R e-usable

https://www.force11.org/group/fairgroup/fairprinciples

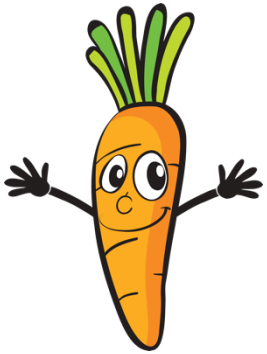
Make your Data FAIR

- **Findable** means data is human and machine readable and attached to persistent identifiers
- **Accessible** means data can be found and retrieved by humans and machines using standard formats
- **Interoperable** means data can be exchanged and used between systems.
- **Reusable** means data can be used by others

Wilkinson, et al., (2016) The FAIR Guiding Principles for scientific data management and stewardship. https://www.nature.com/articles/sdata201618

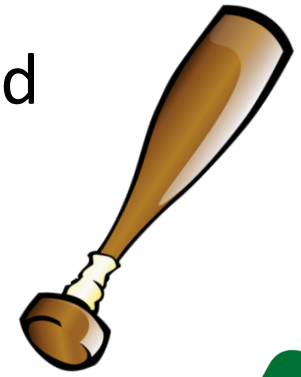
Credit: Melissa Haendel

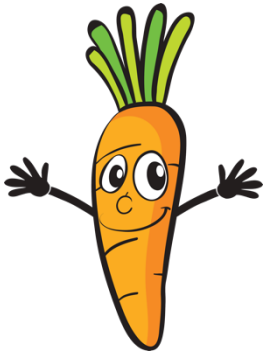
What's in it for YOU?



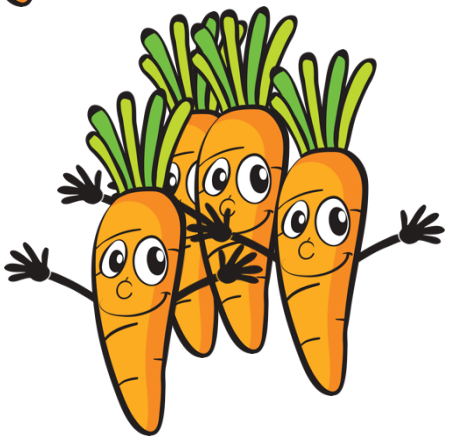
More citations of YOUR work, increasing your visibility in the research community.

Easily comply with journal and funding requirements.





Less time spent fulfilling requests for data.



We all benefit from data sharing -- higher rated Grants and Publications (and hopefully promotion)

How to Make Your Published Data FAIR

- Use standard formats
- Supply complete **metadata**
- Embrace ontologies
- Use persistent and unambiguous identifiers
- Put your data in a long-term stable repository
- Cite, share freely and encourage others

1. Understand “Machine Readable”

This IMAGE of a table is NOT Machine Readable
(Published March 12, 2019 in PLOS one)

Species	Ensembl Plants Id's	Gene		cDNA		CDS	
		Length in bp (chr. no.)	Similarity (%)	Length in bp	Similarity (%)	Length in bp	Similarity (%)
Monocots							
Z. mays	Zm00001d043442_T001	3522 (3)	100	2191	100	1719	100
T. aestivum -A sub-genome	TraesCS3A02G274300	3732 (3)	65.98	2196	78.44	1683	87.19
- B sub-genome	TraesCS3B02G308000.1	3748 (3)	63.95	2210	77.82	1683	86.71
-D sub-genome	TraesCS3D02G273500.1	3718 (3)	65.42	2196	79.33	1683	86.77
T. urartu	TRIUR3_28465-T1	2088 (3)	75.81	1404	80.84	1404	80.84
Ae. tauschii	EMT16146	3172 (3)	72.06	1524	85.31	1524	87.53
O. sativa	OS01T0746400-00	3109 (1)	72	1710	87.66	1710	89.05
B. distachyon	BRADI2G49670.1	3577 (2)	68	2140	80.13	1713	86.23
S. bicolor	Sb03g034400.1	3545 (3)	75.91	1867	91.48	1740	94.76
Dicots							
A. thaliana	AT4G32810.1/Max4	3265 (4)	52.8	2026	56.59	1713	61.99
G. max	GLYMA06G09000.2	3891 (6)	52.72	2049	60.53	1692	65.88
V. vinifera	VIT_04s0008g03380.t01	2823 (4)	58.83	1782	64.65	1641	67.59
S. lycopersicum	Solyc08g066650.2.1	3075 (8)	52.36	1907	57.96	1674	61.56
T. cacao	EOY29749 (TCM_037195)	3680 (9)	52.04	2051	58	1680	63.75
P. trichocarpa	POPTR_0006s25490.1	3983 (6)	54.84	1674	63.79	1674	64.84
P. persica	EMJ23585 (PRUPE_ppa006042mg)	2893 (1)	56.11	2436	58.41	1296	67.28
M. truncatula	AES73861 (MTR_3g109610)	3439 (3)	52.31	2057	57.35	1698	63.28

