



Standards for distributed Plant Phenotyping data integration: challenges and solutions.

Cyril Pommier

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<https://hal.science/hal-01779751>

Submitted on 5 Jun 2020

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Standards for Distributed Plant Phenotyping data integration



Challenges and Solutions

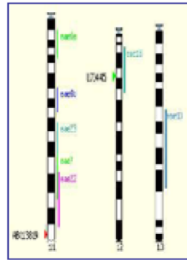
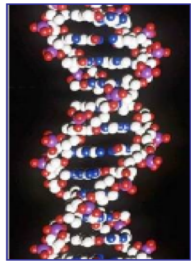


Outline

- FAIR principles
- Data model
- Standards
- Use cases
 - ◆ Information systems : traceability and integration
 - ◆ Standard File format
 - ◆ Web services for analysis and interoperability
 - ◆ Semantic Web & RDF
- Perspectives



Phenotyping $P = G \times E \times C$

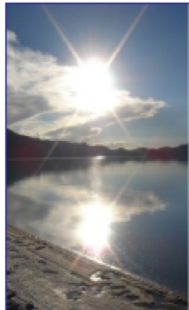


Plant Genotype

Interactions



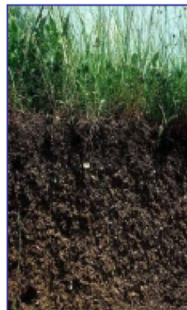
Environment



Climate



Cultural
Practice



Soil



Stress

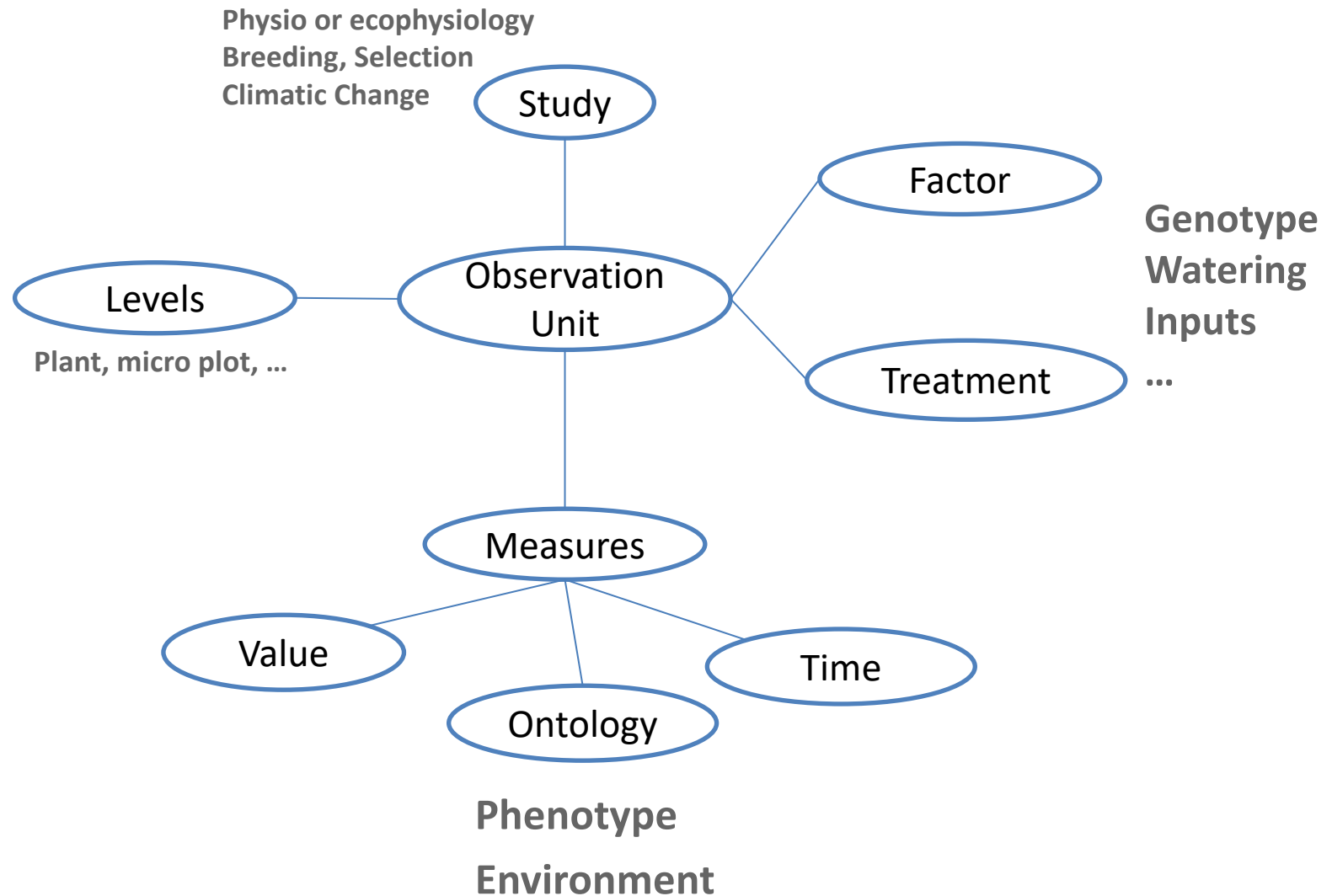
Phenotype



Phenology, Structure, Biochemical content

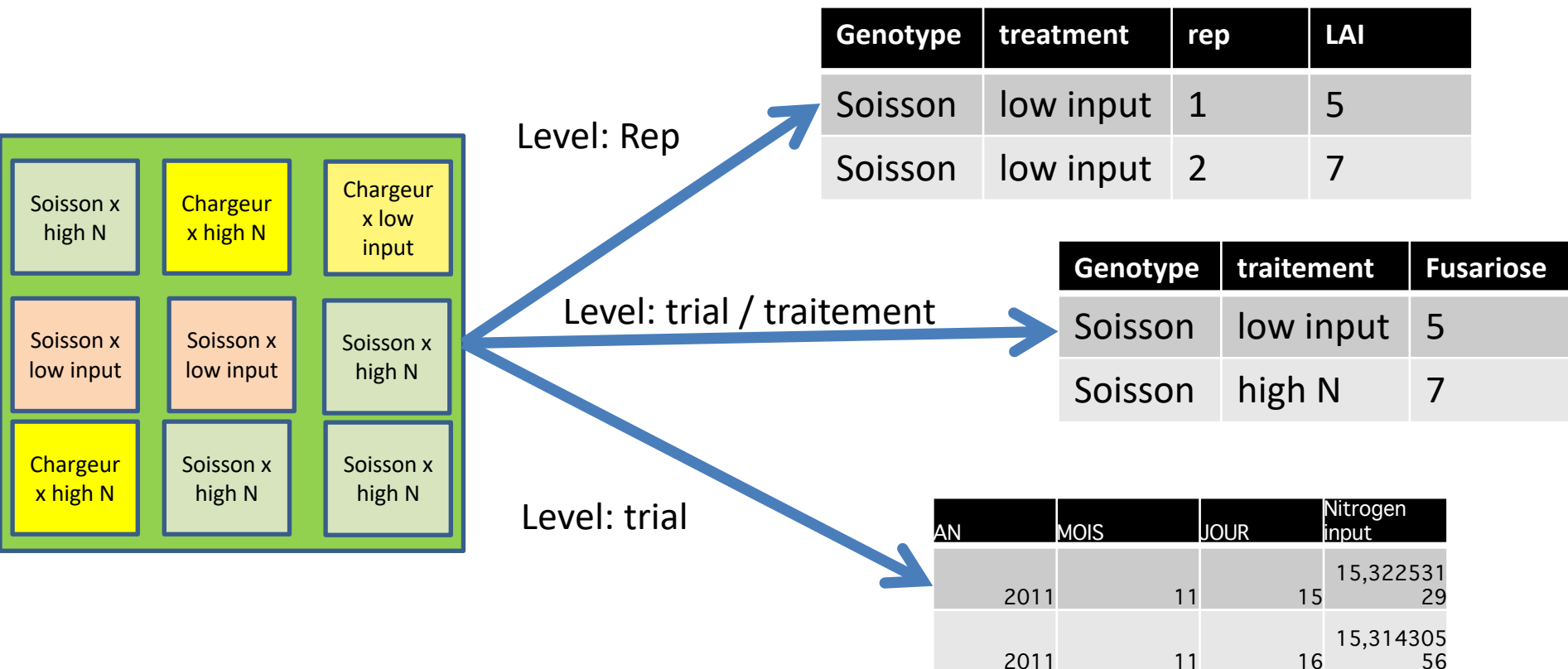
- Trait/Variable : a definition of an observable characteristic
 - ♦ Yield
- Phenotype : A trait/Variable with a value
 - ♦ Yield = 15 Kg by hect

Study/Trial organisation



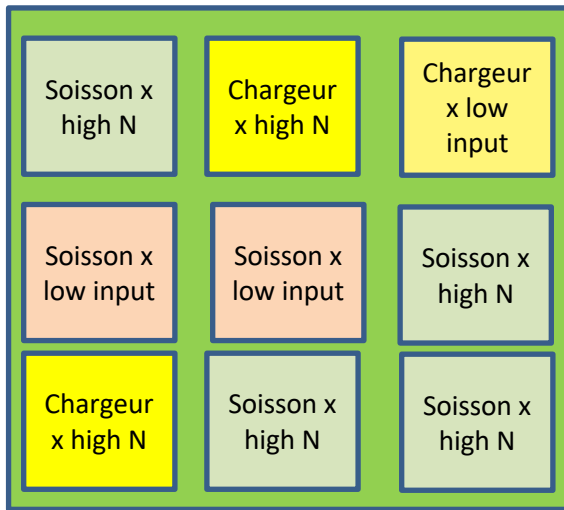
Data life cycle

Raw data

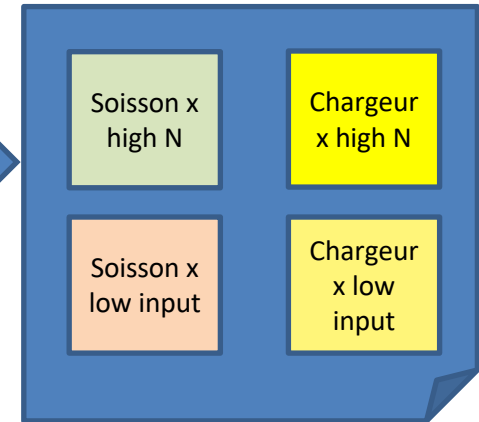


Data Elaboration

Raw data



Elaborated data



Genotype	treatment	rep	LAI
Soisson	fi	1	5
Soisson	fi	2	7

Genotype	treatment	LAI
Soisson	low input	6

Data elaboration

- NIRS

Individual	Genotype	Repetition	Date	4000	4002	4004	4006
662200657-1	662200657	1	Nov11	0.790383794657 181	0.790834341907 288	0.791261293580 598	0.791659233526 804
662200657-2	662200657	2	Nov11	0.817254078896 638	0.817865344054 208	0.818450087726 549	0.819007314250 037
662200659-1	662200659	1	Nov11	0.822434379133 726	0.822871701993 426	0.823268552780 517	0.823649256266 632

