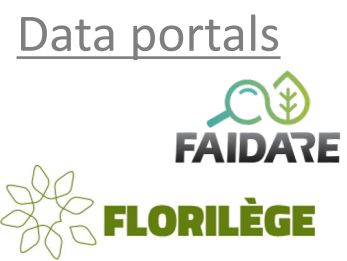
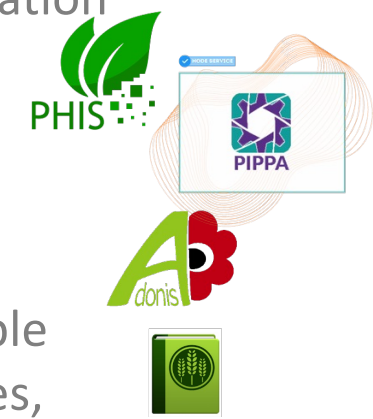


➤ FAIR Plant Phenomics Data Management Tools and Guidelines

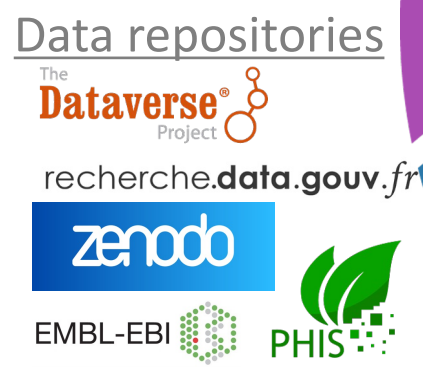
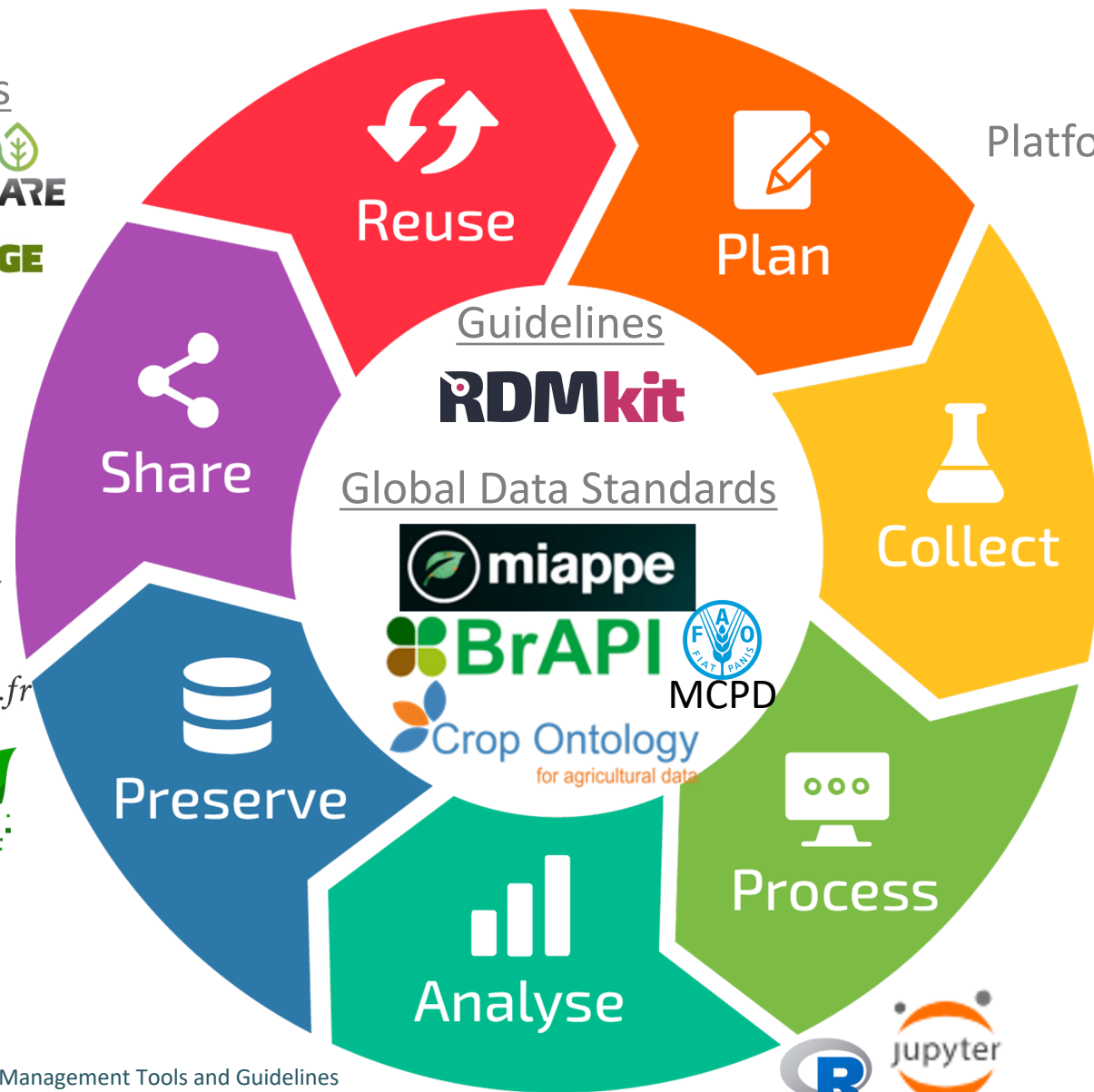
Some current practices in Elixir and Emphasis European Infrastructures



Platform Information Systems

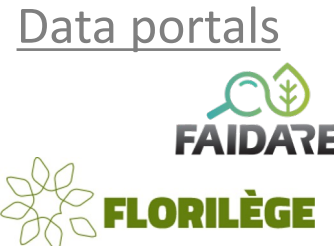


Portable devices, sensors, ...



Scripts and Workflows





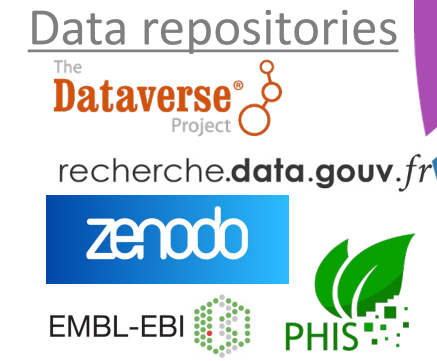
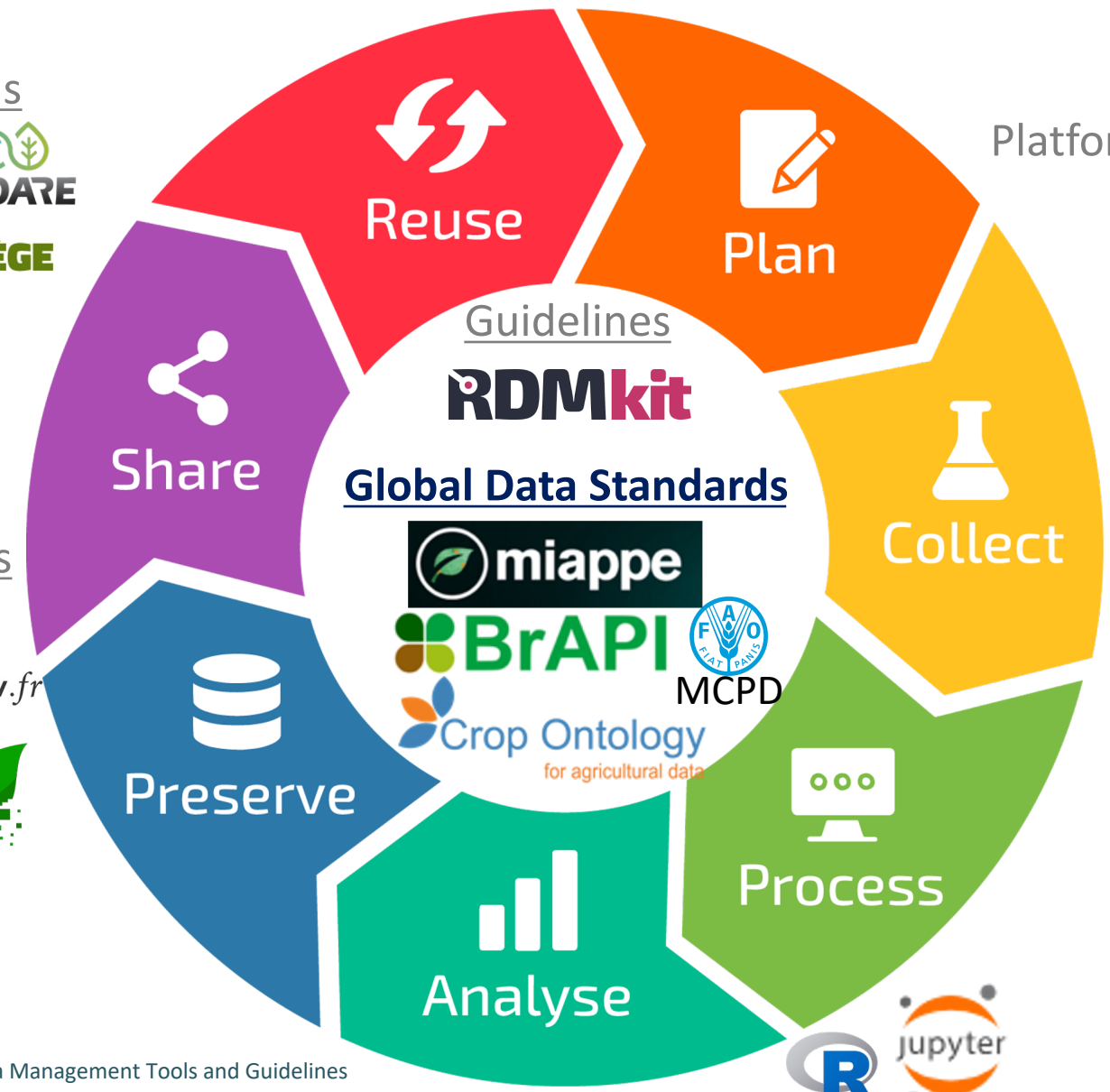
Platform Information Systems



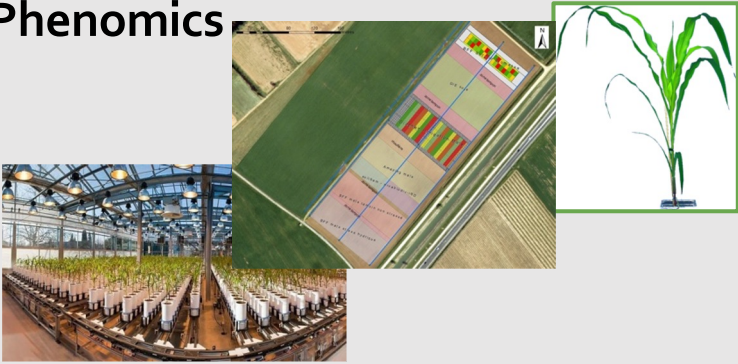
Portable devices, sensors, ...



