### Tools to manage trial, phenotyping and marker datasets: FAIRness in the Legume Generation consortium

**James Brett** 



Biotechnology and Biological Sciences Research Council

Earlham Institute, Norwich Research Park, Norwich, Norfolk, NR4 7UZ, UK www.earlham.ac.uk









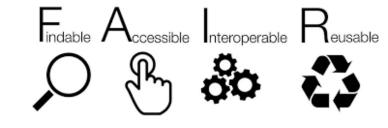
**Decoding Living Systems** 





### Trial and marker data management:

"Data access plays a crucial role in aiding breeders to make informed decisions in their breeding programmes, which results in improved and accelerated crop improvement."



"...extracting useful knowledge requires integration and contextualisation"

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		Simon Griffiths	Paragon x Watkins 272	Paragon x Watkins RLS	Designing Future Wheat

### the "Legume Generation Knowledge centre"

		Genotyping Data	roject Searcl							
Show 10 v entries					Search:					
Genotyping Data Project Name	Description	Breeding program	Folder	Year	Location	Genotyping Facility				
Tinker_QTL_2021	SNP	QTL mapping	AAFC Ottawa		2021					
Metabolomics-Oat6K	SNP	Infinium	Cornell University		2020					
Spain_2020	SNP	Instituto De Agricultura Sostenible	Spanish Counci for Scientific Research	i i	2020					
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### Data problems

- Increased computational capacity is leading to more data getting produced
- Complex problem to store and make this data accessible
- How to make it appropriate for increasing rise of machine learning?



# Solutions for data storage – phenotyping and field trials

Here at EI we tackle this problem by developing software and services to address these challenges using FAIR principles

• Grassroots



### **Dr Simon Tyrrell**

Wheat Initiative Software Engineer, Data Science Group



# FAIR data principles - Findable

The first step in (re)using data is to find them.

- Data are described with rich metadata
- Metadata and data should be easy to find for both humans and computers.
- Machine-readable metadata are essential for automatic discovery of datasets and services



# FAIR data principles - Accessible

Once the user finds the required data, they need to know how can they be accessed, possibly including authentication and authorization.

- (Meta)data are retrievable by their identifier using a standardized communications protocol
- Metadata are accessible, even when the data are no longer available



# FAIR data principles - Interoperable

The data usually need to be integrated with other data.

- Able to be easily integrated with applications or workflows for analysis, storage, and processing.
- (Meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.



# FAIR data principles - Reusable

The ultimate goal of FAIR is to optimize the reuse of data.

- Metadata and data should be well-described so that they can be replicated and/or combined in different settings
- Metadata and data are associated with detailed provenance



### Grassroots

- Grassroots infrastructure is a lightweight architecture to share both distributed data and services across multiple servers.
- The scientific functionality of the Grassroots is provided by services
  - Field Trials
  - Parental Genotypes
  - Field Pathogenomics
  - Blast
  - SamTools



# Field Trial Experiments

Experiments where different crops are planted in plots within a field, differing treatments applied and then traits are measured.

- Standardised template for submitting the genotype (the genetic material of the crop) and the phenotype (the characteristics that you want to measure) data
- To facilitate publishing of data compliant with FAIR sharing principles



# Field Trial Experiments

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- Standardised template for submitting the genotype (the genetic material of the crop) and the phenotype (the characteristics that you want to measure) data
- To facilitate publishing of data compliant with FAIR sharing principles
- Main DFW/DSW goal is to make all data openly available



### **Grassroots - Programmes**



- The high level organization or group that is responsible for conducting trials and studies.
  - Designing Future Wheat, Delivering Sustainable Wheat, Wheat Genetic Information Network (WGIN), BBSRC Low Protein Wheat, Legume Generation.

### Metadata such as

- Name
- Crop
- Objective
- Principal Investigator
- Etc.



### **Grassroots - Findable**



The experimental data can be accessed using a map-based view and a searchable table of the data...





## **Grassroots - Findable**

... or via a text-based search web page...



#### SEARCH FIELD TRIALS

A service to search field trial data

For more information and help, go to the user documentation

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2	Field Trial	DFW WP3 - DFW Academic Toolkit Trials	DFW WP3	View Field Trial
3	Field Trial	DFW WP3 - DFW Breeders Toolkit Trials	DFW WP3	View Field Trial
4	Field Trial	Andrew Riche - DFW Academic Toolkit RRes	Andrew Riche	View Field Trial
			Black Horse	
5	Study	DFW Academic Toolkit Trial H2019	St Albans United Kingdom	View Study
			AL3 7PX	
			Black Horse	
6	Study	DFW Toolkit lines 2nd year	St Albans United Kingdom	View Study
			AL3 7PX	
-			Meadow, Rothamsted Experimental Farm	
7	Study	DFW Academic Toolkit RRes Harvest 2020	Redbourn	View Study



# **Grassroots - Findable**



... or programmatically

- Curl
- Python
- C/C++
- R
- etc.