- After Calibration and Analysis

Individual	Genotype	Repetition	Gluc_sol	Gluc_solub	Gluc_hydrol	NIRS_id	Date
662200659-1	662200659	1	0.064074733	0.38557928	0.321504547	2274	Nov11

Data elaboration

- LIDAR
 - ◆ Very Big files
 - ◆ Plant Architecture
 - ◆ Raw extraction :
 - Leaf area, leaf angle
 - ◆ Elaboration → % interception
- Metabolomic
 - ◆ MSI Compliant Full description
 - ◆ Elaboration →
 - Leaf Protein concentration
 - Root Cellulose concentration

Data elaboration

- Transformation and computation operation
- Future new analysis to elaborate new variables.
 - Raw data long term conservation
- Need
 - ◆ Reproducibility
 - ◆ Traceability
 - ◆ Provenance

→ FAIR

FAIR Data Principles

Ids
Metadata
Index

F_{indable}



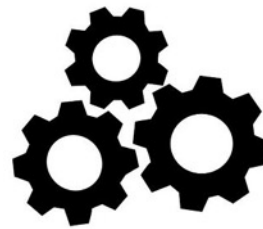
Open Protocols
Persistent Metadata

A_{ccessible}



Semantics
Linked Data
Vocabularies

I_{nteroperable}



License
Well described
Provenance
Standards

R_{eusable}



- Avoid Data Silos
- Interoperable Data and Tools Integration
 - ◆ Linked data
- Repositories Complementarity
 - ◆ Volume and Variety Burden Sharing

FAIR: DATA STANDARDS



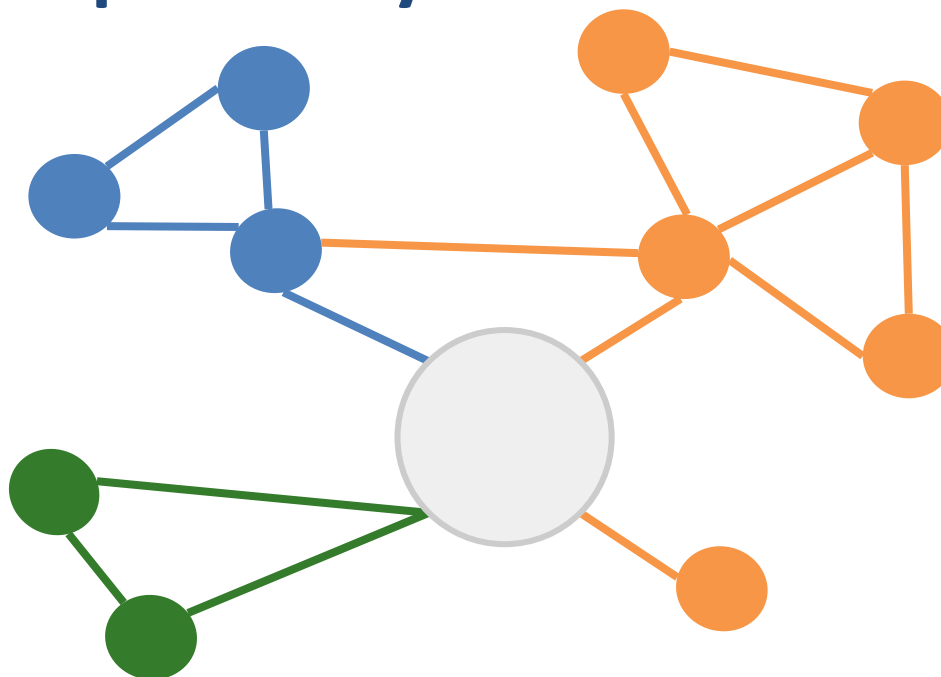
Metadata
Semantic

Interoperability in International network

National Networks



European Networks



Global Networks



International data standards



Minimal information



Controlled vocabularies
Trait dictionaries



MCPD



WheatIS standards

- <http://wheatis.org/DataStandards.php>
- Phenotypes guidelines
- MIAPPE
- Croponontology
- Breeding API

Wheat Data Interoperability Guidelines

[Home](#)
[Guidelines](#)
[Ontologies & Vocabularies](#)
[Use cases](#)
[Getting involved](#)
[About](#)
[Home](#) / [Phenotypes](#)

Phenotypes

Phenotypes are the characteristics of an organism resulting from interactions between genes and the environment. Plant phenotyping can be used in several fields, such as breeding and crop improvement. Phenotypes (traits and associated value) can be used in several fields of agricultural research in multi-location environments, germplasm bank and crop improvement. Furthermore, phenotypes are in interaction, like for instance in the case of gene-environment interactions.

[Getting Involved](#)


1. Data formats

We recommend following minimum format principles with data representation: each variable (trait along with method, units and scales or environmental conditions) should be represented by a unique identifier. This principle has been formalized in the [MIAPPE](#) under improvement.

The [Breeding API](#), described below, is a MIAPPE compliant web service API specification.

There is also an emerging initiative to produce a semantic web version of MIAPPE through a [to RDF transformation](#) (new!).

See the [germplasm recommendations](#) for data format regarding germplasm information.

- Reuse for other crops: Rice, ...

Wheat Data Interoperability Guidelines

[Home](#) [Guidelines](#) ▾ [Ontologies & Vocabularies](#) [Use cases](#) ▾ [Getting involved](#) [About](#) ▾

[Home](#) / [Getting involved](#)

Getting involved

See who endorses the guidelines

To stay relevant and useful for the wheat data community, it is important that the recommendations contained here are maintained. This will be especially true as new technologies are developed requiring standards to be agreed. The maintenance of the guidelines will depend on an ongoing process of monitoring practices across the wheat community, and maintaining communication with those who are producing and using wheat data. There are many ways you can help.

Become an adopter: Please let us know why and how these guidelines are helpful to you and your institution. See the [Current list of adopters](#)

Give your feedback: You can contact us either by email or by leaving a comment on a specific page. This is an easy way to propose improvements or corrections, update the state of the art and share best practices.

Getting Involved



Whe

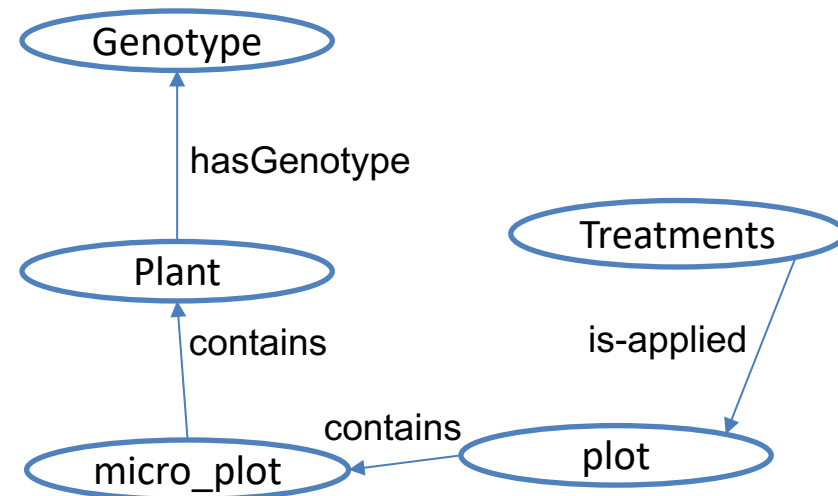
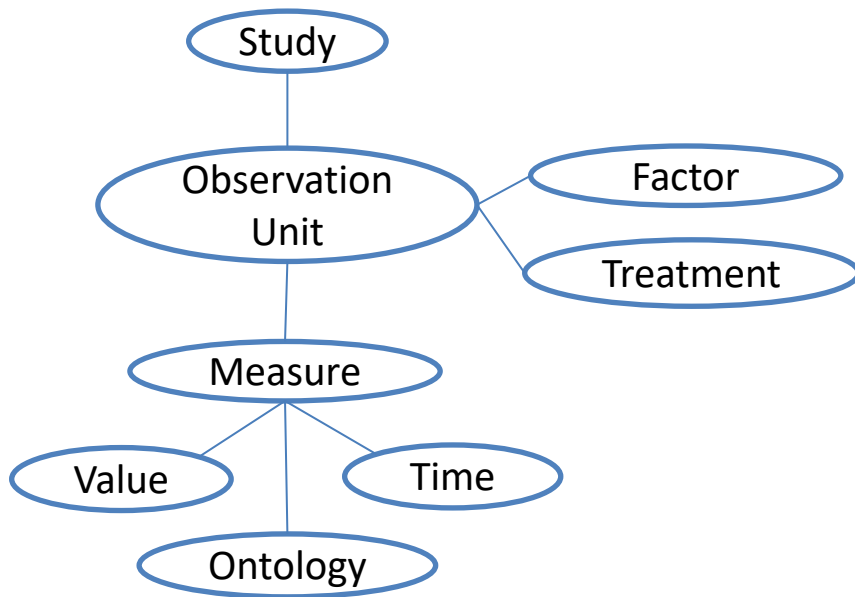
INTEROPERABILITY: SEMANTIC