Scripts and Workflows



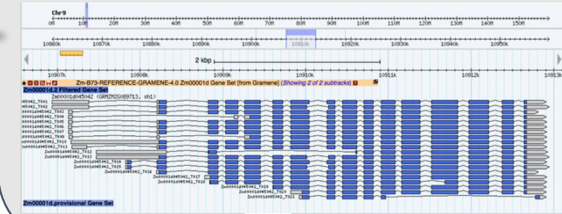
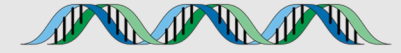
Phenomics



F_{indable} A_{ccessible} I_{nteroperable} R_{eusable}



Genetics Genomics Omics



Dispersed (no central repo)
Heterogenous
Getting Standardized

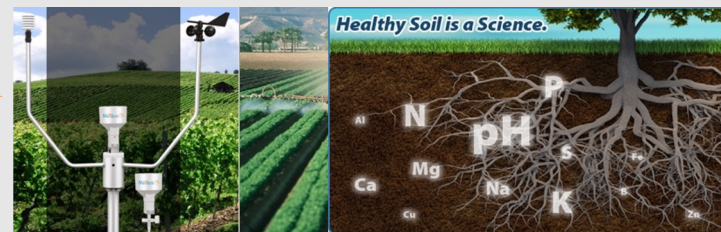
Mostly centralized
Homogenous data
Heterogenous metadata

Plant Breeding
Genetic variations by Traits

Climate Change Studies
Genotype by Environment

F_{indable} A_{ccessible} I_{nteroperable} R_{eusable}

Environment



Dispersed
Heterogenous

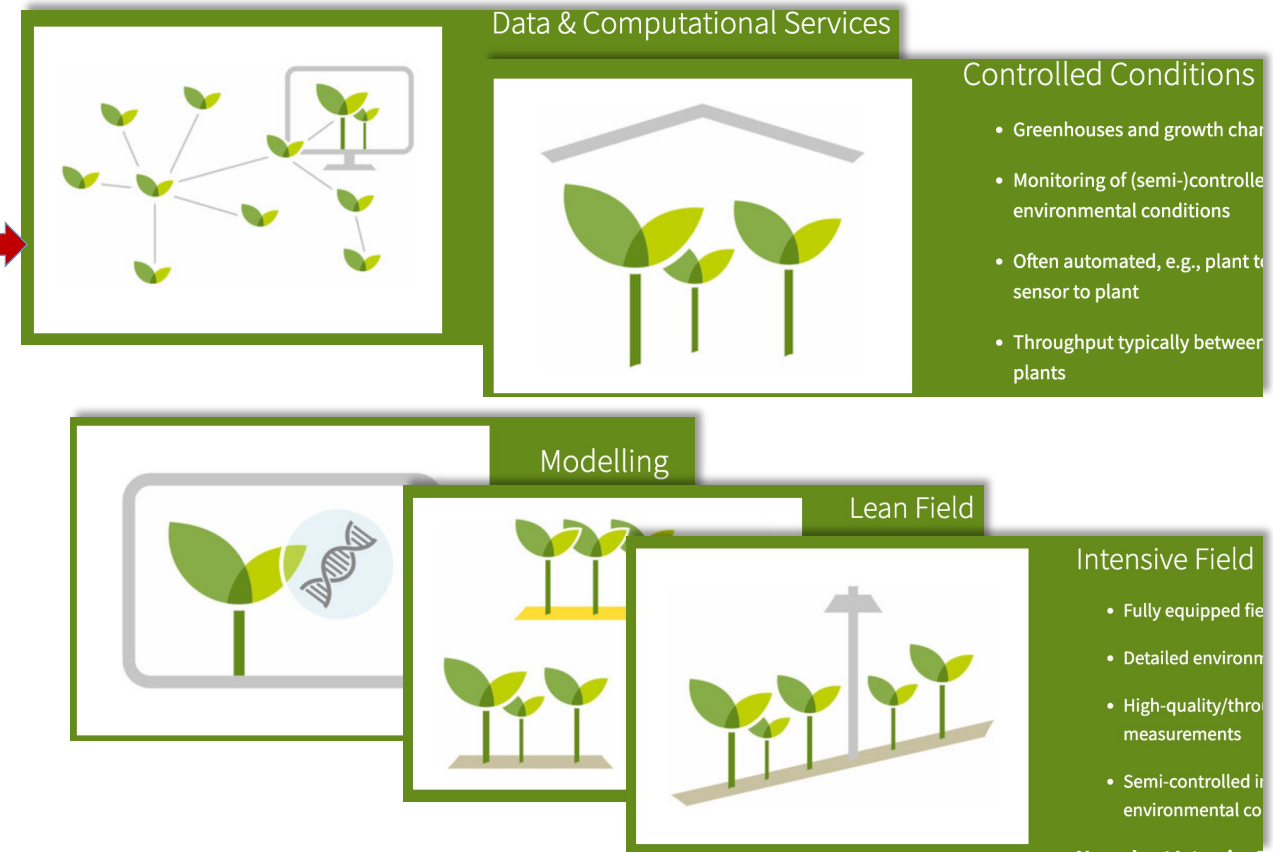
Gathered to solve Pheno to Omic data management and integration

• ELIXIR

- European Infrastructure for life sciences data
- Slovenia , France, Germany, Portugal, UK, Belgium, Italy, NL...
- <https://elixir-europe.org/communities/plant-sciences>
- FAIR data management, software, training, ...

• EMPHASIS IPPN

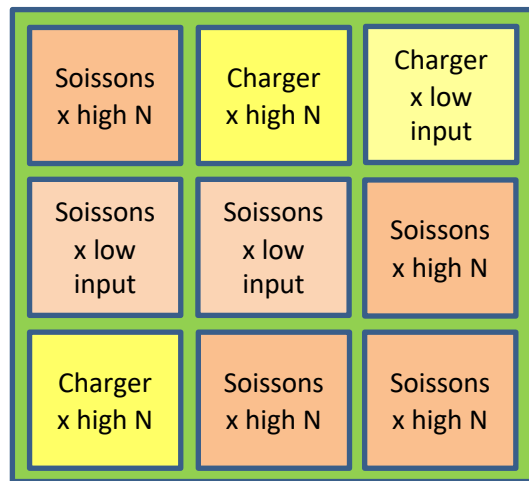
- European Infrastructure for Plant Phenotyping
- France, Germany, Belgium, UK, ...
- <https://www.plant-phenotyping.eu>



Data Acquisition

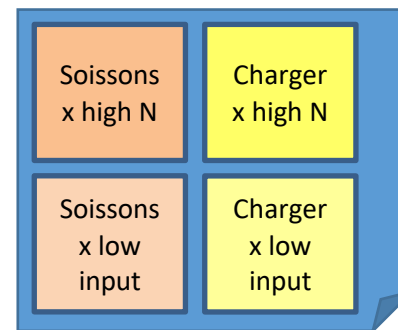
Data computation/Integration

« Raw » data, pheno/env measurement, variables



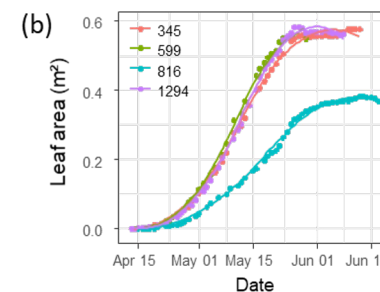
Derivation, Reduction

« Derived » data, indicators



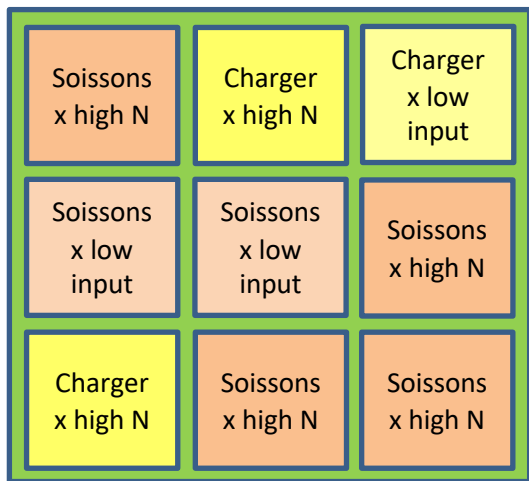
Genotype	Treatment	N input	Date	Rep	Fusariose
Soissons	low input	15,3225129	15/11/2011	1	5
Soissons	low input	15,3430556	16/11/2011	2	7

Genotype	Treatment	Fusariose
Soissons	low input	6



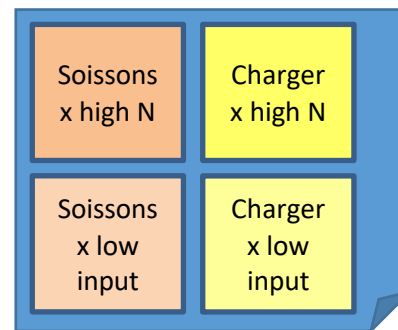


« Raw » data, pheno/env measurement, variables



Derivation, Reduction

« Derived » data, indicators

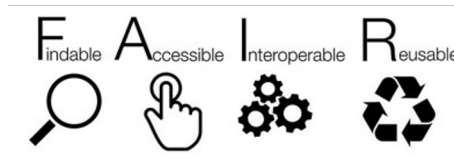
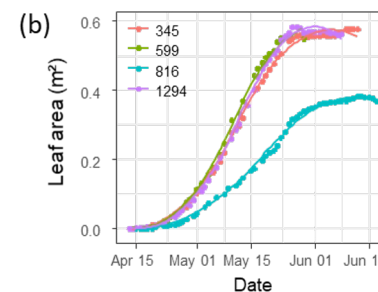


Publication

Variety charger is resistant to fusariose under intensive cultural practice

Genotype	Treatment	N input	Date	Rep	Fusariose
Soissons	low input	15,3225129	15/11/2011	1	5
Soissons	low input	15,3430556	16/11/2011	2	7

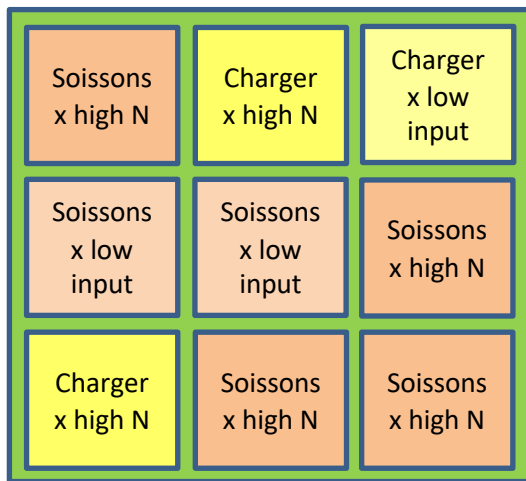
Genotype	Treatment	Fusariose
Soissons	low input	6



Wilkinson et al.
The FAIR Guiding Principles for scientific data management and stewardship.
Scientific Data 3 (2016)

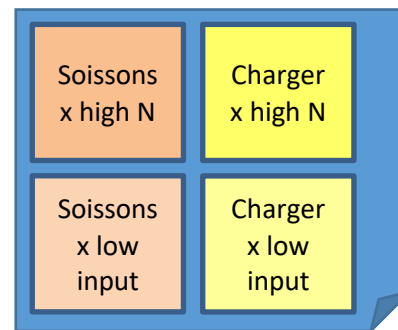


« Raw » data, pheno/env measurement, variables

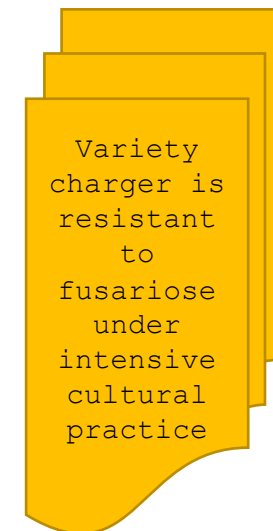


Derivation, Reduction

« Derived » data, indicators



Publication



Genotype	Treatment	N input	Date	Rep	Fusariose
Soissons	low input	15,3225129	15/11/2011	1	5
Soissons	low input	15,3430556	16/11/2011	2	7

Genotype	Treatment	Fusariose
Soissons	low input	6

VARIABLES

- Raw Measures Pheno & Env
- Data cleaning
- Traceability, Reproducibility & Provenance

INDICATORS

- New computation for each scientific question
- One experimental dataset → many derived dataset

Semantic

- ◆ Description of the data
- ◆ Controlled vocabularies: term name and definitions
- ◆ Ontologies: semantic links between terms
- ◆ *Biologist driven*



Structure



- Formatting and Organizing the data
- Data Models
- Standards : CSV, VCF, GFF, MIAPPE (www.miappe.org) , etc...
- *Biologist & Computer scientist driven*



Persistent Unique Identifiers

DOI, URI, gene ID, accessions ID, Trait ID, ...