https://doi.org/10.1371/journal.pone.0213531.t001

1. Understand “Machine Readable”. Using Standard Formats (SNP example)

SNP: A chromosome number and genome position, an alternative allele relative to the allele in the reference genome used, and the genotypes of the lines tested.

CHROM	POS	REF	ALT	Line 1	Line 2
Chr01					A
Chr03					C
Chr10					U

CHROM	POS	REF	ALT	Line 1	Line 2
Gm01	12345	A	C	0/0	0/0
Gm03	67891	C	T	0/1	0/0
Gm10	23456	G	T	1/1	./.

Use the File format STANDARD for your data type

VCF: Variant Call Format is the STANDARD

Note: PDF images are not findable or accessible. Use tables but beware of Excel (e.g., hidden characters)

1. Understand “Machine Readable”

This Bar Code and QR Code are Machine Readable but NOT human readable

Wilkinson et al (2016).
FAIR Data Principles. *Nature*

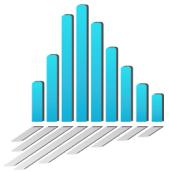
2. Put Data in the right repository

Data goes into Data repositories:

- Nucleotide sequences

Plant SNPs → European Variation Archive

- Protein/Proteomics/Metabolomics



MetaboLights

- General Repositories

Get a DOI

- Not sure?

re3data.org
REGISTRY OF RESEARCH DATA REPOSITORIES

FAIRsharing.org
standards, databases, policies

Journals

nature
International weekly journal of science

PLOS

Contact YFD

3. Supply Complete Metadata

Metadata = Information about the data

Data (Phenotype): Plant is 170 cm tall

Metadata:

Species = xxx
Germplasm = xxx
Age = xxx
Dev. Stage = xxx
Field location = xxx
Environment = xxx
Measurement method = xxx

Data without Metadata is NOT FAIR

Use ontologies!

Same word, different meanings

Cell

Different words, same concept

Berenjena

Eggplant

Aubergine

Ontologies to the rescue!

Controlled Vocabulary
Hierarchy of terms & explicit relationships among them, understood by computers

3. Supply Complete Metadata

Metadata = Information about the data

- Supply enough Metadata so that your experiment can be accurately reproduced
- Use community Standards for your data type. Examples:
  - MIxS: Minimal Information about any Sequence
  - MIAPPE: Minimum Information About a Plant Phenotyping Experiment
- Use Ontologies (GO, PO, TO, EO)
- Don't Know? Ask us!