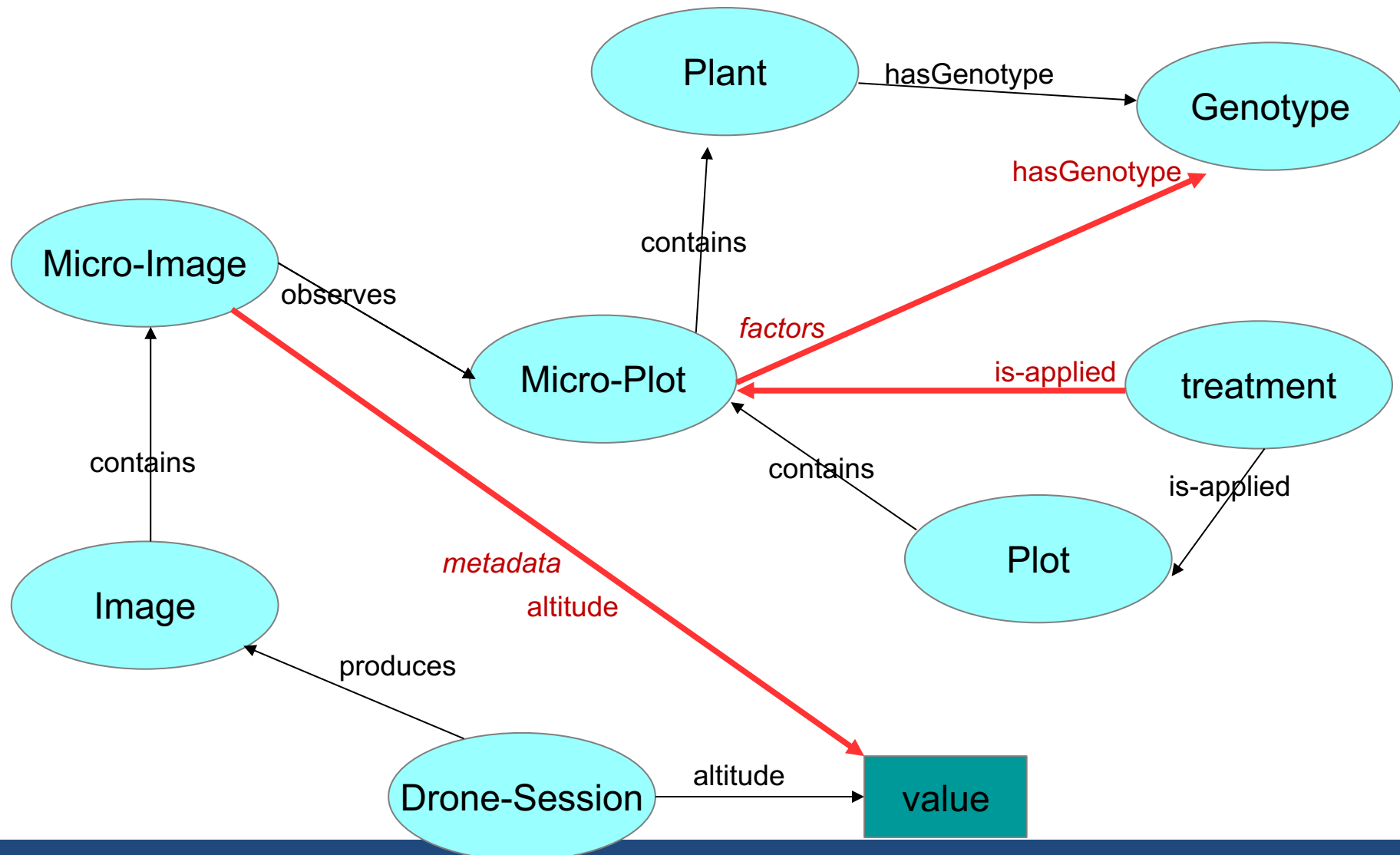
FAIR

Semantic

- Define concepts: plant, micro_plot, phenotype, experiment, event
- Define Relations: micro_plot contains plant
- Common Vocabularies and ontologies
 - ◆ Agrovoc, Plant Ontology, Crop Ontology, Environment Ontology, ...



Semantic Inference



Semantic Inference

- Enables Provenance and Reuse
- Uncouple
 - ◆ Data capture
 - ◆ Data analysis
 - ◆ Data reuse
- Inference allows to format the data for a target use

Phenotype data in breeding

Germplasm ID	PH	PH2	GCOL	GY
24530	80	1	2	35
85432	120	3	4	48
78452	95	2	4	43
56093	100	2	1	50

The height of the plant

The color of the grain

The grain yield

Annotation must explain:

1/ What is the observation about ?

=

TRAIT or Environment

Elizabeth Arnaud et al.

Phenotype data in breeding

Annotation must explain:

Germplasm ID	PH	PH2	GCOL	GY
24530	80	1	2	35
85432	120	3	4	48
78452	95	2	4	43
56093	100	2	1	50

2/ How is the trait observed ?

=

METHOD

With a
measuring tape

Estimated
visually

Calculated
Panicle weight x panicle
density

Elizabeth Arnaud et al.

Phenotype data in breeding

Annotation must explain:

Germplasm ID	PH	PH2	GCOL	GY
24530	80	1	2	35
85432	120	3	3	48
78452	95	2	3	43
56093	100	2	1	50

cm

1 = short (<90cm)
2 = medium
(>90cm and <110cm)
3 = tall (>110cm)

1 = white
2 = cream
3 = yellow

g/m²

3/ How is the trait observation expressed?

=

SCALE

Community Species Ontologies

Elizabeth Arnaud et al.

Phenotype data in breeding

Germplasm ID	PH	PH2	GCOL	GY
24530	80	1	2	35
85432	120	3	3	48
78452	95	2	3	43
56093	100	2	1	50

1 VARIABLE

=

1 TRAIT/ENV

+ 1 METHOD

+ 1 SCALE

Woody Plant Ontology ONTOLOGY

Ontology name	Woody Plant Ontology
Authors	Célia Michotey
Version	v1
Licence	CC BY 4.0
Links	CropOntology TVD5 format Adonis format

Traits, methods and scales

Search terms...

Woody Plant Ontology ONTOLOGY

Agronomical TRAIT CLASS

Fertility TRAIT CLASS

Morphological TRAIT CLASS

Other TRAIT CLASS

Phenological TRAIT CLASS

Physiological TRAIT CLASS

Quality TRAIT CLASS

Stress TRAIT CLASS

Stress: Abiotic stress TRAIT CLASS

Stress: Biotic stress TRAIT CLASS

Bacterial canker girdling index TRAIT

Bacterial canker lesion length TRAIT

Game damages TRAIT

Nests presence TRAIT

NID: Nests presence VARIABLE

NID: Nests presence VARIABLE

Identifier	WOODY:0000067
Name	NID
Synonyms	Nests presence NID[Adonis]
Context of use	Trial evaluation
Status	Standard for INRA
Institution	INRA
Scientist	Célia Michotey
Date	13/03/2017
Crop	Woody Plant

Nests presence TRAIT

Identifier	WOODY:1000056
Name	Nests presence
Description	Presence or absence of nests
Main abbreviation	NID
Status	Standard for INRA
Class	Stress: Biotic stress

Visual scoring METHOD

Identifier	WOODY:2000003
Name	Visual scoring
Description	Visual assessment with a reference scoring scale
Class	Estimation

Presence/ absence SCALE

Identifier	WOODY:3000003
Name	Presence/Absence
Data type	Nominal
Decimal places	0
Min	0

INTEROPERABILITY: STANDARD



Minimum Information About Plant Phenotyping Experiment

- Standard
 - ◆ Data exchange and traceability
 - ◆ Repositories
- Input and output for analysis pipelines developed for phenotyping and genetic
 - ◆ Transplant, Elixir : European eInfrastructure for life science
 - ◆ EPPN and Emphasis European eInfrastructure (ESFRI) for plant Phenotyping
 - ◆ CGIARs
- Implementations
 - ◆ File Archive
 - ◆ Web Service
 - ◆ RDF

Measures for interoperability of phenotypic data: minimum information requirements and formatting

Hanna Ćwiek-Kupczyńska, Thomas Altmann, Daniel Arend, Elizabeth Arnaud, Dijun Chen, Guillaume Cornut, Fabio Fiorani, Wojciech Frohmberg, Astrid Junker, Christian Klukas, Matthias Lange, Cezary Mazurek, Anahita Nafissi, Pascal Neveu, Jan van Oeveren, Cyril Pommier, Hendrik Poorter, Philippe Rocca-Serra, Susanna-Assunta Sansone, Uwe Scholz, Marco van Schriek, Ümit Seren, Björn Usadel, Stephan Weise, Paul Kersey and Paweł Krajewski ✉

Plant Methods 2016 12:44 | DOI: 10.1186/s13007-016-0144-4 | © The Author(s) 2016

Received: 15 April 2016 | Accepted: 18 October 2016 | Published: 9 November 2016



Cy

Towards recommendations for metadata and data handling in plant phenotyping



Paweł Krajewski^{1,*}, Dijun Chen², Hanna Ćwiek¹, Aalt D.J. van Dijk³, Fabio Fiorani⁴, Paul Kersey⁵, Christian Klukas², Matthias Lange², Augustyn Markiewicz⁶, Jan Peter Nap³, Jan van Oeveren⁷, Cyril Pommier⁸, Uwe Scholz², Marco van Schriek⁷, Björn Usadel^{4,9} and Stephan Weise²

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[Table of Contents](#)

This Article

J. Exp. Bot. (2015) 66 (18): 5417-5427.
doi: 10.1093/jxb/erv271
First published online: June 4, 2015
This article appears in: [Special](#)