Technical

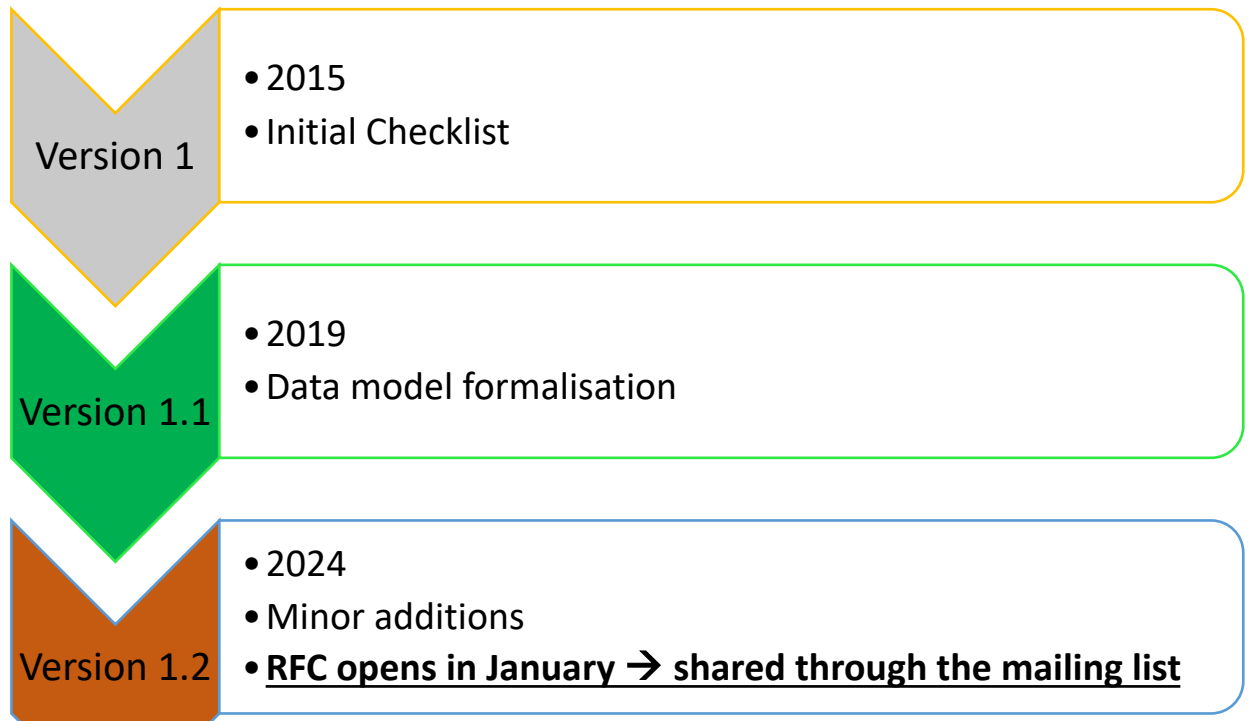
- Data integration and sharing
- Interoperability : tools and systems
 - GA4GH 
 - Breeding API www.brapi.org 
 - Computer scientist driven

Phenotype Structure Standard

Minimal Information About Plant Phenotyping Experiments

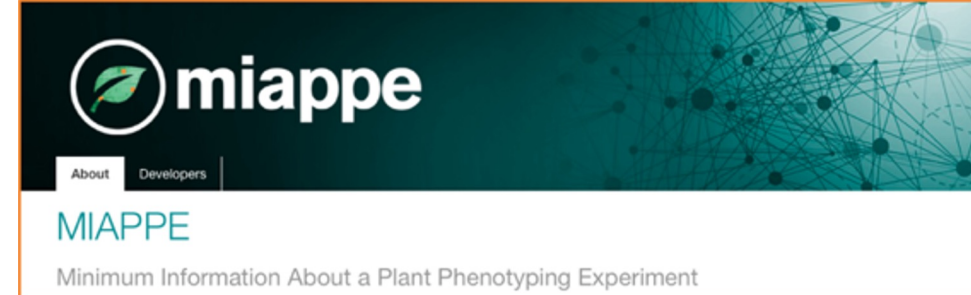


- www.miappe.org
- Crops and woody plants
- Single experiment
- Multilocal multiyear network
- Field
- Greenhouse
- Many stakeholders
 - Elixir, Emphasis, Bioversity CGIAR, North American PPN
- Open Community
 - Request for comments
 - Github Feature requests
 - Mailing lists
 - Meetings & Workgroups



Line #	MIAPPE Check list	Definition	MIAPPE Example	Format	Cardinality
OM-1	Investigation	Investigations are research programmes with defined aims. They can exist at various scales (for example, they could encompass a grant-funded programme of work, the various components comprising a grant-reviewed publication, or a single experiment).			1 per MIAPPE submission
OM-2	Investigation unique ID	Identifier comprising the unique name of the institution/database holding the submission of the investigation data, and the accession number of the investigation in that institution.	EM-12345678	Unique identifier	0-1
	Investigation title	Human-readable string summarising the investigation.	Acquisition of Maize in Temperate Climate, Mail Density Genome-Wide Association Genetics and Density Patterns Revealed Key Genetic Features, with	Free text (short)	1
Environment					
ENV-1 Non-exhaustive list of Environment Parameters.					
ENV-2	Environment parameters				
Growth facility					
ENV-3	Air temperature	List of hourly air temperature throughout the experiment.	22 °C	Numeric	
ENV-4	Organ temperature	List of hourly organ temperatures throughout the experiment.	18 °C	Numeric	
Experimental Factors					
TR-1 Non-exhaustive list of Experimental Factors that can be applied.					
TR-2	Factor type				
TR-3	Seasonal environment	A plant treatment (EO:0001001) involving an exposure to a given conditions of regional seasons.	Spring season; dry season	Plant Environment Ontology:'EO_0007036'	
TR-4	Air treatment regime	The treatment involving an exposure to wind/air with varying degree of temperature, which may depend on the study type or the regional environment.	28/25°C (Day/Night)	Plant Environment Ontology:'EO_0007161'	
TR-5	Soil temperature regime	A physical plant treatment (EO:0007316) involving an exposure to varying degree of temperature, which may depend on regional environment.	27/25°C (Day/Night)	Plant Environment Ontology:'EO_0007161'	

• Phenotype Structure Standard



Minimum Information for Biological and Biomedical Investigations

A collection of the historical MIBBI foundry reporting guidelines. The minimum information standard is a set of guidelines for reporting data derived by relevant methods in biosciences. If followed, it ensures that the data can be easily verified, analysed and clearly

- **Biologist Friendly**
 - Clear definitions and examples
 - Excel templates
 - Trainings
- **Computer scientist friendly**
 - Model, implementations, formalisation
- **Minimal and sufficient list of metadata:**
 - The objective of the experiment
 - Who contributed to the experiment
 - What were the experimental procedures
 - What was the biological material experimented
 - ...

Phenotype Technical Standard, MIAPPE Implementations

Ontology, OWL Implementation

- <https://github.com/MIAPPE/MIAPPE-ontology>
- <http://agroportal.lirmm.fr/ontologies/PPEO>
- Data model representation
- Formal concepts and constraints

File Archive

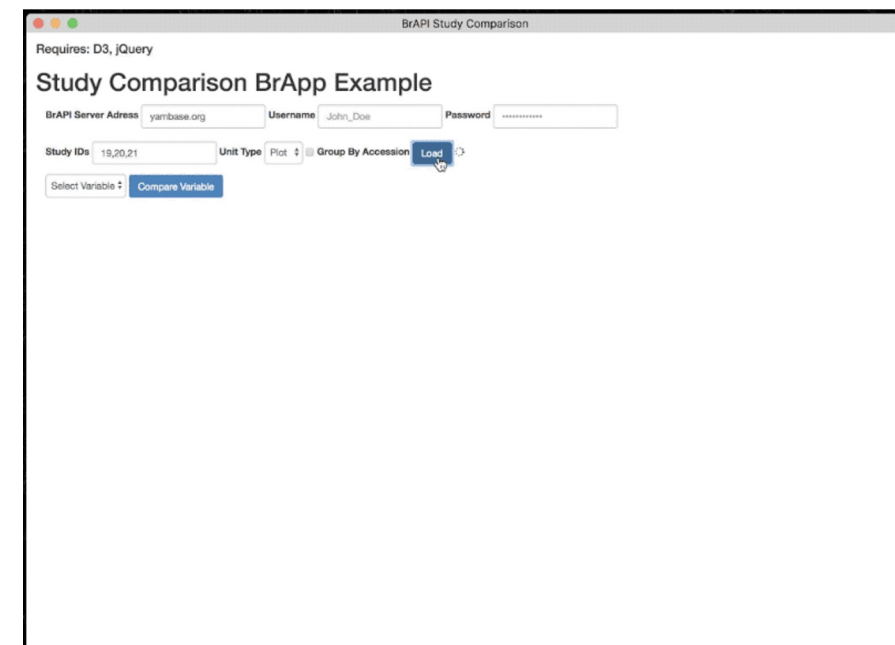
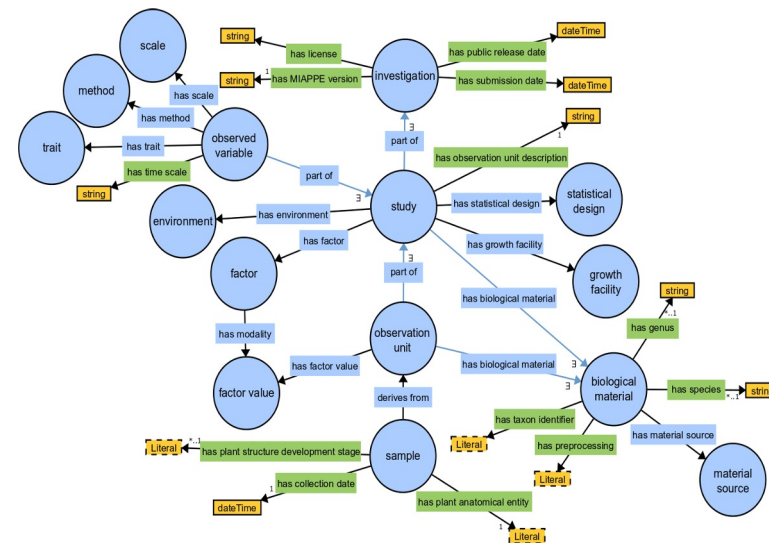
- ISA Tab: data + metadata
- RO Crate

Web Services

- Breeding API
- International collaboration
- Standard Open Web Service API
- Information Exchange, Main target: Breeding
- Excellence in Breeding platform (CGIAR, Pet)

Data repositories

- Any BrAPI compliant DB (GnpIS, PHIS, PIPPA, ...)
- Generic data repositories (Dataverse, Zenodo, e!Dale, ...)