JSON request to run a given service

```
"services": [{
  "so:name": "Search Grassroots",
    "start_service": true,
    "parameter_set": {
        "parameters": [{
            "parameters": [{
            "param": "SS Keyword Search",
            "current_value": "Paragon"
        }]
    }
}]
```



### **Grassroots - Accessible**



- All data is openly available
- All Field Trials, Studies, etc. have a unique identifier and are accessible through standard web technologies



# **Grassroots - Interoperability**

The Field Trials data and metadata is exposed using many APIs such as

- Grassroots
- <u>BrAPI</u> which is a community-driven standardized RESTful web service API specification to enable interoperability among plant breeding databases.
- Frictionless Data
  - Schemas published at <u>https://grassroots.tools/frictionless-data/</u>
- CSV files

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currentPage:	1 2023
pageSize:	44
totalCount:	44
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studyName:	"1st vs 3rd wheat take-all resistance trial"
studyDbId:	"5dd8009ade68e75a927a8274"
locationName:	"Stackyard RES"
locationDbId:	"5d67a6f124ce205d7f6bbc53"
<pre> additionalInfo:</pre>	
study_design:	"Randomised block design"
<pre>w phenotype_gathering_notes:</pre>	"Sponsors to take plant samples. Farm to record yields."
▼ trialName:	"DFW - Designing Future Wheat - Work package 2 (WP2) - Added value and resilience"
trialDbId:	"5d5ac41c24ce20420b23322a"
▼ 1:	
<pre>studyName:</pre>	"2017 DFW Paragon x Watkins Mapping Populations 6th Year"
studyDbId:	"5ef1d9de02700f433d408463"
locationName:	"Meadow, Rothamsted Experimental Farm"
locationDbId:	"5ef1dbb702700f447d624323"
commonCropName:	"wheat"
startDate:	"2016-10-19"
endDate:	"2017-08-15"
active:	"false"
<pre>additionalInfo:</pre>	
study_design:	"Split plot randomised & blocked"
▼ so:description:	"7 PxW Mapping populations grown at 2 N levels plus 2 Robigus x Watkins mapping populations"
	Earlham Institute

### **Grassroots - Reusability**



- Using as many standard ontologies as possible
  - <u>Schema.org</u>
  - Crop Ontology
  - Plant Experimental Conditions Ontology
  - Environment Ontology
  - <u>Software Ontology</u>
  - <u>Agronomy Ontology</u>
- Custom ontological terms that will be submitted to the Crop Ontology



### Grassroots - Reusable data

### Plot data is standardized using ontological terms for each plot

#### PLOT DETAILS

Row: 20 Column: 1 Length: 3.594m Width: 1.8m Study Design: Sowing Date: 2019-10-30 Harvest Date: 2020-08-10 Treatment: Comment: Slight height segregation



Replicate	Rack	Accession	Pedigree	Gene Bank	Links
1 (Current Plot)	1	DFW SEL 0208		Germplasm Resources Unit	
3 <u>(Plot Row:3 - Col:23)</u>	1	DFW SEL 0208		Germplasm Resources Unit	
2 <u>(Plot Row:14 - Col:15)</u>	1	DFW SEL 0208		Germplasm Resources Unit	



×



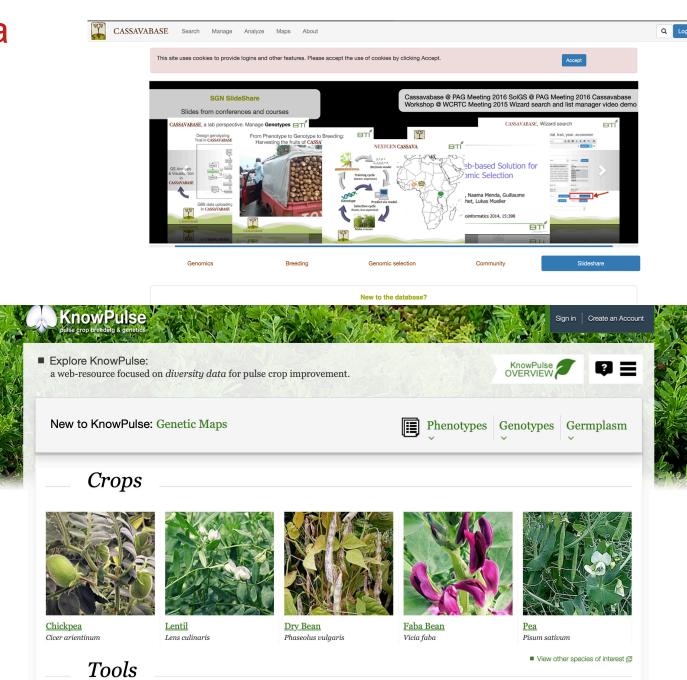
### **Databases Storing Genetic Data**

• Still deciding which database software to work with.

Two that we are considering and have already been used successfully to house genetic information on various crops:

- Breedbase -> <u>https://cassavabase.org</u>
- Tripal3 -> <u>https://knowpulse.usask.ca</u>

Integrate with Grassroots database and can perform downstream analyses on data e.g. BLUPS/BLUEs and genomic selection.



# Acknowledgements

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#### **James Brett**

Legume Breeding Data Manager

James.brett@earlham.ac.uk



Earlham Institute, Norwich Research Park, Norwich, Norfolk, NR4 7UZ, UK www.earlham.ac.uk







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