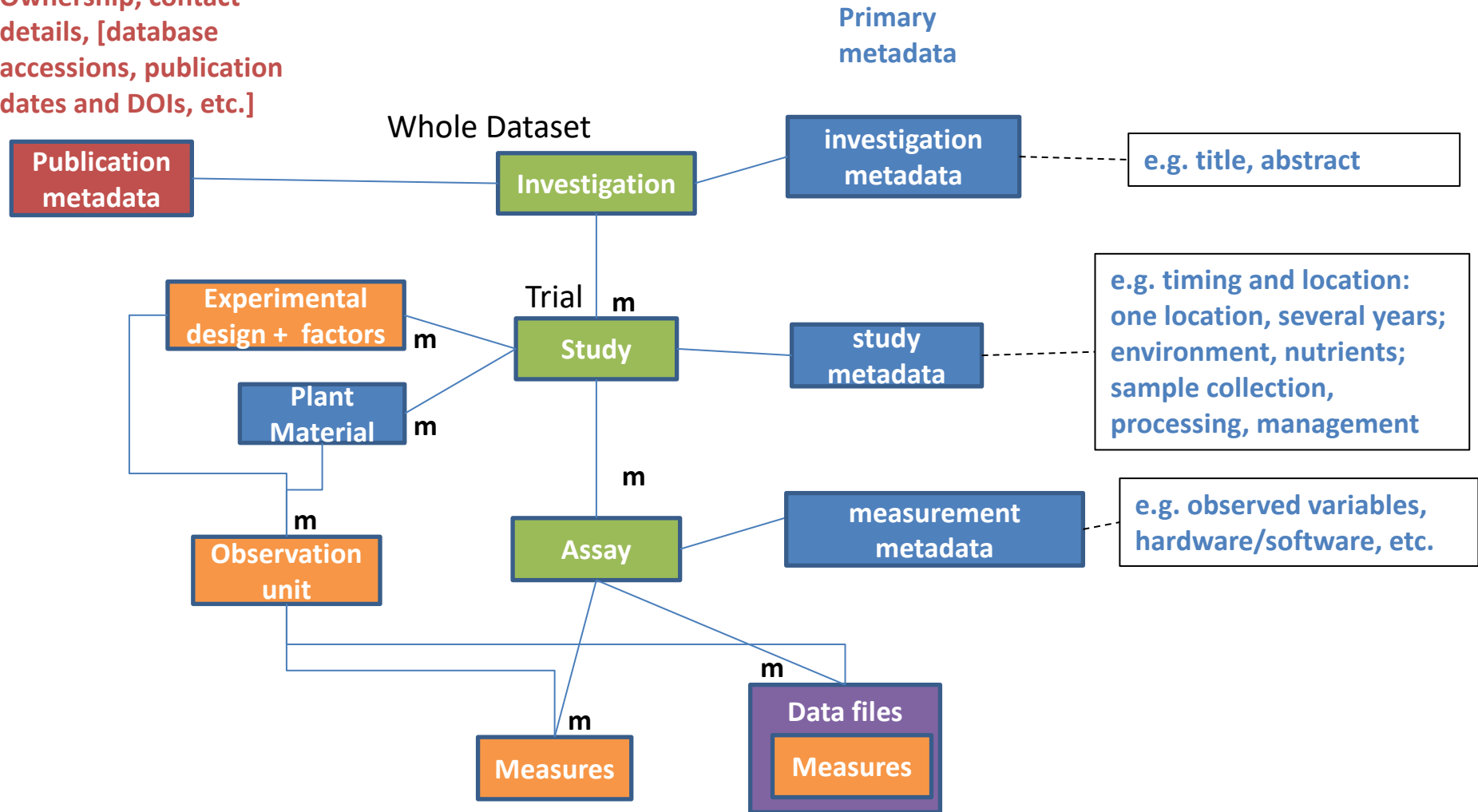
MIAPPE Construction

- Contribution
 - ◆ European Infrastructures : Elixir (Bioinformatics), Emphasis/EPPN (Phenotyping)
 - ◆ National Institutes: France, Germany, Poland, UK, Portugal, Slovenia, Nederland, Belgium, Italy
- Steering committee
 - ◆ Elixir: European Bioinformatic infrastructure
 - ◆ Emphasis: European plant phenotyping infrastructure
 - ◆ Bioversity International - CGIAR
 - ◆ Elizabeth Arnaud, Paul Kersey, Pawel Krajewsky, Matthias Lange, Cyril Pommier, Bjorn Usadel
- Current Versions
 - ◆ Version 1 : Transplant + EPPN + Phenome
 - ◆ Version 1.1 : Elixir, validation in progress
 - Documentation and model: Biologist friendly
 - Adaptations to new implementations
 - Proposal open for consultation contribution welcomed
 - See <http://www.miappe.org> for providing feedback.



MIAPPE v1.1 Overview

Ownership, contact details, [database accessions, publication dates and DOIs, etc.]



MIAPPE v1.1 Overview

Plant Material

- **Biosource : Plant Material identification**
- Multi Crop Passport Descriptor (MCPD) compliant
 - ♦ <https://www.biodiversityinternational.org/e-library/publications/detail/faobiodiversity-multi-crop-passport-descriptors-v21-mcpd-v21/>
 - ♦ FAO & Biodiversity International
 - ♦ Genebanks
- ID Field are reused in MIAPPE
- Key : Identification
 - ♦ 0. Persistent unique identifier : PUID = URI/DOI
 - ♦ 1. Institute code
 - ♦ 2. Accession number
 - ♦ 5. Genus
 - ♦ 6. Species
 - ♦ 7. Subspecies : 'subsp.' (for subspecies); 'convar.' (for convariety); 'var.' (for variety); 'f.' (for form); 'Group' (for 'cultivar group')
 - ♦ 28. Remarks
- Suitable for non Genbank collections : breeder varietal list, laboratory collection, ...

MIAPPE v1.1 Overview

Variables

- Observation Variables
 - ◆ Phenotype & environment
 - ◆ Trait : What is measured
 - ◆ Method : How is it measured
 - ◆ Scale : How is it observed
 - ◆ Variable : trait + method + scale

Traits, methods and scales

DOWNLOAD SHOW OBSOLETE TERMS English

- Wheat traits
 - Abiotic stress traits
 - Acid soil tolerance
 - AcidTol Estimation (method_of)
 - Aluminum tolerance
 - Boron tolerance
 - Cold tolerance
 - Drought tolerance
 - Frost damage
 - Hail damage
 - Heat tolerance
 - Herbicide damage
 - Leaf rolling incidence

Term information

AcdTol Estimation

Identifier CO_321:0000299

Method class Estimation

Method description Observe the growth low pH (acid) soil fi

Method name AcdTol Estimation

Method reference Reynolds et al., 200

Traits, methods and scales

Search terms...

Woody Plant Ontology ONTOLOGY

Woody Plant Ontology ONTOLOGY

Ontology name Woody Plant Ontology

Authors Célia Michotey

Version v1

Licence CC BY 4.0

Links [CropOntology.TVD5 format](#)
[Adonis format](#)

Physiological TRAIT CLASS

Quality TRAIT CLASS

Stress TRAIT CLASS

Stress: Abiotic stress TRAIT CLASS

Stress: Biotic stress TRAIT CLASS

Bacterial canker girdling index TRAIT

Bacterial canker lesion length TRAIT

Game damages TRAIT

NID: Nests presence VARIABLE

Identifier WOODY:0000067

Name NID

Synonyms Nests presence
NID[Adonis]

Context of use Trial evaluation

Status Standard for INRA

Institution INRA

Scientist Célia Michotey

Date 13/03/2017

Crop Woody Plant

Nests presence TRAIT

Identifier WOODY:1000056

Name Nests presence

Description Presence or absence

Main abbreviation NID

Status Standard for INRA

Class Stress: Biotic stress

Visual scoring METHOD

Identifier WOODY:2000003

Name Visual scoring

Description Visual assessment
scoring scale

Class Estimation

Presence/ absence SCALE

Identifier WOODY:2000003

MIAPPE v1.1 overview:

Metabolomic

- Existing standards
 - ◆ Metabolights, Minimum information MSI
 - ◆ Full traceability
 - ◆ Sample treatment : temperature, tissue processing, molecule extraction protocol, measurement protocol....
- MIAPPE
 - ◆ Elaborated data
 - ◆ Elaborated, computed variables: Leaf Sugar content by microplot
 - ◆ Link to Metabo archive
 - Metabolight
 - Metabohub
 - ...

USE CASES



Information Systems for publication and traceability

File archive

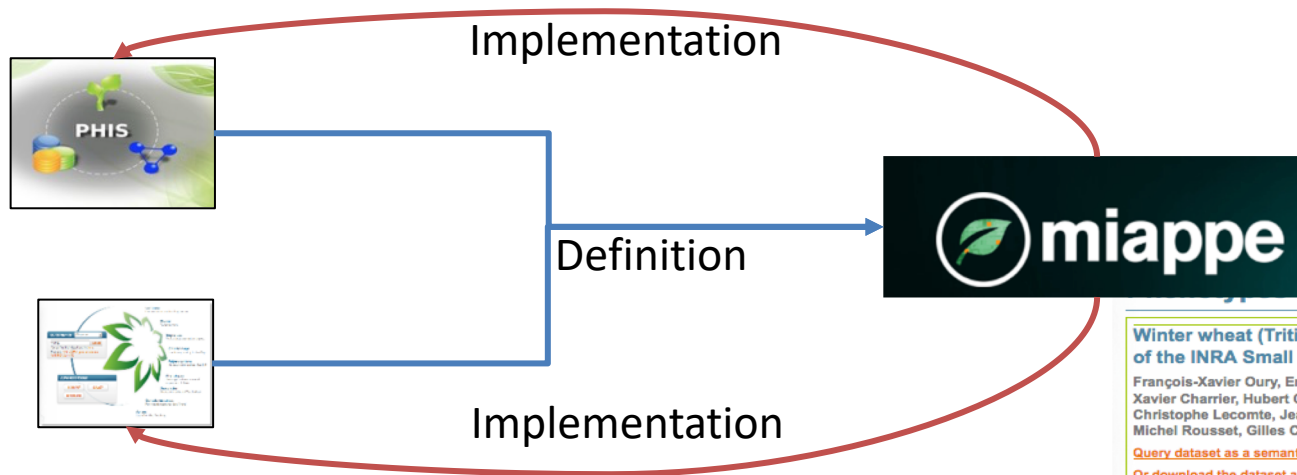
Web services

Semantic web and RDF

USE CASE: DATA REPOSITORIES



MIAPPE: Databases



- Production databases
 - ◆ PHIS
- Cleaned data publication repositories
 - ◆ GnpIS
 - <http://dx.doi.org/10.15454/1.4489666216568333E12>
 - ◆ eDale
 - ◆ PlantPhenoDB
- Implementation
 - ◆ Internal
 - ◆ Web services API

Winter wheat (*Triticum aestivum* L) phenotypic data from the multiannual, multilocal trial of the INRA Small Grain Cereals Network.

François-Xavier Oury, Emmanuel Heumez, Bernard Rolland, Jérôme Auzanneau, Pierre Bérard, Maryse Brancourt, Xavier Charrier, Hubert Chiron, Camille Depatureaux, Laurent Falchetto, Olivier Gardet, Stéphane Gilles, Alex Girard, Christophe Lecomte, Jean-Yves Morlais, Pierre Pluchard, Didier Tropée, Maxime Trottet, Patrice Walczak, Gérard Michel Rousset, Gilles Charmet

[Query dataset as a semantic graph.](#)
[Or download the dataset as RDF archive.](#)

Abstract
 Published 2015 by INRA

[Back to Form](#)

Search parameter(s):

Geolocation

DATA SETS: 4

Network Data Set :
[INRA Wheat Network BRC accession \(A series\)](#)

Network Data Set :
[INRA Small Grain Cereals Network](#)
 DOI: <http://dx.doi.org/10.15454/1.4489666216568333E12>

Network Data Set :
[INRA Wheat Network not BRC accession \(B and C series\)](#)

Origin site Collecting site Evaluation site

Phenotyping campaign(s)

2000 x 2001 x 2002 x 2003 x 2004 x 2005 x 2006 x 2007 x
 2009 x 2010 x 2011 x 2012 x 2013 x 2014 x 2015 x

[remove all](#) [add all](#)

Trial list **Phenotypic data**

[ZURGI](#) [GnpIS](#) 813 trials

Name	Campaign	Site	Direct
BTH Champagne-céréales 2004 SetA1	2004	Champagne-céréales	
BTH Champagne-céréales 2005 SetA1	2005	Champagne-céréales	

MIAPPE databases & FAIR

- Findable: Indexed metadata
- Interoperable : Vocabularies/Ontologies, Plant material ID

Phenotypes

Genotype **Variable** **Trial** Reset Form Results

Traits, methods and scales

Search terms...