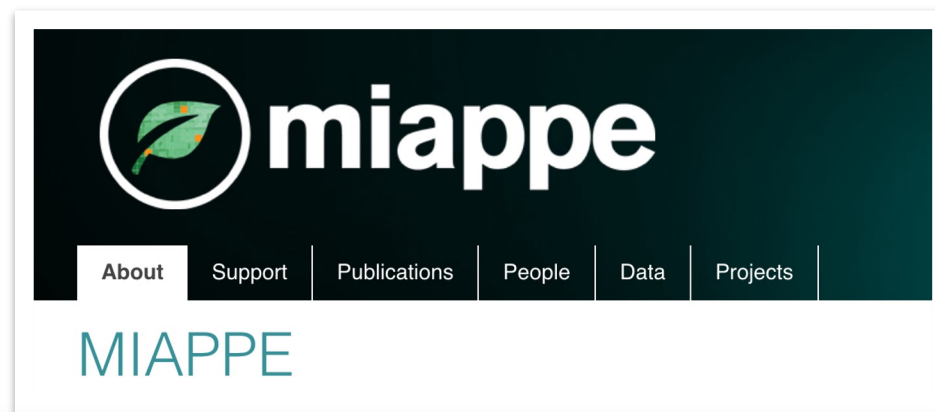
• MIAPPE Specifications

- www.miappe.org

MIAPPE primers

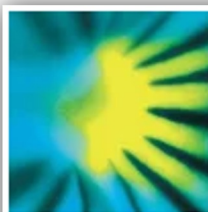
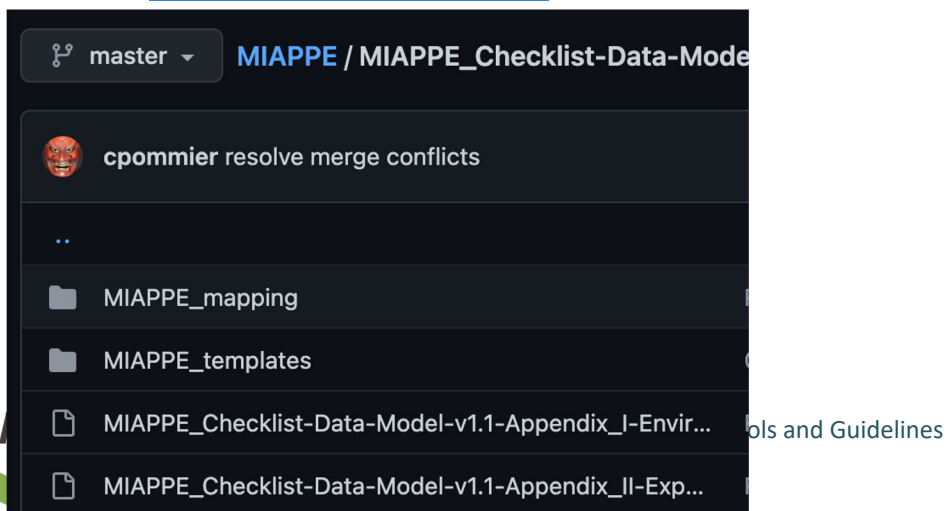
See the [support page](#) for full informations

- The latest specifications, [data model overview](#)
- The latest specifications [field list with description](#)



- Github

- https://github.com/MIAPPE/MIAPPE/tree/master/MIAPPE_Checklist-Data-Model-v1.1



New Phytologist

Methods | [Open Access](#) |

Enabling reusability of plant phenomic datasets with MIAPPE 1.1

Evangelia A. Papoutsoglou✉, Daniel Faria, Daniel Arend, Elizabeth Arnaud, Ioannis N. Athanasiadis, Inês Chaves, Frederik Coppens, Guillaume Cornut, Bruno V. Costa, Hanna Ćwiek-Kupczyńska, Bert Droesbeke, Richard Finkers, Kristina Gruden, Astrid Junker, Graham J. King, Paweł Krajewski, Matthias Lange, Marie-Angélique Laporte, Célia Michotey, Markus Oppermann, Richard Ostler, Hendrik Poorter, Ricardo Ramírez-Gonzalez, Živa Ramšak, Jochen C. Reif, Philippe Rocca-Serra, Susanna-Assunta Sansone, Uwe Scholz, François Tardieu, Cristobal Uauy, Björn Usadel, Richard G. F. Visser, Stephan Weise, Paul J. Kersey, Célia M. Miguel, Anne-Françoise Adam-Blondon, Cyril Pommier✉ ... [See fewer authors](#) ^

First published: 14 March 2020 | <https://doi.org/10.1111/nph.16544> | Citations: 10

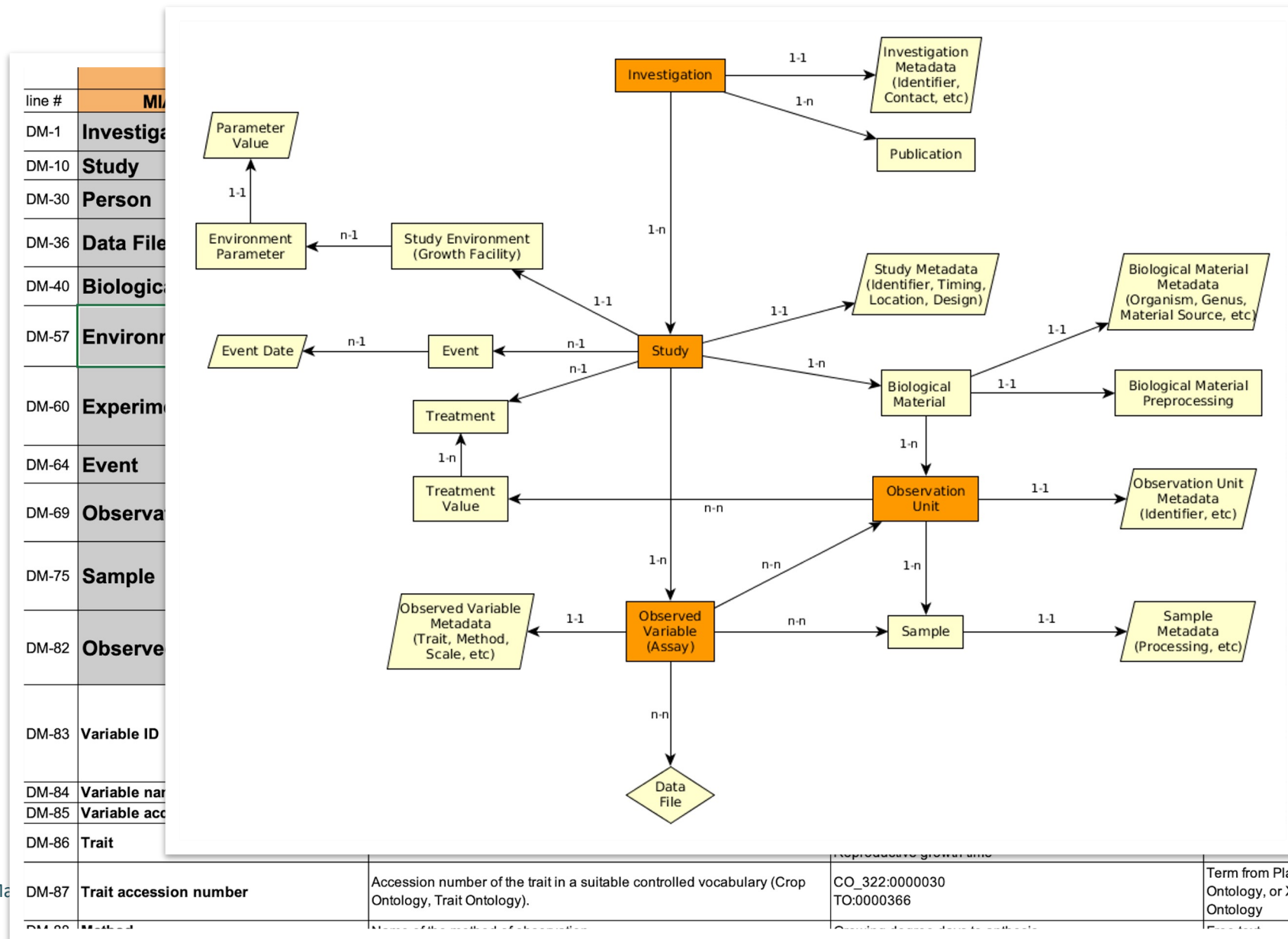
MIAPPE Specifications

- Specification table
- Sections
- Metadata Fields

line #	MIAPPE Check list	MIAPPE			Cardinality
		Definition	Example	Format	
DM-1	Investigation	Investigations are research programmes with defined aims. They can exist at various scales (for example, they could encompass a grant-funded programme of work, the various components comprising a peer-reviewed publication, or a single experiment).			1 per MIAPPE submission
DM-10	Study	A study (or experiment) comprises a series of assays (or measurements) of one or more types, undertaken to answer a particular biological question.			1+ per investigation
DM-30	Person	A human involved in the investigation or specifically any of its studies.			1+ per investigation / 0+
DM-36	Data File	A file or digital object holding observation data recorded during one or more assays of the study, typically in tabular form. Multiple data files may be provided per study, and each file can include observations for several observation units and several observed variables.			0+ per study
DM-40	Biological Material	The biological material being studied (e.g. plants grown from a certain bag or seed, or plants grown in a particular field). The original source of that material (e.g., the seeds or the original plant cloned) is called the material source, which, when held by a material repository, should have its stock identified.			1+ per study; 0+ per observation unit
DM-57	Environment	Environmental parameters that were kept constant throughout the study and did not change between observation units or assays. Environment characteristics that vary over time, i.e. environmental variables, should be recorded as Observed Variables (see below).			0-1 per study
DM-60	Experimental Factor	The object of a study is to ascertain the impact of one or more factors on the biological material. Thus, a factor is, by definition a condition that varies between observation units, which may be biotic (pest, disease interaction) or abiotic (treatment and cultural practice) in nature. Depending on the level of the data, an experimental factor can be either "what is the factor applied to the plant" (i.e. Unwatered), or the "environmental characterisation" (i.e. if no rain on unwatered plant : Drought ; if rain on unwatered plant: Irrigated)			0+ per study; 0+ per observation unit
DM-64	Event	An event is discrete occurrence at a particular time in the experiment (which can be natural, such as rain, or unnatural, such as planting, watering, etc). Events may be the realization of Factors or parts of Factors, or may be confounding to Factors. Can be applied at the whole study level or to only a subset of observation units.			0+ per study/observation unit
DM-69	Observation Unit	Observation units are objects that are subject to instances of observation and measurement. An observation unit comprises one or more plants, and/or their environment. There can be pure environment observation units with no plants. Synonym: Experimental unit.			1+ per study
DM-75	Sample	A sample is a portion of plant tissue harvested, non-harvested or extracted from an observation unit for the purpose of sub-plant observations and/or molecular studies. A sample must be used when there is a physical sample that needs to be stored and traced. Otherwise, observations made at the sub-plant level should be recorded as plant level observations using the observed variables to characterize the object of the observation (e.g. Berry sugar content, Fruit weight, Grain Protein content, Leaf 1 width, Leaf 2 width, Leaf 2 length).			0+ per observation unit
DM-82	Observed Variable	An observed variable describes how a measurement has been made. It typically takes the form of a measured characteristic of the observation unit (plant or environmental trait), associated to the method and unit of measurement. Multiple variables with the same combination of trait, method and scale can be used in association with different plant parts (leaf 1, leaf 2), when this distinction is necessary for observations referring to different parts of the same observation unit.			1+ per study
DM-83	Variable ID	Code used to identify the variable in the data file. We recommend using a variable definition from the Crop Ontology where possible. Otherwise, the Crop Ontology naming convention is recommended: <trait abbreviation>_<method abbreviation>_<scale abbreviation>. A variable ID must be unique within a given investigation.	Ant_Cmp_Cday	Unique identifier	1
DM-84	Variable name	Name of the variable.	Anthesis computed in growing degree days	Free text	0-1
DM-85	Variable accession number	Accession number of the variable in the Crop Ontology	CO_322:0000794	Crop Ontology term	0-1
DM-86	Trait	Name of the (plant or environmental) trait under observation	Anthesis time Reproductive growth time	Free text	1
DM-87	Trait accession number	Accession number of the trait in a suitable controlled vocabulary (Crop Ontology, Trait Ontology).	CO_322:0000030 TO:0000366	Term from Plant Trait Ontology, Crop Ontology, or XML Environment Ontology	0-1