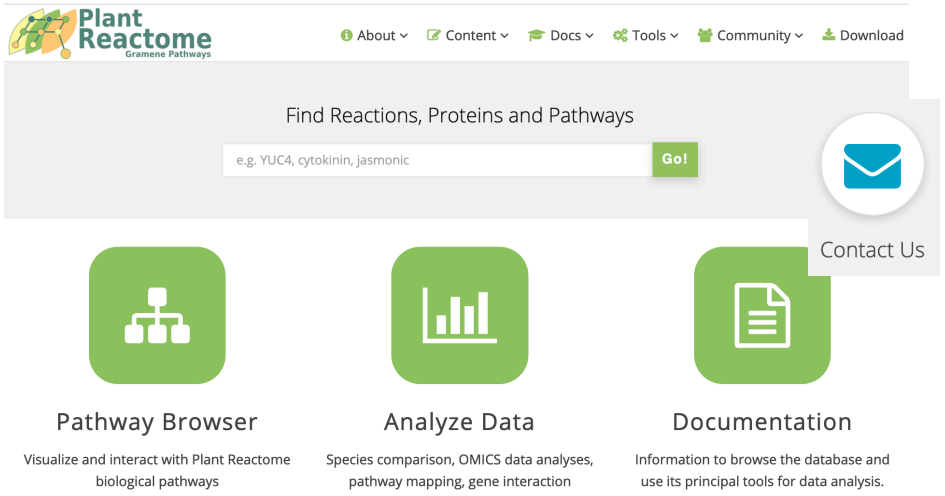
MIxS

MIAPPE

Budget TIME to provide Metadata

5. Check Standards Set Forth by Species Communities – Let Curators Know About Your Work

- Don’t RE-name genes! Check out gene nomenclature standards for your species