☐ Wheat Inra Phenotype Ontology **ONTOLOGY**

☐ Abiotic stress **TRAIT CLASS**

☐ Frost susceptibility **TRAIT**

☐ Lodging score **TRAIT**

☐ LS_score: Lodging score,Susceptibility to lodging **TRAIT**

☐ Agronomical **TRAIT CLASS**

☐ Biotic stress **TRAIT CLASS**

☐ Morphological **TRAIT CLASS**

☐ Other **TRAIT CLASS**

☐ Quality **TRAIT CLASS**

LS_score: Lodging score,Susceptibility to lodging **VARIABLE**

Ontology name: Wheat Inra Phenotype Ontology
 Identifier: WIPO:0000099
 Name: LS_score
 Synonyms: Lodging score,Susceptibility to lodging
 Institution: INRA
 Scientist: Jacques Le Gouis
 Date: 15/06/2016
 Crop: Wheat

Lodging score **TRAIT**

Identifier: WIPO:0010030
 Name: Lodging score
 Class: Abiotic stress

Direct measure **METHOD**

Identifier: WIPO:0020016
 Name: Direct measure
 Description: Mesure directe # ModeOp Arvalis
 Echelle de 1-10 prenant en compte
 %surface versée et l'angle de vers

1 to 9 note **SCALE**

Identifier: WIPO:0030006
 Name: 1 to 9 note
 Data type: Ordinal
 Min: 1
 Max: 9
 Categories: 1 = Resistant
 2 = susceptible

Phenotypes

Genotype **Variable** **Trial** Reset Form Results

Add accession by Genus Reset Tab

Choose a species

Add accession by Panel

Add accession by Collection

Add accession by Name

Paste your Accession Name list

Accession

1-10 of 2,556

Accession Number	Accession Name	Taxon Name
TX816	02438-6HD-106-1	Triticum aestivum aestivum
TX817	02438-6HD-132-1	Triticum aestivum aestivum
TX818	02438-6HD-141-1	Triticum aestivum aestivum
TX811	02438-6HD-15-1	Triticum aestivum aestivum
TX812	02438-6HD-32-1	Triticum aestivum aestivum
TX813	02438-6HD-56-1	Triticum aestivum aestivum
TX814	02438-6HD-78-1	Triticum aestivum aestivum
TX815	02438-6HD-80-1	Triticum aestivum aestivum

MIAPPE databases & FAIR

- Accessible
- Reusable: License, File standard
- Whole Phenotyping Network

Phenotypes

Winter wheat (*Triticum aestivum* L) phenotypic data from the multiannual, multilocal field trials of the INRA Small Grain Cereals Network.

François-Xavier Oury, Emmanuel Heumez, Bernard Rolland, Jérôme Auzanneau, Pierre Bérard, Maryse Brancourt-Hulmel, Xavier Charrier, Hubert Chiron, Camille Depatureaux, Laurent Falchetto, Olivier Gardet, Stéphane Gilles, Alex Giraud, Christophe Lecomte, Jean-Yves Morlais, Pierre Pluchard, Didier Tropée, Maxime Trottet, Patrice Walczak, Gérard Doussinault, Michel Rousset, Gilles Charmet

[Query dataset as a semantic graph.](#)

[Or download the dataset as RDF archive.](#)

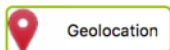
Abstract

Winter wheat phenotypic data from a French experimental network. It includes observations for different characters (agronomic, quality, disease, phenology,...) on more than 10 experimental locations during more than 15 years and for more than 1700 winter wheat genotypes.

Published 2015 by INRA

[Back to Form](#)

Search parameter(s):



DATA SETS: 4

Network Data Set :

[INRA Wheat Network BRC accession \(A series\)](#)

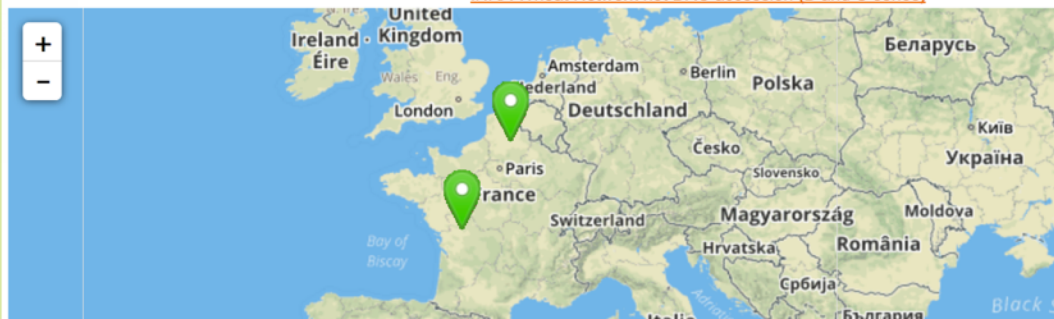
Network Data Set :

[INRA Small Grain Cereals Network](#)

DOI:<http://dx.doi.org/10.15454/1.4489666216568333E12>

Network Data Set :

[INRA Wheat Network not BRC accession \(B and C series\)](#)



Origin site

Collecting site

Evaluation site

2000

2001

2002

2003

2004

2005

2006

2007

2009

2010

2011

2012

2013

2014

2015

remove all

add all

Trial list

Phenotypic data

LEVEL: TRIAL

1-10 of 52,875

Display 10 results per page

Lot Number	Accession Number	Accession Name	Itk	Trial Name
AO13047	39291	AO13047	t: traite	BTH_Champagne-céréal
AO14001	AO14001	AO14001	t: traite	BTH_Champagne-céréal
Bermude	TX9	Bermude	fi: faible intrant	BTH_Clermont-Ferrand_2
AO13030	39286	AO13030	t: traite	BTH_Clermont-Ferrand_2
AO13031	AO13031	AO13031	fi: faible intrant	BTH_Clermont-Ferrand_2
ARKEOS	36693	ARKEOS	t: traite	BTH_Clermont-Ferrand_2
DI13002-2	39307	DI13002-2	fi: faible intrant	BTH_Dijon_2015_SetA1
ARKEOS	36693	ARKEOS	t: traite	BTH_Dijon_2015_SetA1
Bermude	TX9	Bermude	t: traite	BTH_Epi-centre_2015_S
AO13022	AO13022	AO13022	nt: non traite fongicides	BTH_Epi-centre_2015_S

Ephesis data export

Ephesis MIAPPE ISA-Tab export

LEVEL: REPLICATION

1-10 of 81,434

Display 10 results per page

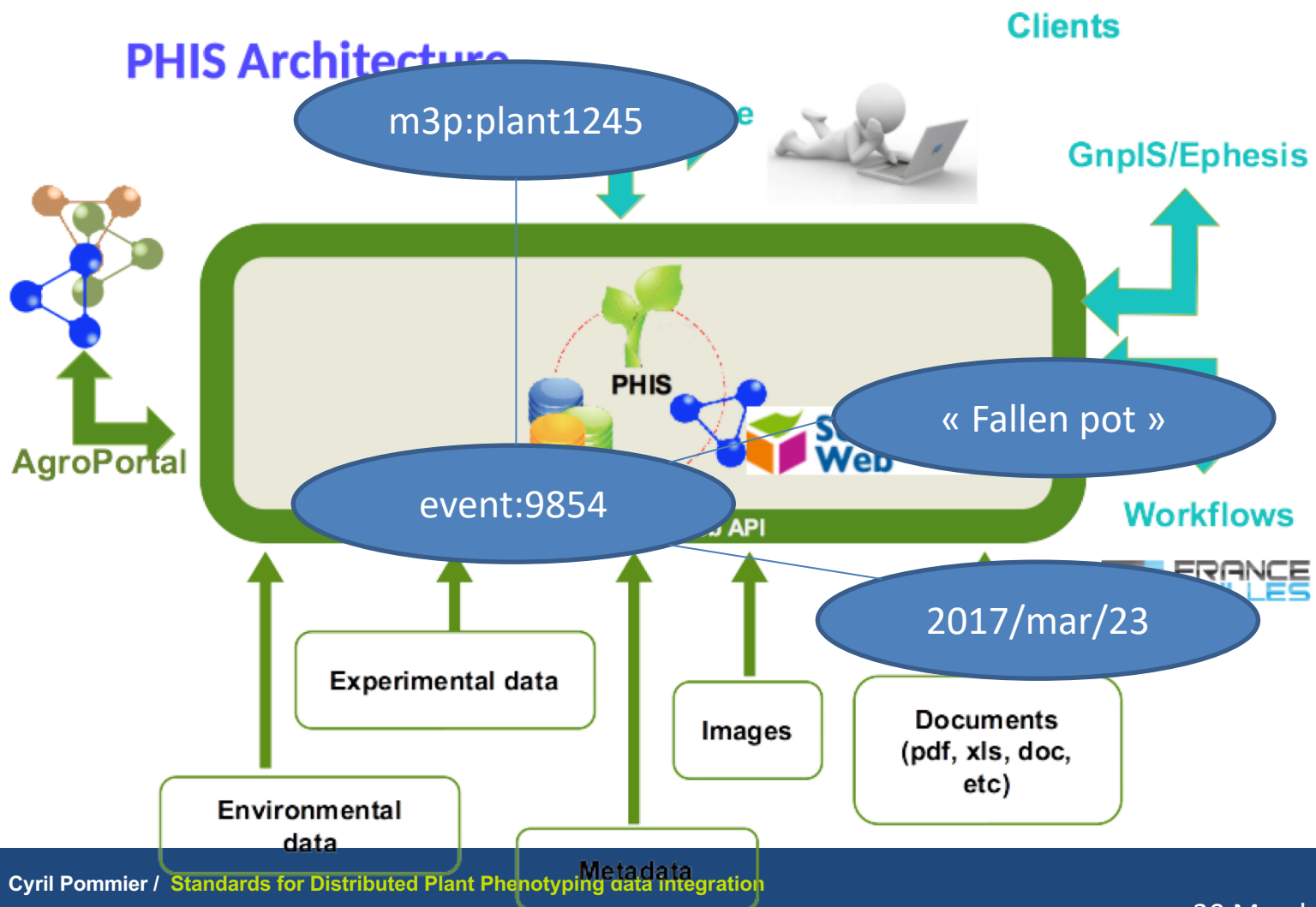
Lot Number	Accession Number	Accession Name	Itk	Trial Name
RE12080	RE12080	RE12080	fi: faible intrant	BTH_Clermont-Ferrand_2
EM11537	37829	EM11537	fi: faible intrant	BTH_Dijon_2015_SetA1
DI13003	39308	DI13003	t: traite	BTH_Dijon_2015_SetA1
AO13015	AO13015	AO13015	t: traite	BTH_Dijon_2015_SetA1
AO13031	AO13031	AO13031	t: traite	BTH_Dijon_2015_SetA1
AO13100	AO13100	AO13100	nt: non traite fongicides	BTH_Epi-centre_2015_S
RUBISKO	36680	RUBISKO	nt: non traite fongicides	BTH_Epi-centre_2015_S
AO11011	37247	AO11011	fi: faible intrant	BTH_Estrées-Mons_2015
DI13003	39308	DI13003	fi: faible intrant	BTH_Estrées-Mons_2015
EM12096	39321	EM12096	fi: faible intrant	BTH_Le_Moulon_2015_S