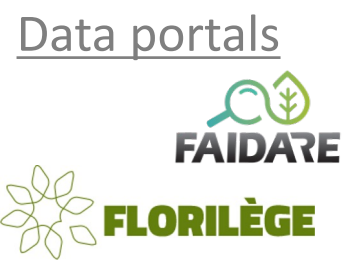
MIAPPE Specifications

- Specification table
- Sections
- Metadata Fields
- Linked and organized

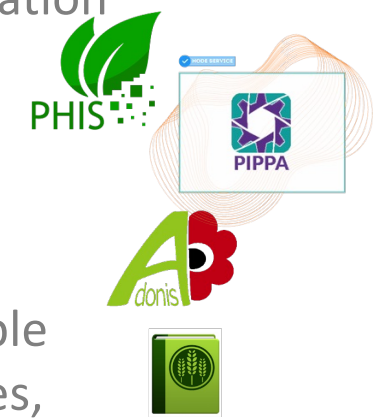


line #	Metadata Field
DM-1	Investigation
DM-10	Study
DM-30	Person
DM-36	Data File
DM-40	Biological Material
DM-57	Environment
DM-60	Experiment
DM-64	Event
DM-69	Observation Unit
DM-75	Sample
DM-82	Observed Variable
DM-83	Variable ID
DM-84	Variable name
DM-85	Variable accession number
DM-86	Trait
DM-87	Trait accession number

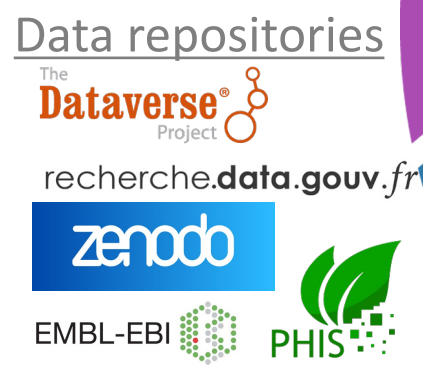
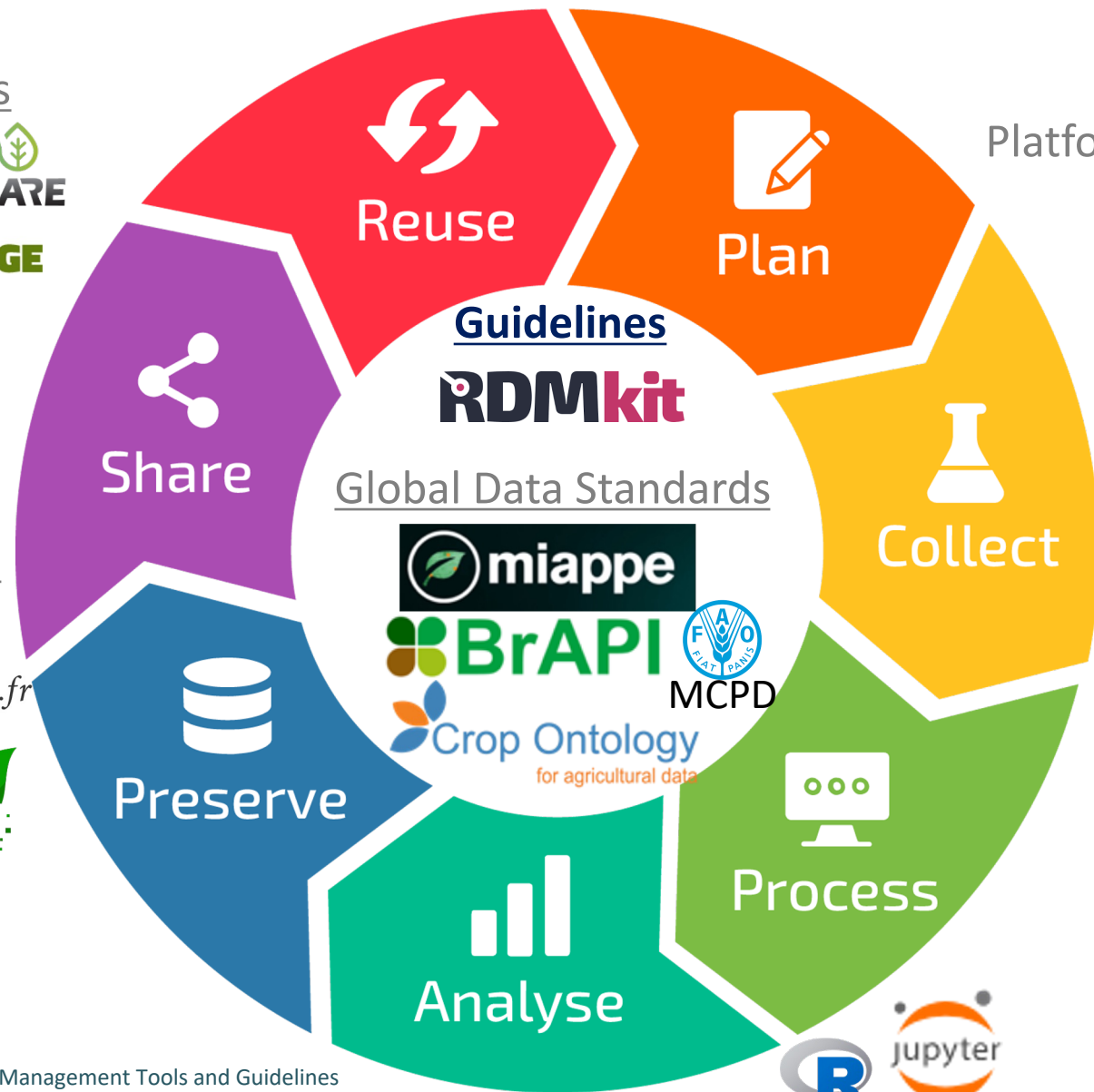
Format	Description	Cardinality
Investigation	Investigation	1 per
Study	Study	1+ per
Person	Person	1+ per
Data File	Data File	0+ per
Biological Material	Biological Material (e.g., the seeds or	1+ per 0+ per
Environment	Environment	0-1 per
Experiment	Experiment	0+ per 0+ per
Event	Event	0+ per
Observation Unit	Observation Unit	1+ per
Sample	Sample	0+ per
Observed Variable	Observed Variable	1+ per
Variable ID	Variable ID	1
Variable name	Variable name	0-1
Variable accession number	Variable accession number	0-1
Trait	Trait	1
Trait accession number	Trait accession number	0-1



Platform Information Systems



Portable devices, sensors, ...

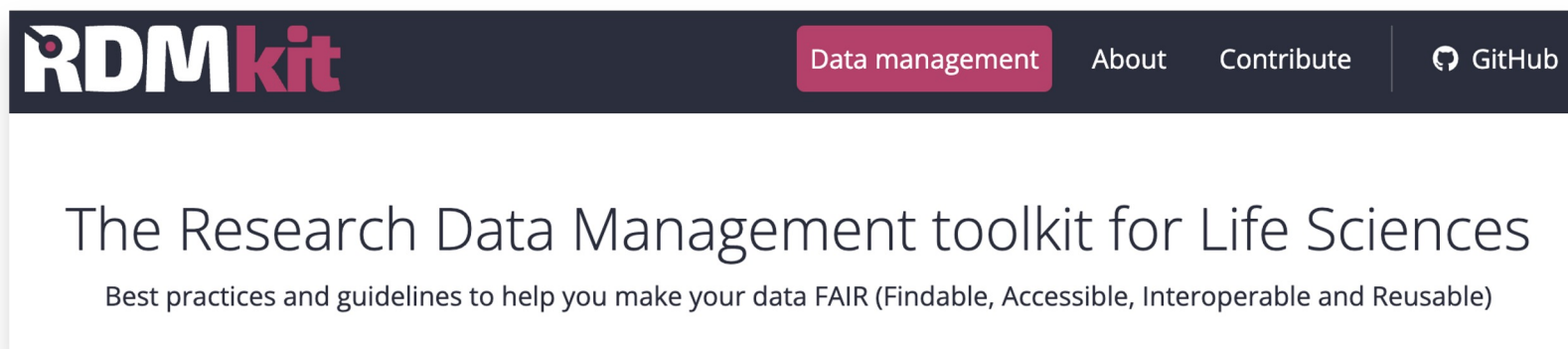


Scripts and Workflows



Community guidelines portal : RDMkit - Best practices and guidelines for FAIR data management

- A “wikipedia-like” knowledge base website, free and open
- Describes how to manage research outputs according to FAIR principles
- Portal to other online resources used by RDM professionals and researchers



URL: <https://rdmkit.elixir-europe.org/>

Recommended in the **Horizon Europe Program Guide** as the “resource for Data Management guidelines and good practices for the Life Sciences”

RDMkit in numbers



- Contributors are experts in RDM and/or in scientific domain in ELIXIR and beyond
- Managed by an editorial board
 - ELIXIR members from several Nodes
 - lead for “FAIR Data & Resources” at the Office of Data Science Strategy at NIH
- The content is curated by members of the ELIXIR RDM Community

Plant Pages

https://rdmkit.elixir-europe.org/plant_sciences

RDMkit Data management About Contribute GitHub Search RDMkit

Data management

- Data life cycle
- Your role
- Your domain

Bioimaging data

Biomolecular simulation data

Epitranscriptome data

Human data

Human pathogen genomics

Intrinsically disordered proteins

Marine metagenomics

Microbial biotechnology

Plant sciences

Your domain

Plant sciences

Introduction

Data management challenges in plant sciences

The plant science domain includes studying the adaptation of plants to their environment, with applications ranging from improving crop yield or resistance to environmental conditions, to managing forest ecosystems. Data integration and reuse are facilitators for understanding the play between genotype and environment to produce a phenotype, which requires integrating phenotyping experiments and genomic assays made on the same plant material, with geo-climatic data. Moreover, cross-species comparisons are often necessary to understand the mechanisms behind phenotypic traits, especially at the genotypic level, due to the gap in genomic knowledge between well-studied plant species (namely Arabidopsis) and newly sequenced ones.

The challenges to data integration stem from the multiple levels of heterogeneity in this domain. It encompasses a variety of species, ranging from model organisms, to crop species, to wild plants such as forest trees. These often need to be detailed at infra-specific levels (e.g. subspecies, variety), but naming at these levels sometimes lacks consensus. Studies can take place in a diversity of settings including indoor (e.g. growth chamber, greenhouse) and outdoor settings (e.g. cultivated field, forest) which differ fundamentally on the requirements and manner of characterizing the environment. Phenotypic data can be collected manually or automatically (by sensors and drones), and be very diverse in nature, spanning physical measurements, the results of biochemical assays, and images. Some omics data can be considered as well

On this page

- Introduction
- Data management planning
- Plant biological materials: (meta)data collection and sharing
- Phenotyping: (meta)data collection and publication
- Genotyping: (meta)data collection and publication
- Related pages
- More information
- Relevant tools and resources