- If you have published on a gene or genes – Let Curators Know
- If you have a dataset that will be useful to others – Let your Community DB Know



The FAIR Data Principles

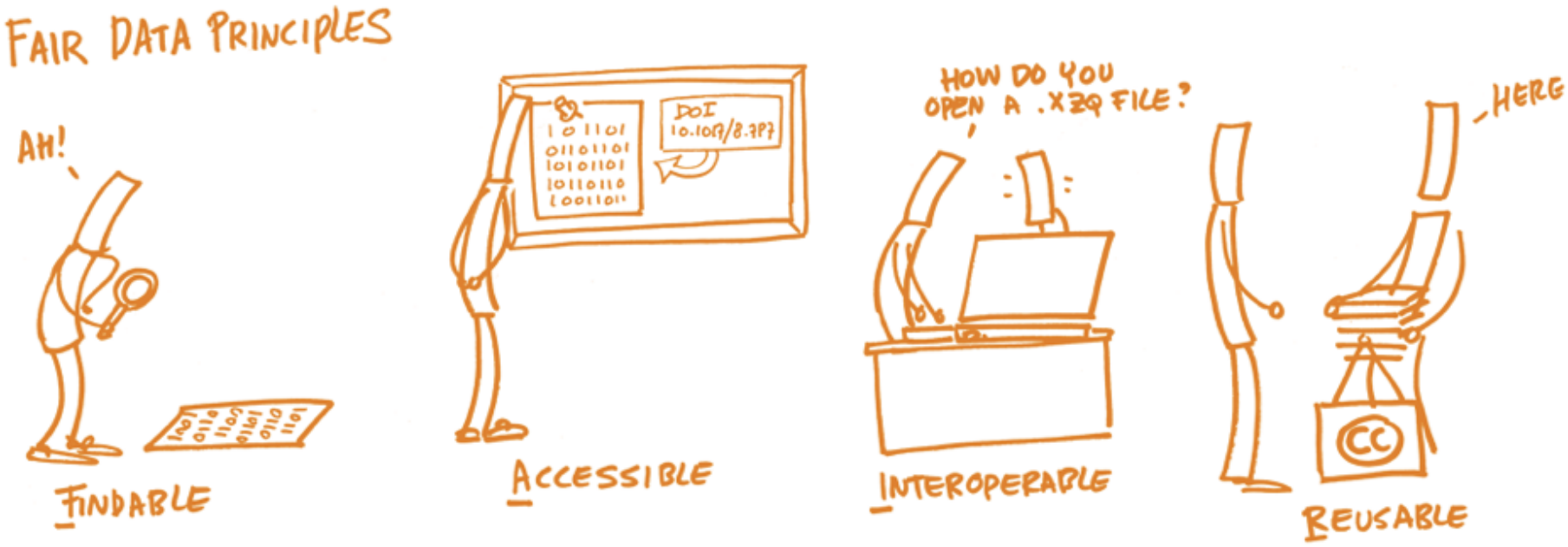
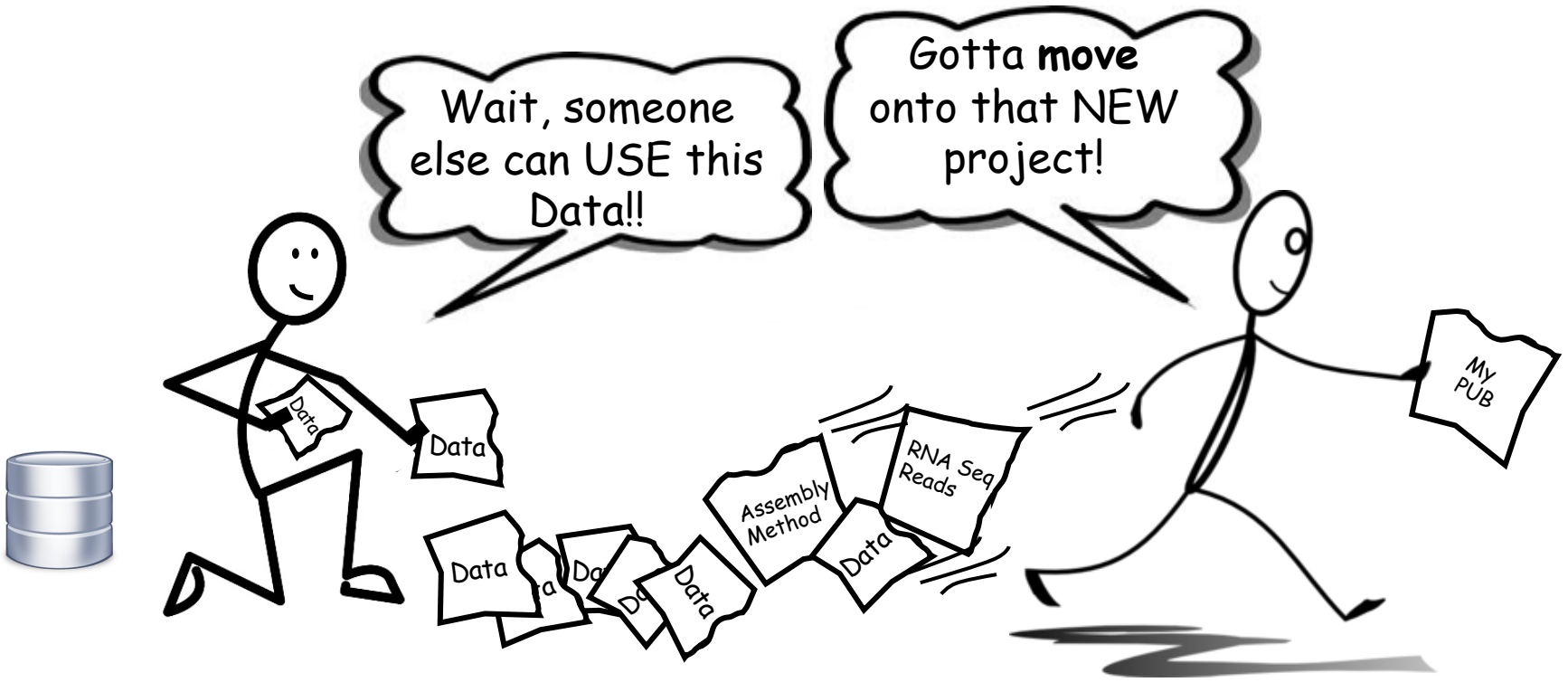