Ephesis data export

Ephesis MIAPPE ISA-Tab export

MIAPPE databases & FAIR

- Reusable: PHIS high tracability
- Annotation of Observation Units



Example : Data set building with GnplS-Ephesis

- GnplS-Ephesis: INRA Information System, part of Phenome and Elixir
 - François-Xavier Oury, Emmanuel Heumez, Bernard Rolland, Jérôme Auzanneau, Pierre Bérard, Maryse Brancourt-Hulmel, Xavier Charrier, Hubert Chiron, Camille Depatureaux, Laurent Falchetto, et al (2015) Winter wheat (*Triticum aestivum* L) phenotypic data from the multiannual, multilocal field trials of the INRA Small Grain Cereals Network. *doi: 10.15454/1.4489666216568333E12*
 - ◆ DOI : <http://dx.doi.org/10.15454/1.4489666216568333E12>
 - ◆ Winter wheat phenotypic French experimental network.
 - ◆ Observations : agronomic, quality, disease, phenology,...
 - ◆ Integration of 10 experimental locations, 15 years, 1700 genotypes.
- 813 trials/study, 81 000 replications

Wheat datasets publications

- Example of multiple datasets+ integration

- ◆ Shared locations
- ◆ Some common varieties

- Successive publications

- ◆ Initial publication: Agronomy and plant breeding

- ◆ **Quality**
 - Breadmaking
 - Technological

- ◆ **Additional Year: 20**

- Example of multiple datasets integration
 - ◆ Shared locations
 - ◆ Some common varieties
- Successive publications
 - ◆ Initial publication: Agronomical breeding
 - ◆ Quality
 - Breadmaking
 - Technological
 - ◆ Additional Year: 2017

The screenshot displays the NmieG data portal interface. At the top, there are tabs for 'Genotype', 'Variable', and 'Trial'. The main section is titled 'Traits, methods and scales' and features a search bar. Below the search bar, a hierarchical ontology of traits is shown, with 'Wheat Inra Phenotype Ontology' selected. The ontology includes categories like 'Abiotic stress', 'Agronomical', 'Biotic stress', 'Morphological', 'Other', and 'Quality'. The 'Quality' category is expanded, showing sub-traits like 'Alveograph Chopin', 'Breadmaking test BIPEA (G)', 'NmieG: Breadmaking test BIPEA: cr', and 'NpainG: Breadmaking test BIPEA: b'. To the right, a table provides metadata for the 'Wheat Inra Phenotype Ontology' dataset, including its identifier (WIPO:0000238), name (NmieG), synonyms (Breadmaking test BIPEA), institution (INRA), scientist (Arnaud Gauffretau, Fran Oury), and date (21/09/2017). At the bottom, a timeline of years from 2000 to 2015 is displayed, with '2017' highlighted as an additional year.

Scientific Question

- Evolution of wheat mean yield for genebank accessions from 2003 to 2007, including disease interaction.

Wheat Yield dataset building

- MIAPPE Plant Material Selection
- Optional Panel or Collections

Phenotypes

[Reset Form](#) [Results](#)

[Genotype](#) [Variable](#) [Trial](#)

[Reset Tab](#)

Add accession by Genus

Choose a species

Add accession by Panel

Add accession by Collection

Add accession by Name

Paste your Accession Name list

Accession

1-10 of 1,729

Accession Number	Accession Name	Taxon Name
Alberic	Alberic	Triticum aestivum aestivum
29843	ALTIGO	Triticum aestivum aestivum
37771	AO00001	Triticum aestivum aestivum
AO01001	AO01001	Triticum aestivum aestivum
AO03001	AO03001	Triticum aestivum aestivum
AO03002	AO03002	Triticum aestivum aestivum
AO03003	AO03003	Triticum aestivum aestivum
AO03004	AO03004	Triticum aestivum aestivum
AO04001	AO04001	Triticum aestivum aestivum
AO05001	AO05001	Triticum aestivum aestivum

[Plant Material Export](#)

Wheat Yield dataset building

- MIAPPE investigation : Genebank/BRC accessions dataset selection

Phenotypes

Genotype

Variable

Trial

Reset Form

Reset Tab

Add trial by Name

Select your trial names

Add trial by Number

Select your trial numbers

Add trial by Campaign

Select your trial campaigns

Add trial by Site

Select your trial sites

Add trial by Data Set

INRA Wheat Network BRC accession (A series) x |

INRA Small Grain Cereals Network
INRA Wheat Network not BRC accession (B and C series)

Add trial by Project

Selected Trials

1-10 of 258

Trial Number	Trial Name	Trial Site
BTH_Champagne-céréales_2004_SetA1	BTH_Champagne-céréales_2004_SetA1	Champagne-céréales
BTH_Champagne-céréales_2005_SetA1	BTH_Champagne-céréales_2005_SetA1	Champagne-céréales

Wheat Yield dataset building

- MIAPPE Assay/Observation variable:
 - ◆ Yield and stress variables selection
 - ◆ See BrAPPS

Genotype
Variable
Trial

Traits, methods and scales

☒
Wheat Inra Phenotype Ontology
ONTOLOGY

☒
Biotic stress
TRAIT CLASS

☒
Disease score Yellow Rust
TRAIT

☒
YR-Score_score: Yellow rust score

☒
Susceptibility to leaf rust
TRAIT

☒
rb: Susceptibility to leaf rust
VARIABLE

Ontology name Wheat Inra Phenotype Ontology
Identifier WIPO:0000162
Name YR-Score_score
Synonyms Yellow rust score
 Susceptibility to stripe rust
Institution INRA
Scientist Jacques Le Gouis
Date 15/06/2016
Crop Wheat

Disease score yellow rust
TRAIT

Identifier WIPO:0010065
Name Disease score Yellow Rust
Class Biotic stress

1 to 9 note
SCALE

Identifier WIPO:0030006
Name 1 to 9 note
Data type Ordinal
Min 1
Max 9
Categories 1 = Resistant
 9 = susceptible

Wheat Yield dataset building

- Easy Subsetting
~ Third of 81 000 replications
- Reuse through
MIAPPE ISA Tab File
export

[Back to Form](#)

☐ [Search parameter\(s\):](#)

Genus:
 Number of Variable(s): 34

Geolocation

DATA SETS: 7
 Network Data Set :
[INRA Wheat Network BRC accession \(A series\)](#)

 Network Data Set :
[INRA Small Grain Cereals Network](#)
 DOI:<http://dx.doi.org/10.15454/1.4489666216568333E12>

 Network Data Set :
[INRA Wheat Network not BRC accession \(B and C series\)](#)

Phenotyping campaign(s)

[remove all](#) [add all](#)

[Trial list](#) [Phenotypic data](#)

Data table view :

LEVEL: REPLICATION

| Display results per page

GENOTYPE ID			TREATMENT		
Lot Number	Accession Number	Accession Name	itk	Trial Name	Trial Site
CF99105	20364	CF99105	untreated, no fungicide	BTH Estrées-Mons 2003_SetA1	Estrées-Mons
Recital	6027	RECITAL	low inputs	BTH Le Moulon 2003_SetA1	Le Moulon
Koreli	29814	KORELI	untreated, no fungicide	BTH Orgeval 2003_SetA1	Orgeval
CF00108	23825	CF00108	untreated, no fungicide	BTH Rennes 2003_SetA1	Rennes
Isengrain	13433	ISENGRAIN	treated	BTH Dijon 2003_SetA2	Dijon
RE02101	23821	RE02101	treated	BTH Le Moulon 2003_SetA2	Le Moulon
EM01288	EM01288	EM01288	treated	BTH Lusignan 2003_SetA2	Lusignan
DI03006	DI03006	DI03006	treated	BTH Clermont-Ferrand 2003_SetB1	Clermont-Ferrand
DI03001	DI03001	DI03001	treated	BTH Dijon 2003_SetB1	Dijon
Caphorn	20443	CAPHORN	untreated, no fungicide	BTH Orgeval 2003_SetB1	Orgeval