Publish in generic data repositories

- **Dataverse**
 - Zenodo
 - e!Dale
- **PAG Computer Demo**
 - Saturday the 13th at 13:30 Town and Country D

https://rdmkit.elixir-europe.org/plant_phenomics_assembly

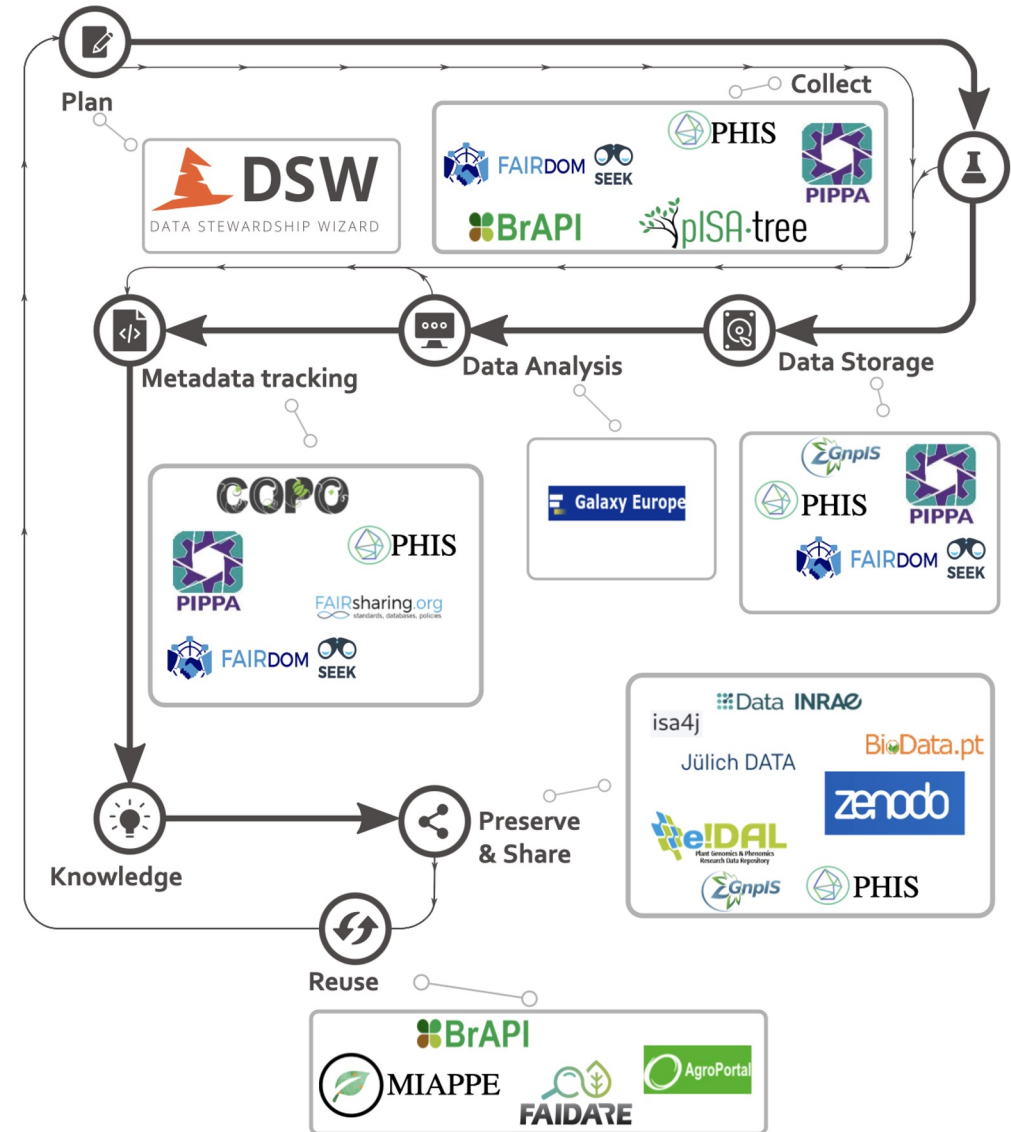


Figure 1. The plant phenomics tool assembly.

Details

Location: Town and Country D

Date: Saturday, Jan 13 1:30 PM

Duration: 2 hours 10 minutes

Presentation

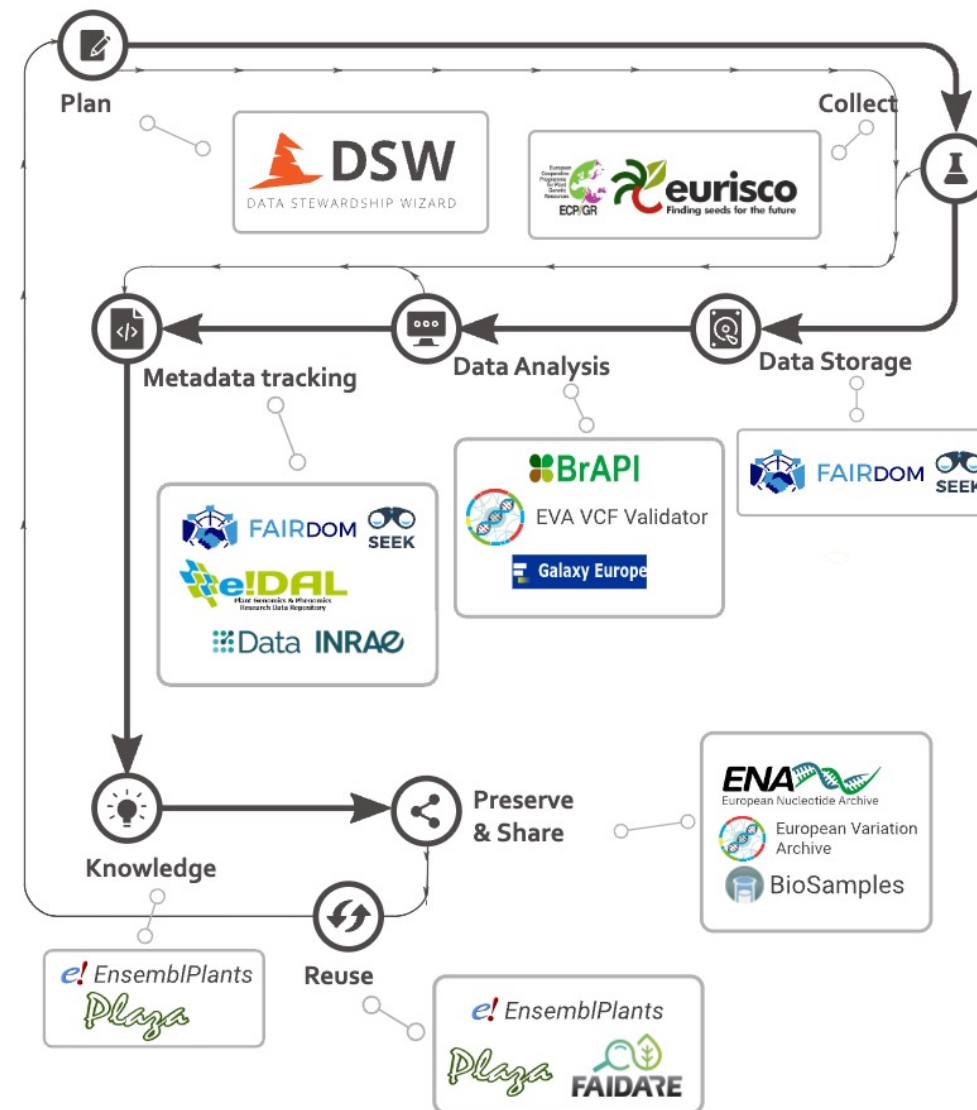


1:30 PM Long Term Plant Phenomic Data Sharing in Generic Data Repositories (Zenodo, Dataverse) Using MIAppe

Publish Sequence and Variation @ EMBL-EBI

- Step by step procedure
- Publish data @ EBI
- Ensure interoperability from Pheno to Geno

https://rdmkit.elixir-europe.org/plant_genomics_assembly





Data portals



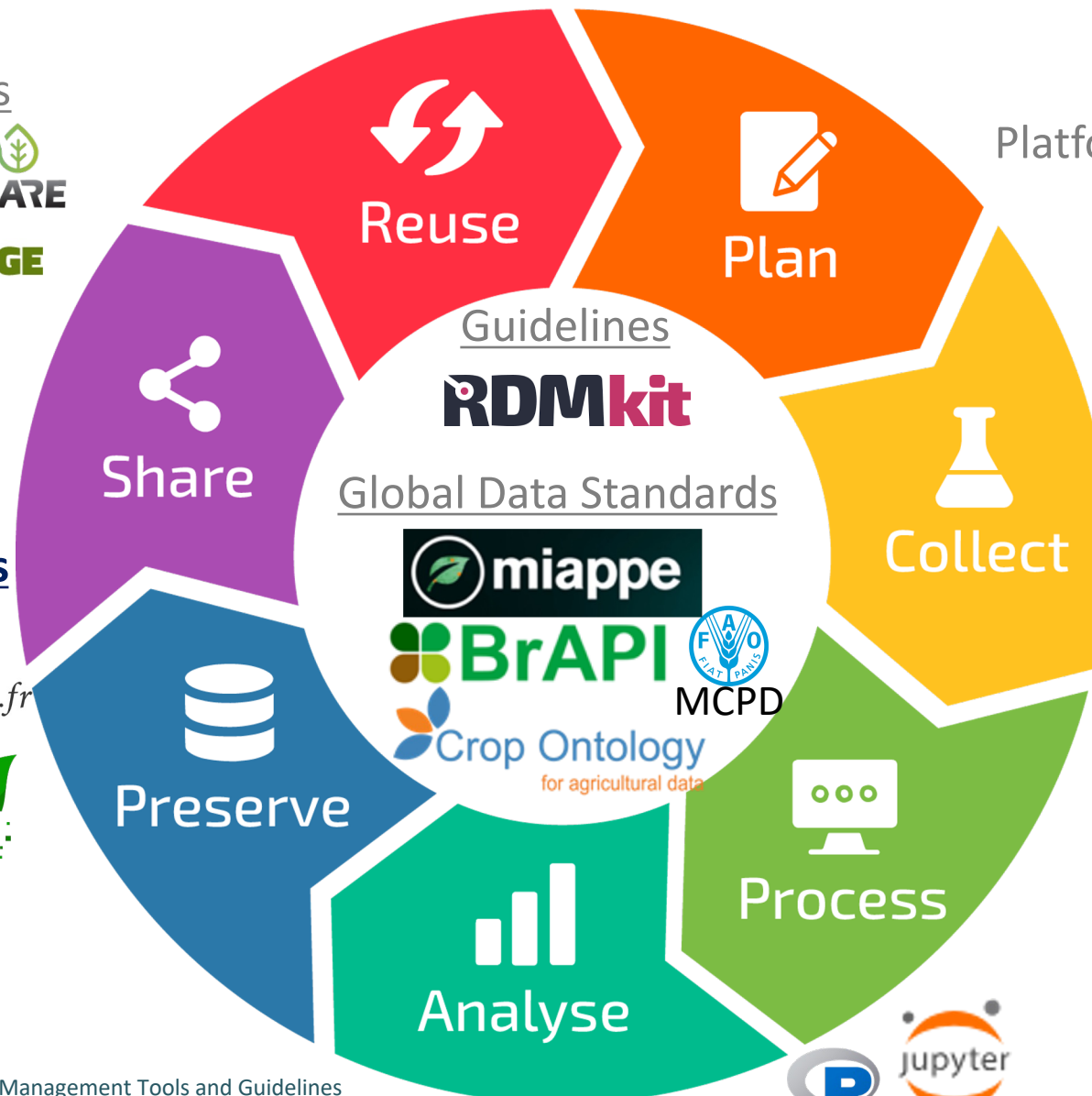
Platform Information Systems



Portable devices, sensors, ...