Image source: https://www.openaire.eu/how-to-make-your-data-fair

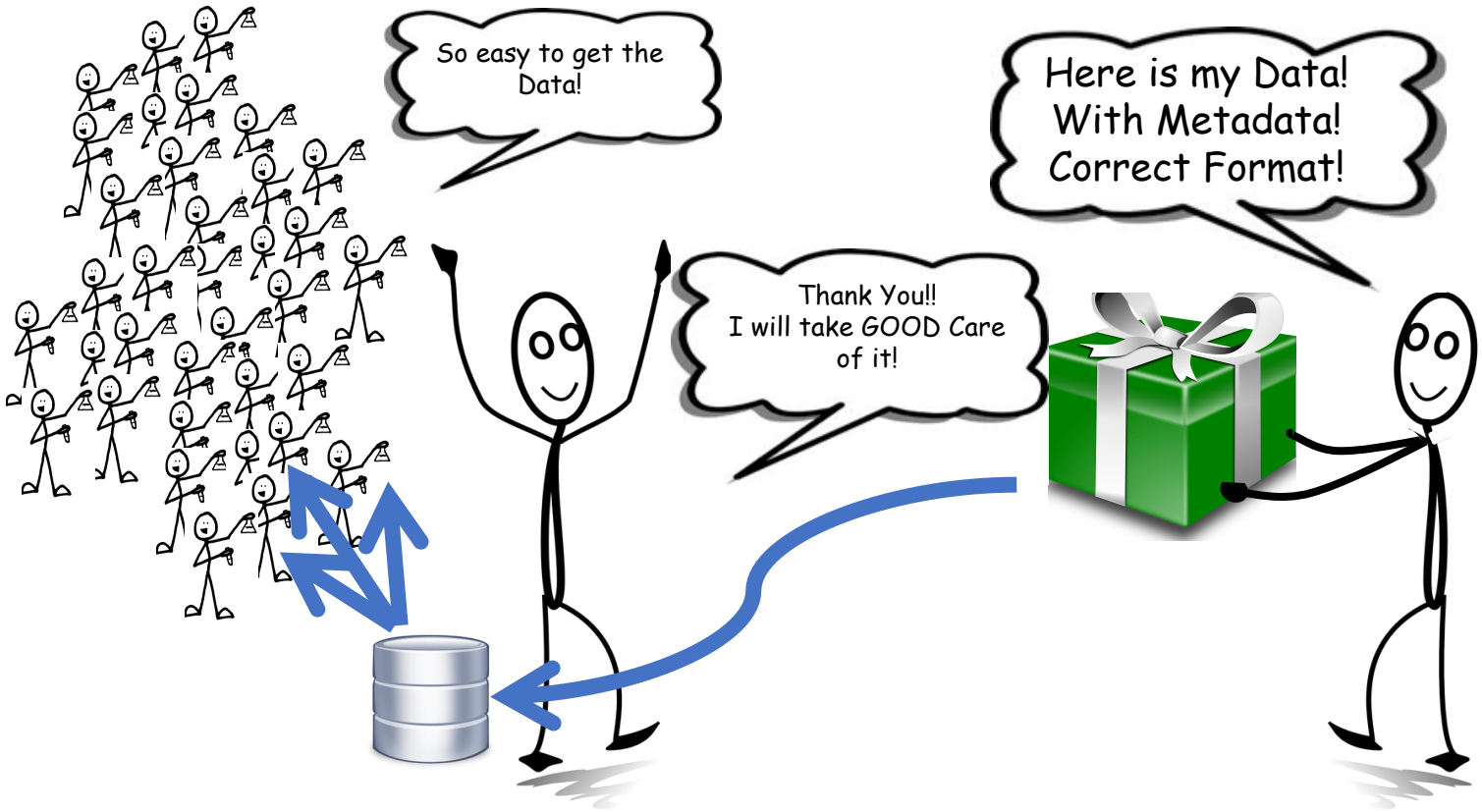
Good Data Stewardship

- Publish Data with the paper
- Describe Data to your fullest ability
- Use the right words to identify Data
- Deposit data in the right Data Repository
- Budget time for Data Management
- Don’t think of it as YOUR data

Databases TODAY…



We Hope… Databases in FUTURE



Good data practices benefit everyone (and help you get funded)

The **Data Management Plan** is an integral part of an NSF grant proposal, which NSF will consider under Intellectual Merit or Broader Impacts.

The plan describes how the proposal will conform to NSF policy on the dissemination and sharing of research results, and may include:

- the types of data, samples, software, curriculum materials, etc.;
- the standards to be used for data and metadata format and content;
- policies for access and sharing;
- policies and provisions for re-use, re-distribution, & production of derivatives;
- plans for archiving data, samples, etc., and preserved access.

BIO Directorate Guidance: https://www.nsf.gov/bio/pubs/BIODMP102015.pdf

Making your Data FAIR

Plantae Webinar by Lisa Harper & Leonore Reiser:

Data Management 101 - Tips for making your published data more Findable, Accessible, Interoperable and Reusable

https://community.plantae.org/video/49923219844245769 36/plantae-seminar-data-management-101-tips-for-making-your-published-data-more-findable-accessible-interoperable-and-reusable-with-lisa-harper-and-leonore-reiser

Thanks!

Lisa Harper

Leonore Reiser

Marcela K. Tello-Ruiz