Ephesis data export
 Ephesis MIAPPE ISA-Tab export

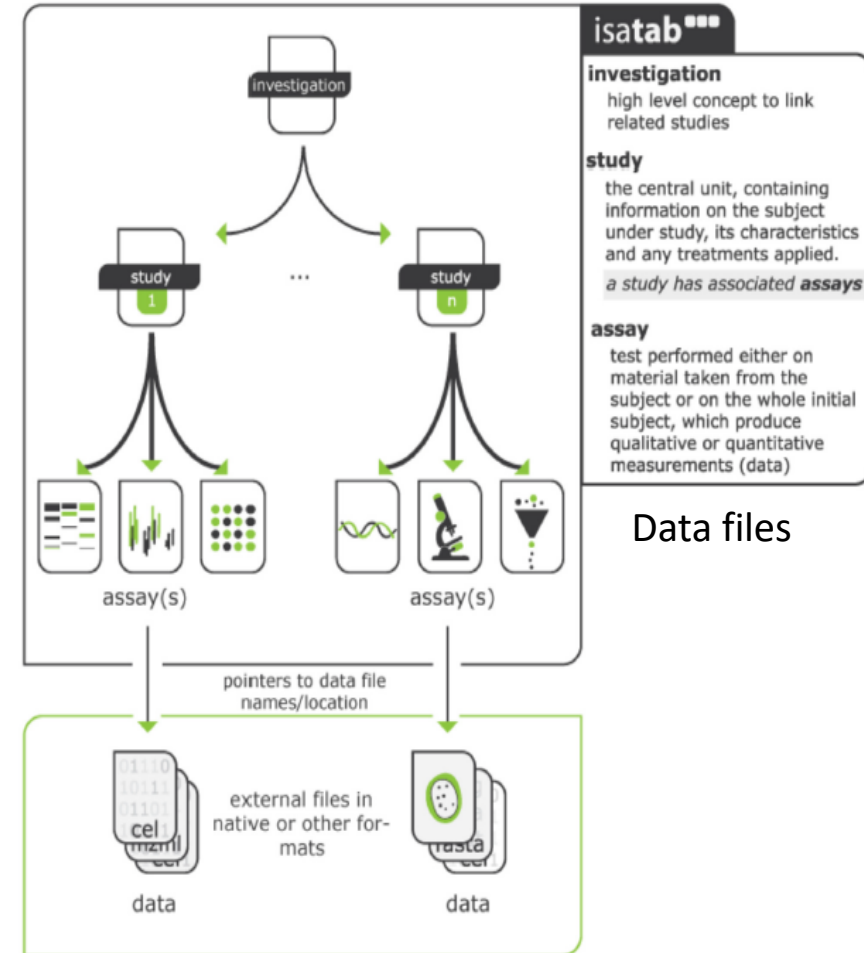
USE CASE: FILE ARCHIVE



MIAPPE ISA Tab

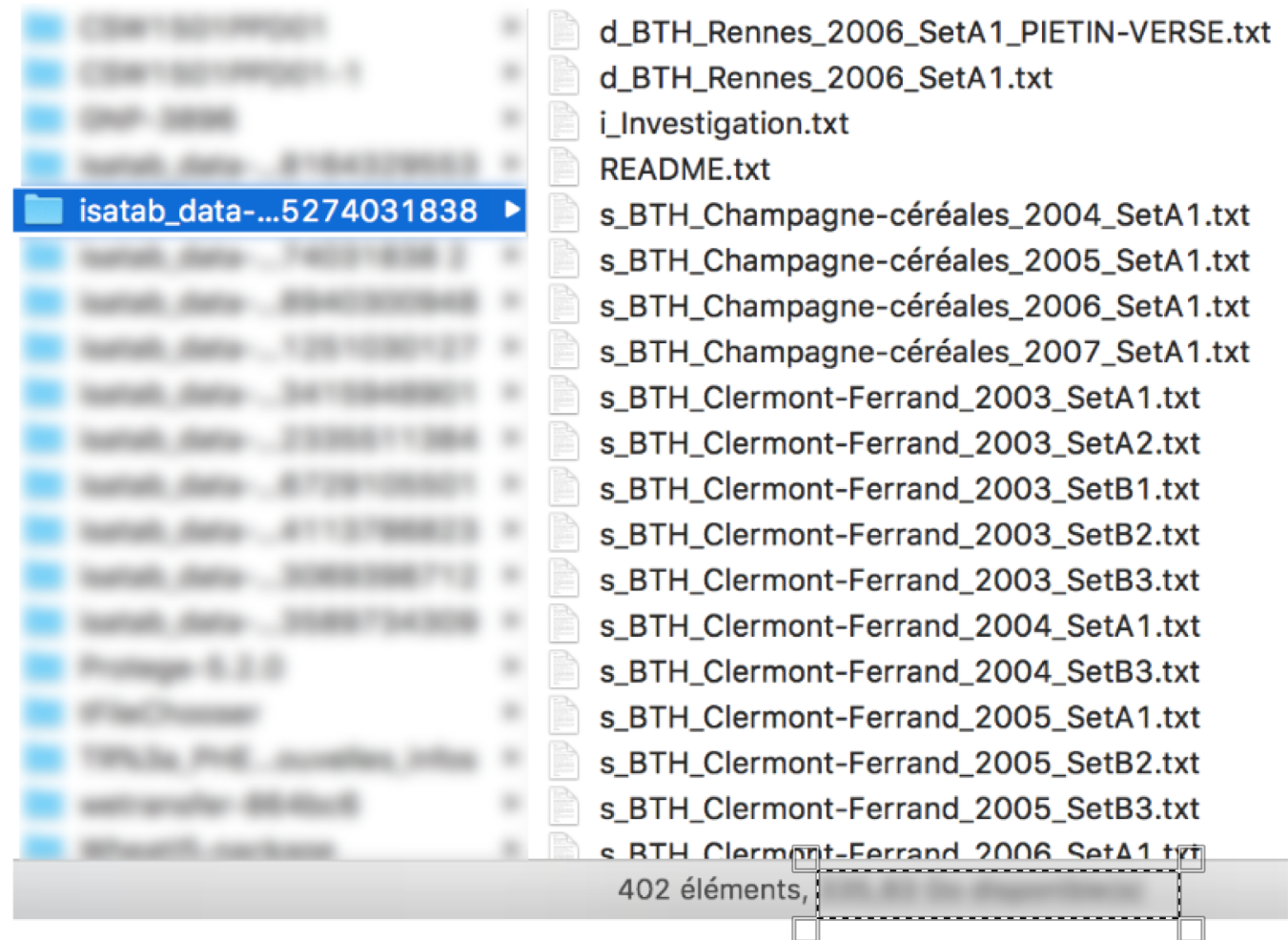
MIAPPE File Archive

- ISA Tab for Phenotyping
 - ◆ Investigation/Study/Assay
 - ◆ Zip Archive
 - MIAPPE Metadata
 - Raw data
 - CSV
 - Images or binary files
 - Reference to image archive (URI/URL)
 - Elaborated data
 - CSV
 - Provenance
- Training and improvements
 - ◆ File and metadata curation
 - Elixir
 - Célia Miguel & Anne Françoise Adam Blondon
 - ◆ BrAPI to IsaTab portable tool
 - Elixir implementation study for MIAPPE Validation
 - Frederik Coppens & H. Parkinson & M. Courtot + Elixir-fr-nl, ISA Framework, ...



MIAPPE File: Wheat Yield dataset

- Zip archive
- 402 files
- README
- i_Investigation.txt :
initial file, bootstrap
- **MIAPPE v1.0**
 - ◆ Not MIAPPE V1.1



MIAPPE File

- Derived data file : d_BTH_Rennes_2003_SetA1.txt

Observation Unit	A	B	C	D	E	F	G	H
Assay Name		Trait Value [r]	Trait Value [rdt]	Trait Value [ht]	Trait Value [prec]	Trait Value [prot]	Trait Value [oid]	Trait Value [knt]
Triticum_aestivum_aestivum-CF00108-CF00108-itk:t-2003		96,6	96,4	80	138	10,2	1	
Triticum_aestivum_aestivum-AO03001-AO03001-itk:nt-2003		103,3	86,2	93	141		1	

- Metadata files

Sample Name	Measurement	Factor Value [itk]	Assay Name	Characteristics [knt]
Triticum_aestivum_aestivum-FARANDOLE-Farandole		untreated, no fungicide	Triticum_aestivum_aestivum-FARANDOLE-Farandole-itk:nt-2003	Farandoleitknt
Triticum_aestivum_aestivum-Ressor-Ressor		low inputs	Triticum_aestivum_aestivum-Ressor-Ressor-itk:fi-2003	Ressoritkfi

A	B	C	D	E
Source Name	Characteristics [Organism]	Characteristics [Infra-specific]	Characteristics [accession number]	Characteristics [accession number]
Triticum_aestivum	Triticum aestivum aestivum	Orvantis	14088	ORVANTIS
Triticum_aestivum	Triticum aestivum aestivum	Recital	6027	RECITAL

- Raw data file: analysis input

Accession Name	itk	Trial Name	Trial Site	X(m)	Y(m)	Campaign	GDD	prot: Grain p	Date [prot]	rdt: Grain yie	Date [rdt]	sept: Se
RECITAL	treated	BTH_Renn	Rennes			2003		10,4		88,4		
TAMARO	untreated, no	BTH_Renn	Rennes			2003				60,7		
DI01022	untreated, no	BTH_Renn	Rennes			2003				95,2		

USE CASE: WEB SERVICES



- Breeding API
- International collaboration
 - ◆ Excellence in Breeding platform (CGIAR)
 - ◆ Coordinator : Peter Selby
 - ◆ Lead: Lukas Mueller, Jan Erik Backlund, Kelly Robbins
- Vision :
 - ◆ Standard Open API
 - ◆ Easy, secure, and efficient
 - ◆ Information Exchange
 - ◆ Between systems and applications
 - ◆ Breeding is the main target

Bill & Melinda Gates Foundation

CassavaBase

T3

IBP

JHI

Bioversity

CIRAD

INRA

IRRI

GOBII

Wageningen

CIP

DaRT

Cornell

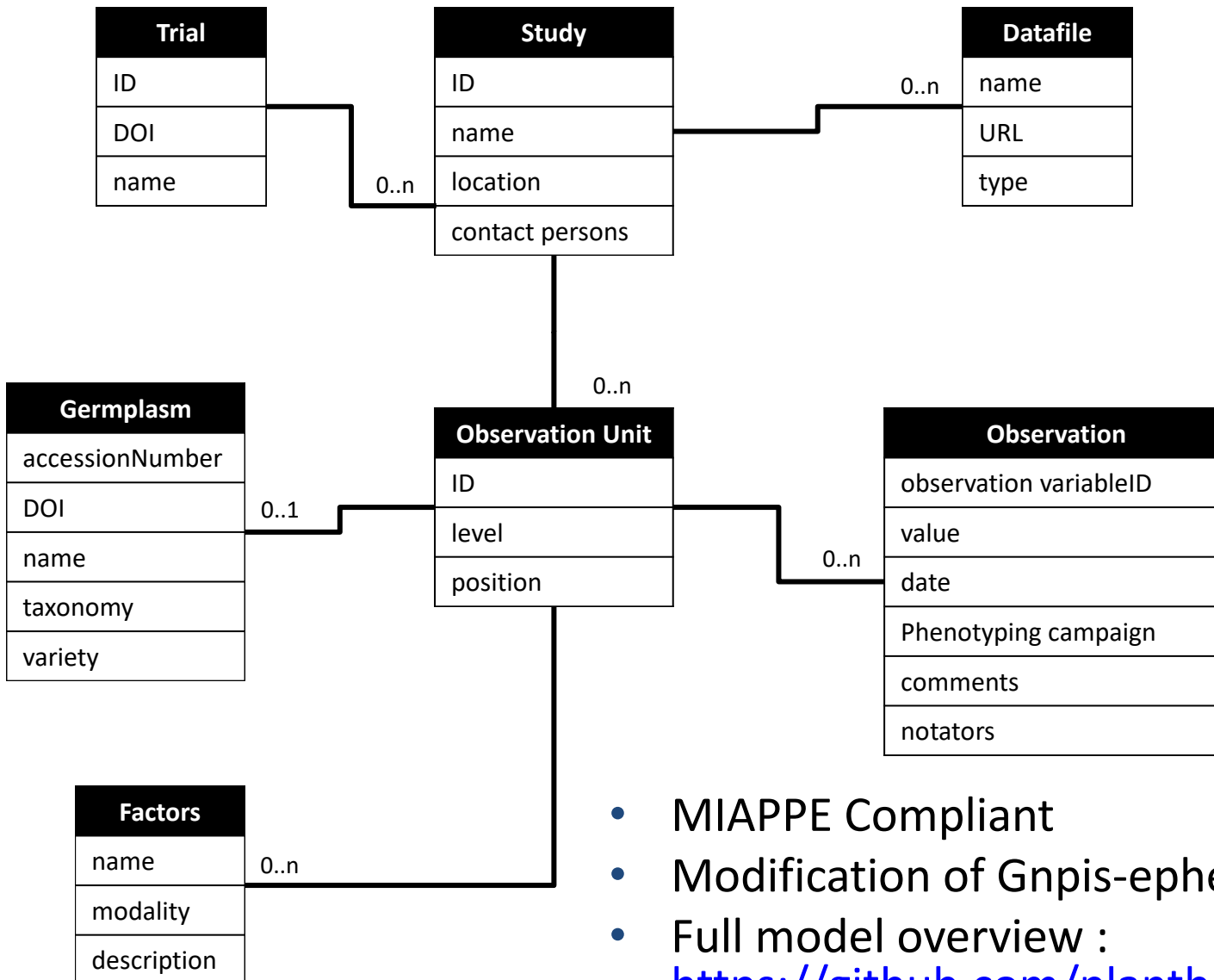
iPlant

BILL & MELINDA
GATES foundation



- Resources
 - ◆ <http://brapi.org/>
 - ◆ Specifications
 - <https://brapi.docs.apiary.io/#reference>
 - <https://github.com/orgs/plantbreeding>
- Servers implementations
 - ◆ CGIARs international network
 - Integrated Breeding Platform, Breeding Management System
 - ◆ Elixir Excelerate
 - ◆ Emphasis: PHIS
 - ◆ Germinate
 - ◆ GnplS
- Clients implementations
 - ◆ Flapjack : genotyping data visualization
 - ◆ Phenome-fppn portal, GnplS
 - ◆ R analysis pipelines
- BrAPPS
 - <https://www.brapi.org/brapps.php>
 - ◆ Ontology Widget
 - <https://github.com/gnpis/trait-ontology-widget>