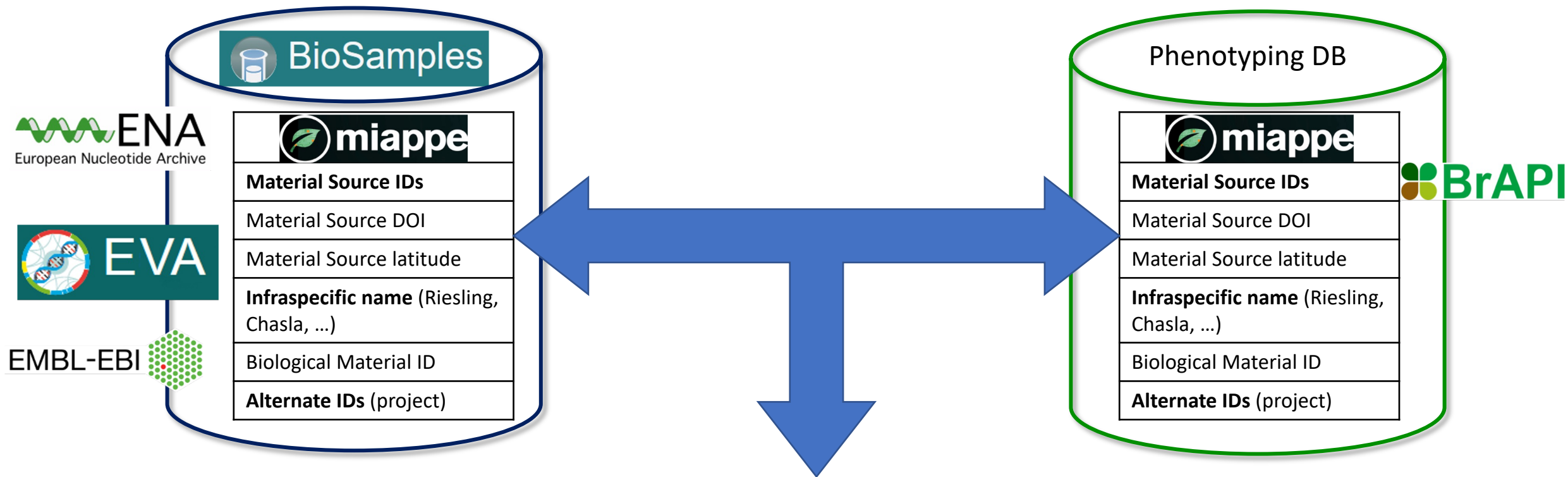


Scripts and Workflows

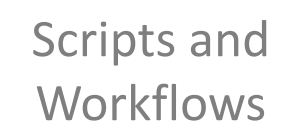
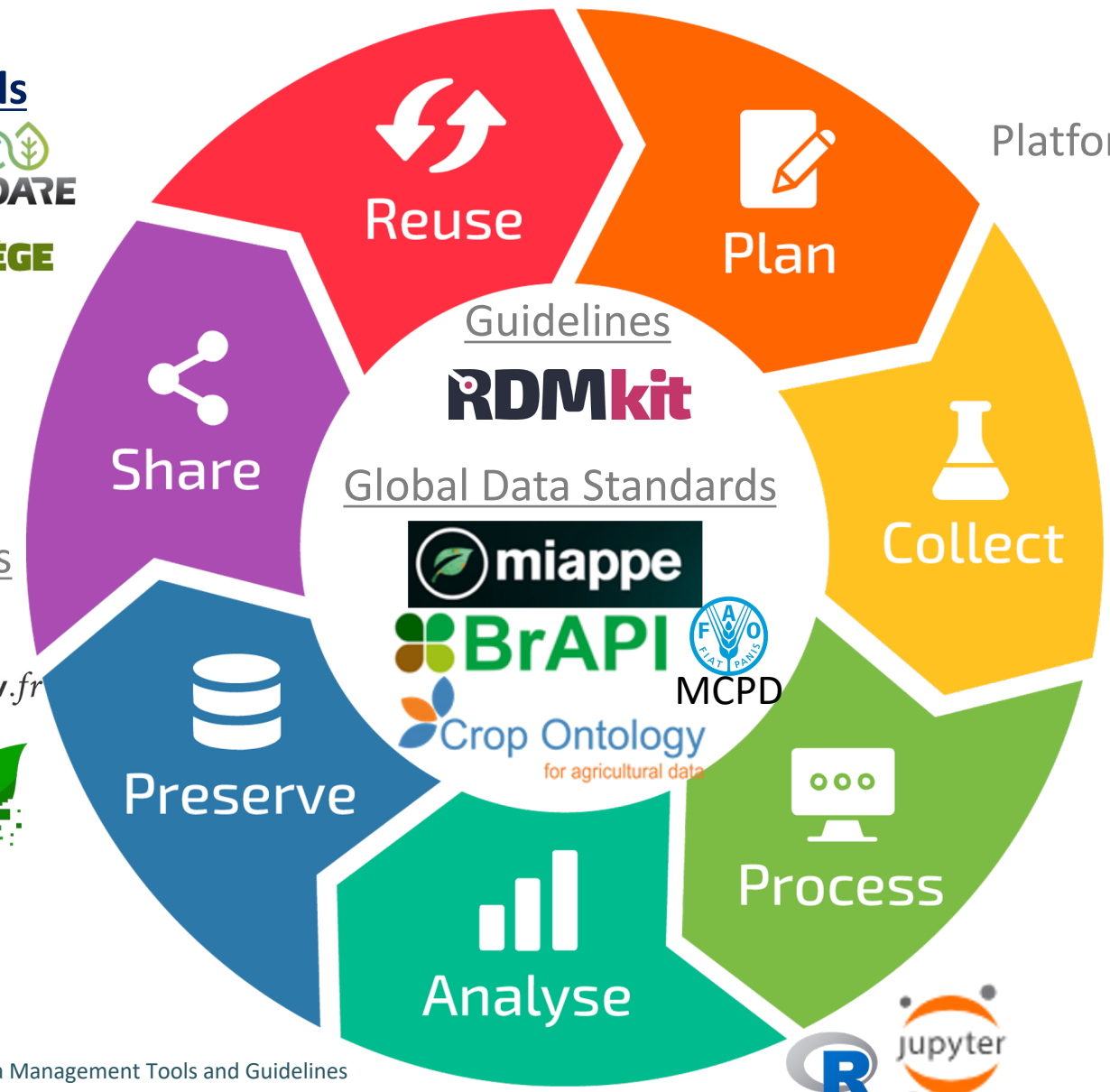
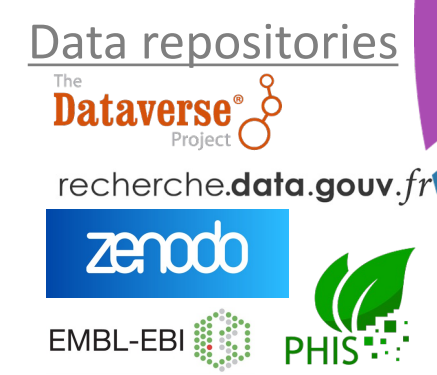
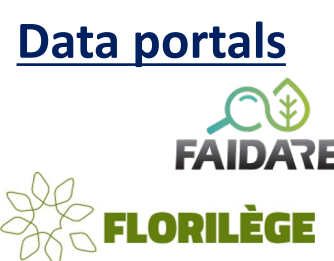


Data repositories

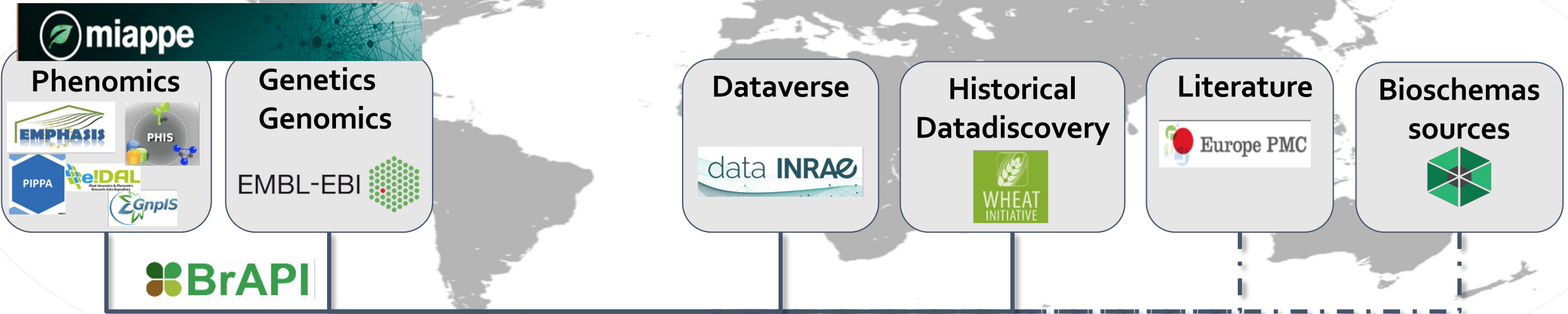




Community data discovery portals



FAIDARE: Global Plant Research Data discovery portal



<https://urgi.versailles.inrae.fr/faidare/>

URGI More...

yield

Results 1 to 20 of 156

Species (21)
Filter on Species...

Data type
 Bibliography [151]
 None [5]

Ontology annotation (20)

10.3389/fpls.2018.00529 - OpenMinTeD@GnpIS
 Bibliography **Triticum Triticum aestivum**
 Global QTL Analysis Identifies Genomic Regions on Chromosomes 4A and 4B H...
 Related Traits Across Different Environments in Wheat (Triticum aestivum L.). 20...
 Genomic Regions on Chromosomes 4A and ... (expand)

10.1186/s12864-019-6005-6 - OpenMinTeD@GnpIS
 Bibliography **Triticum Triticum aestivum**
 Genome-wide association study reveals new loci for **yield**-related traits in Sichu...
 stripe rust stress. 2019 Genome-wide association study reveals new loci for **ye**...

Ontology variable selection

Filter English

- Woody Plant Ontology **Ontology**
 - Biochemical **Trait class**
 - Morphological **Trait class**
 - Other **Trait class**
 - Phenological **Trait class**
 - Budflush **Trait**
 - BF_score_BI: Broadleaves budflush scoring **Variable**
 - Budget date **Trait**
 - BS_date: Budget date **Variable**

Identifier CO_357:1000009
 Name Budget date
 Description Assessment of the date when budget score will be reached for the first time
 Entity bud
 Attribute budget
 Class Phenological
 Main abbreviation BS_date
 Status Standard for INRAE
 Bud date protocol **Method**
 Identifier CO_357:2000014
 Name Bud date protocol
 Description Estimated date from polynomial regression of a time series of budflush or budget scores
 Class Computation
 Calendar day **Scale**
 Identifier CO_357:3000043
 Name Calendar day
 Data type Date
 Min 0
 Max 0
 Documentation [https://urgi.versailles.inrae...](https://urgi.versailles.inrae.fr/...)
 Context of use Research-intensive characterization
 Trial evaluation
 Breeding criterion
 Status Standard for INRAE

OK Cancel

Full text
 +
 Fine criteria
 +
Link back



- 33 databases indexed all over the world






Database (33)

Filter on Database...




Data provider

- INRAE-URGI [47,461,178]
- EBI [12,794,551]
- IPK [402,128]
- Gramene [257,561]
- T3 [223,013]
- UWA [167,167]
- PGSB [140,138]
- Rothamsted Research [137,917]
- EVA [66,510]
- GrainGenes [23,339]
- WUR [6,660]
- CIMMYT [1,788]
- TERRA-REF [1,098]
- CIRAD [722]
- NIB [694]
- VIB [692]
- IBET [67]
- DDBJ [58]
- IPGPAS [8]





France

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Germany

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United Kingdom

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United States

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Mexico

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France

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Europe

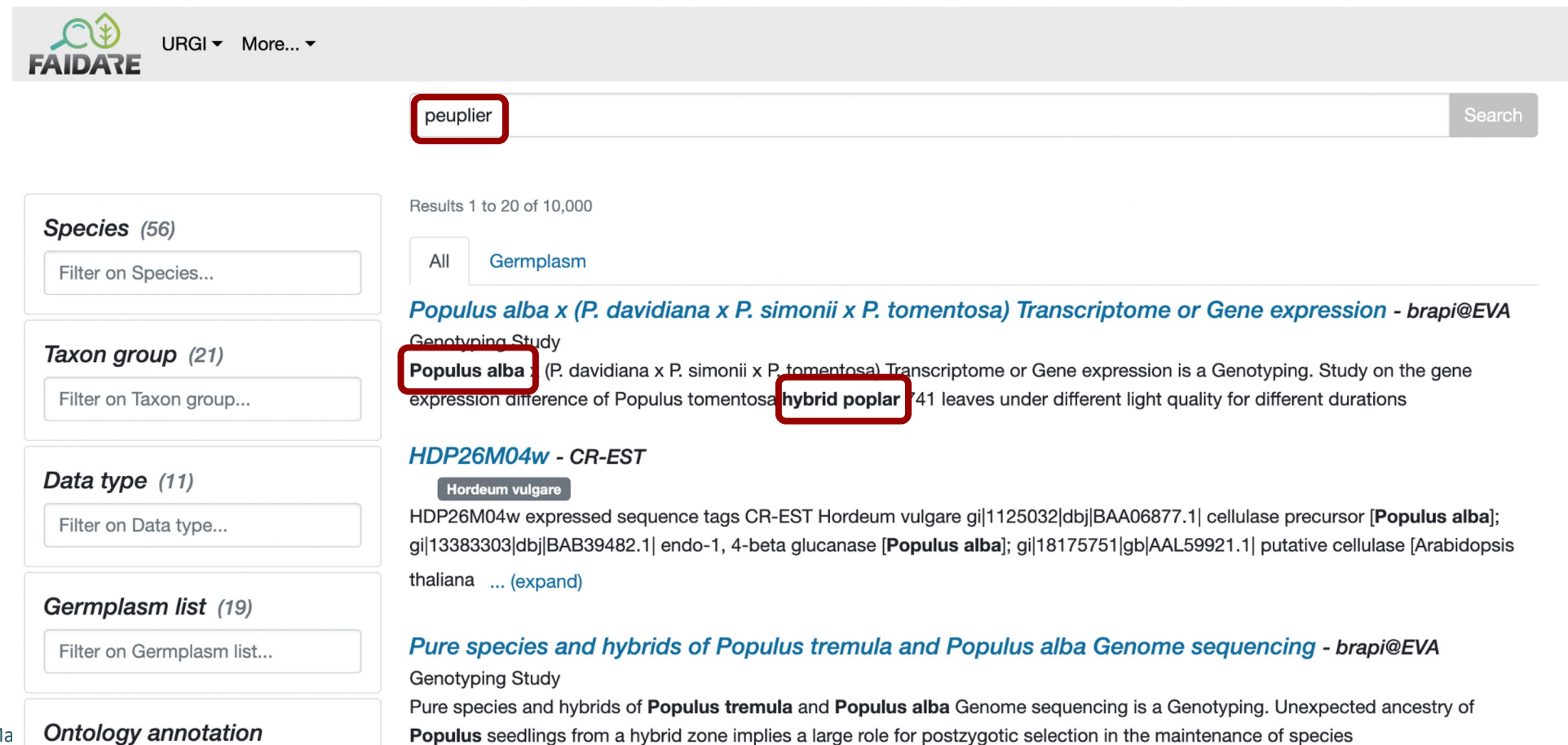
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United States

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Minimal generic (Data Discovery)

- 33 databases indexed all over the world
- Simple full text search
 - Ontology based synonyms



The screenshot shows the FAIDARE search interface. At the top, there is a search bar with the text "peuplier" entered and a "Search" button. Below the search bar, the results are displayed as "Results 1 to 20 of 10,000". On the left side, there are several filter panels: "Species (56)", "Taxon group (21)", "Data type (11)", "Germplasm list (19)", and "Ontology annotation". Each panel has a "Filter on..." button. On the right side, there are search results. The first result is titled "Populus alba x (P. davidiana x P. simonii x P. tomentosa) Transcriptome or Gene expression - brapi@EVA". Below the title, it says "Genotyping Study". The text of the result is "Populus alba (P. davidiana x P. simonii x P. tomentosa) Transcriptome or Gene expression is a Genotyping. Study on the gene expression difference of Populus tomentosa hybrid poplar 41 leaves under different light quality for different durations". The second result is titled "HDP26M04w - CR-EST" and includes a tag "Hordeum vulgare". The text of the result is "HDP26M04w expressed sequence tags CR-EST Hordeum vulgare gi|1125032|dbj|BAA06877.1| cellulase precursor [Populus alba]; gi|13383303|dbj|BAB39482.1| endo-1, 4-beta glucanase [Populus alba]; gi|18175751|gb|AAL59921.1| putative cellulase [Arabidopsis thaliana ... (expand)". The third result is titled "Pure species and hybrids of Populus tremula and Populus alba Genome sequencing - brapi@EVA" and includes the text "Genotyping Study" and "Pure species and hybrids of Populus tremula and Populus alba Genome sequencing is a Genotyping. Unexpected ancestry of Populus seedlings from a hybrid zone implies a large role for postzygotic selection in the maintenance of species".

- 33 databases indexed all over the world
- Simple full text search
 - Ontology based synonyms
- Dedicated filters
 - Data type
 - Taxonomy
 - Genetic resources
 - Crop Ontology
 - Gene Ontology
 - ...

Data type (37)

gen|

- Genome annotation [14,181,486]**
- Gene annotation [3,298,434]
- Gene [117,609]
- Genotyping Study [748]
- Genetic map [165]
- Genotyping Experiment [13]

Data type (37)

ph|

- Physical map feature [2,157,405]**
- Bibliography [2,988]
- Phenotyping Experiment [2,179]
- Phenotyping study [829]
- Phenotyping Study [816]
- Physical map [12]

Species (661)

Filter on Species...

Taxon group (156)

Filter on Taxon group...

- Triticum [20,150,119]**
- Hordeum [88,286]
- Brachypodium [67,367]
- Oryza [53,579]
- Sorghum [52,772]
- Setaria [48,627]
- Italica [48,625]
- Zea [46,973]

Other results are available. Refine your search.

Ontology variable selection

Filter English

- Wheat Crop Ontology **Ontology**
 - Abiotic stress **Trait class**
 - Agronomical **Trait class**
 - Grain weight **Trait**
 - Grain yield **Trait**
 - Lodging incidence **Trait**
 - LS_score: Lodging score **Variable**
 - Plant height **Trait**
 - Precocity **Trait**
 - Biotic stress **Trait class**
 - Other **Trait class**
 - Quality **Trait class**

LS_score **Variable**

Ontology name Wheat Crop Ontology

Identifier CO_321:1000099

Name LS_score

Synonyms Lodging score
Susceptibility to lodging

Institution INRA

Scientist Jacques Le Gouis

Date 15/06/2016

Crop Wheat

Cross reference WIPO:0000099

Lodging incidence **Trait**

Identifier CO_321:0000167

Name Lodging incidence

Description Indicates incidence of lodged plants.

Entity Plant

Attribute Lodging incidence

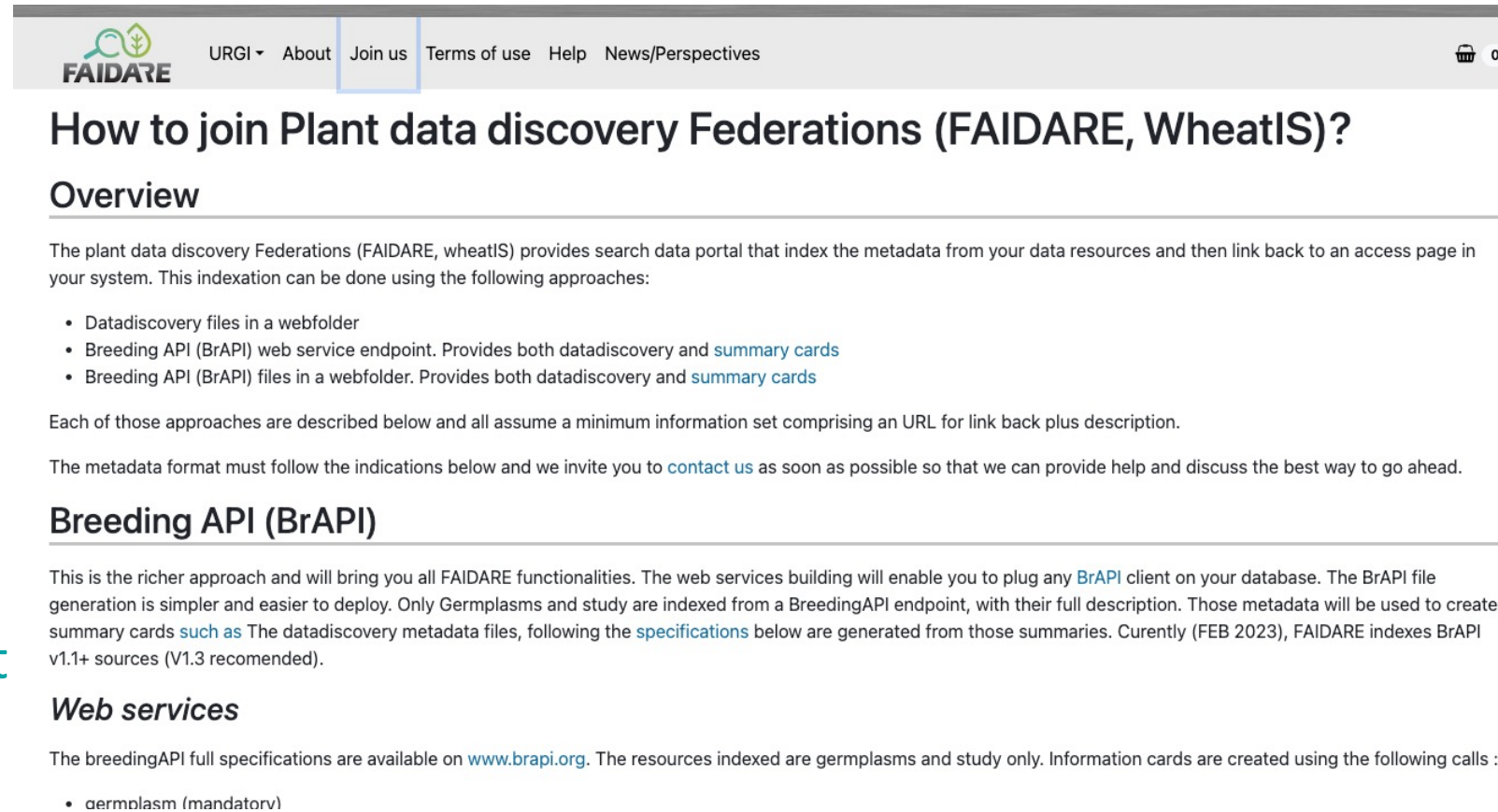
Class Agronomical

Main abbreviation Lodg

Alternative LOD

OK Cancel

- 33 databases indexed all over the world
- Simple full text search
 - Ontology based synonyms
- Dedicated filters
 - Data type
 - Taxonomy
 - Genetic resources
 - Crop Ontology
 - Gene Ontology
 - ...
- Friendly community management
 - Join the Federation support



The screenshot shows the FAIDARE website header with navigation links: URGI, About, Join us, Terms of use, Help, and News/Perspectives. The 'Join us' link is highlighted with a blue box. Below the header is the article title 'How to join Plant data discovery Federations (FAIDARE, WheatIS)?' and the section 'Overview'. The overview text describes the plant data discovery Federations and lists three approaches: Datadiscovery files in a webfolder, Breeding API (BrAPI) web service endpoint, and Breeding API (BrAPI) files in a webfolder. It also mentions that each approach is described below and that the metadata format must follow the indications below. The section 'Breeding API (BrAPI)' follows, explaining that this is the richer approach and will bring all FAIDARE functionalities. The 'Web services' section mentions that the breedingAPI full specifications are available on www.brapi.org.

Aknowledgments

Elixir Plant community & platforms

Beier S., Gruden C., Pommier C., Coppens F, Scholz U, Lange M., Contreras B., Adam Blondon AF, Faria D, Chavez I, Miguel C, Droedsbek B, Finkers R, Papoutsoglou E, Olster R, Ramsak Z, ...



H2020 AGENT



N. Stein (IPK, coord), P. Kersey (RBGK), M. Alaux (INRAE), S. Weise (IPK), C. Pommier (INRAE), M. Lange (IPK), R. Finkers (WUR), J. Destin (INRAE)

MIAPPE community



ELIXIR Plant Community, Krajewsky P, Cwiek H, Tardieu F, Usadel B, Arend D, Arnaud E, Junker A, King G, Laporte MA, Poorter H, Reif J, Rocca-Serra P, Sansone SA, Kersey P, And many more!



Breeding API

Selby P, Mueller L, Robbins K, Backlund JE, ... , And many more!

Crop Ontology



Arnaud E, Laporte MA, ...

Emphasis



Tardieu F, Usadel B, Arend D, Junker A, Poorter H, Neveu P, Pierushka R, Shur U... And many more!