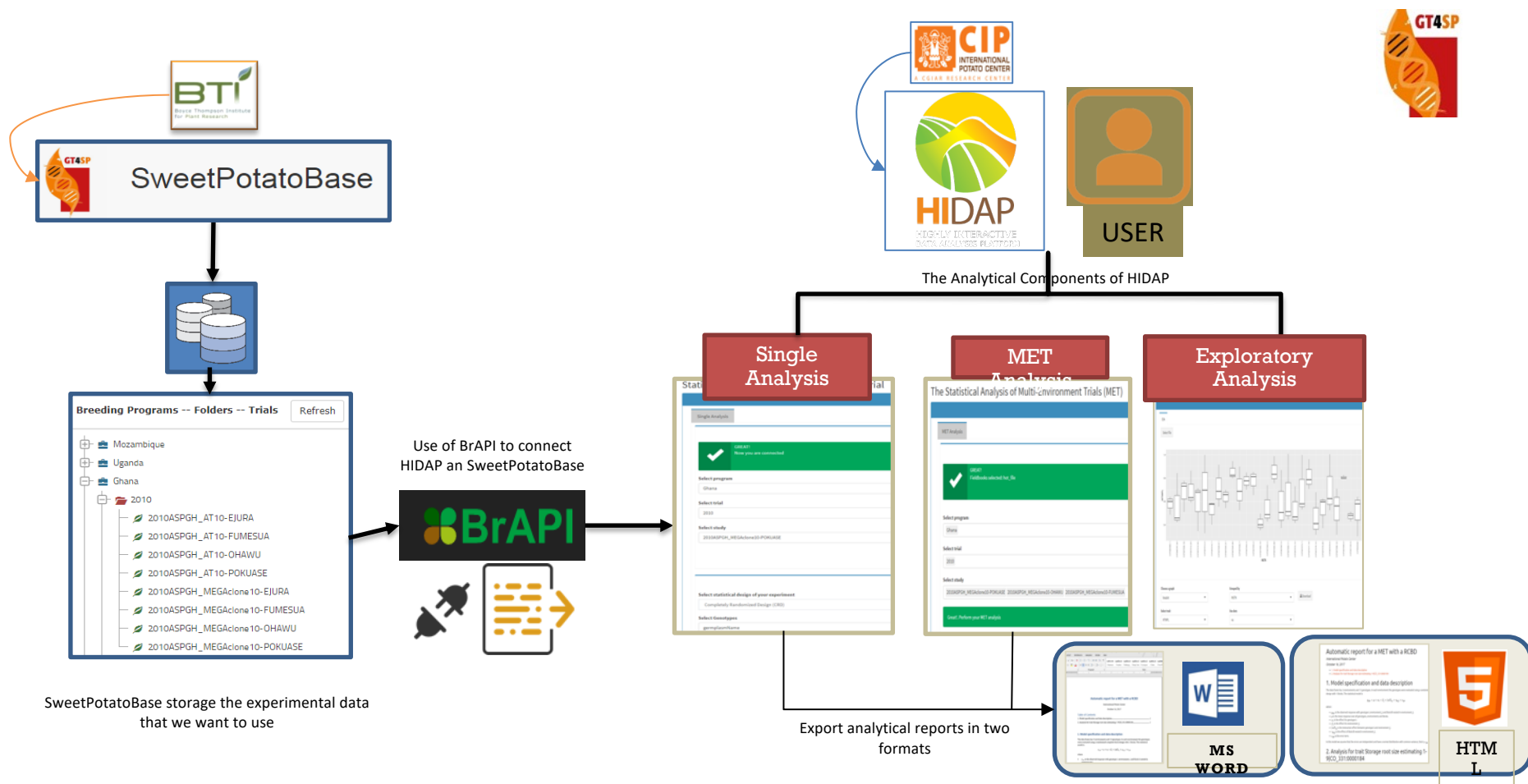
Implicit Phenotyping Model overview



- MIAPPE Compliant
- Modification of Gnpis-ephephesis publication
- Full model overview : <https://github.com/plantbreeding>

USE case WS1: BrAPI for R analysis

Workflow HIDAP-SweetPotatoBase



Brapi/v1/study/table web service → ISA Raw data file

R brapi libraries: on github

Hub, Inc. [US] | <https://github.com/CIP-RIU/brapi>

README.md

BrAPI R package

build passing build passing coverage 51%

This version is still under development. The implementation sometimes changes minor details.

README

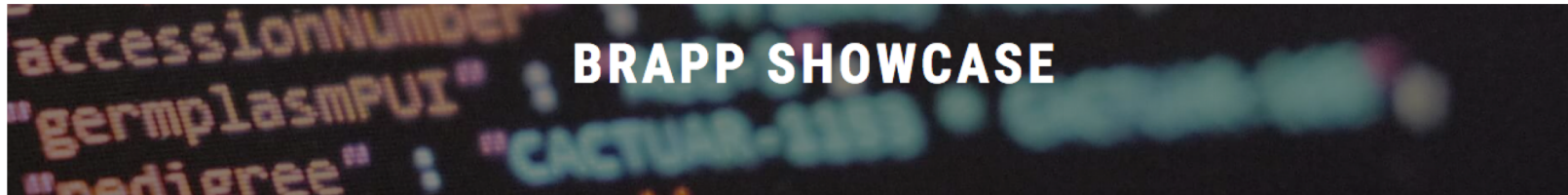
An R package to use the [Breeding API \(BrAPI\)](#) for accessing plant breeding data.

It can be installed using:

```
install.packages("devtools")
devtools::install_github("CIP-RIU/brapi")
```

USE case WS2: BrAPPS

- Tools integrable in any BrAPI compliant System
 - ◆ <https://www.brapi.org/brapps.php>



Welcome to the BrAPI Application Showcase, or BrAPPs for short. Each of these BrAPPs is an independent tool which can run on its own or can be easily integrated with a larger system. And of course, each BrAPP is completely BrAPI driven and can be used with any BrAPI compliant system. The goal is to keep the BrAPI community informed about what tools are available and encourage functionality sharing. If you have a BrAPP you would like to share with the community please reach out to a [BrAPI Coordinator](#)



GRAPHICAL FILTERING TOOL

FROM [CASSAVABASE](#)

DEMO SOURCE DOCS

Built by CassavaBase, this is a fully BrAPI compliant tool for graphically building complex search and filter queries of Observational Data.



STUDY COMPARISON TOOL

FROM [CASSAVABASE](#)

DEMO SOURCE DOCS

Built by CassavaBase, this is a fully BrAPI compliant tool for comparing the performance of germplasm across studies.



VARIABLE ONTOLOGY WIDGET

FROM [URGI - INRA](#)

DEMO SOURCE DOCS

Built by URGi - INRA, this is a JavaScript widget displaying all the observation variables of a BrAPI endpoint.



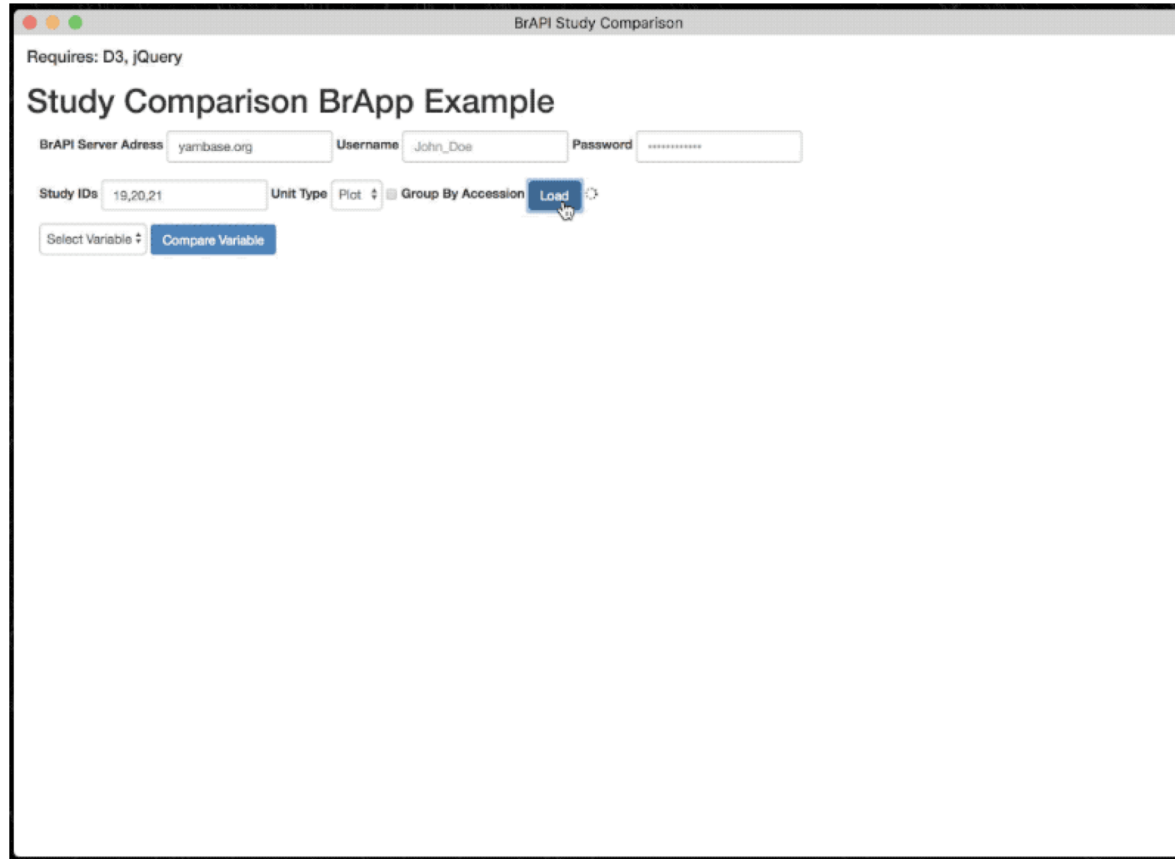
PEDIGREE VIEWER

FROM [CASSAVABASE](#)

DEMO SOURCE DOCS

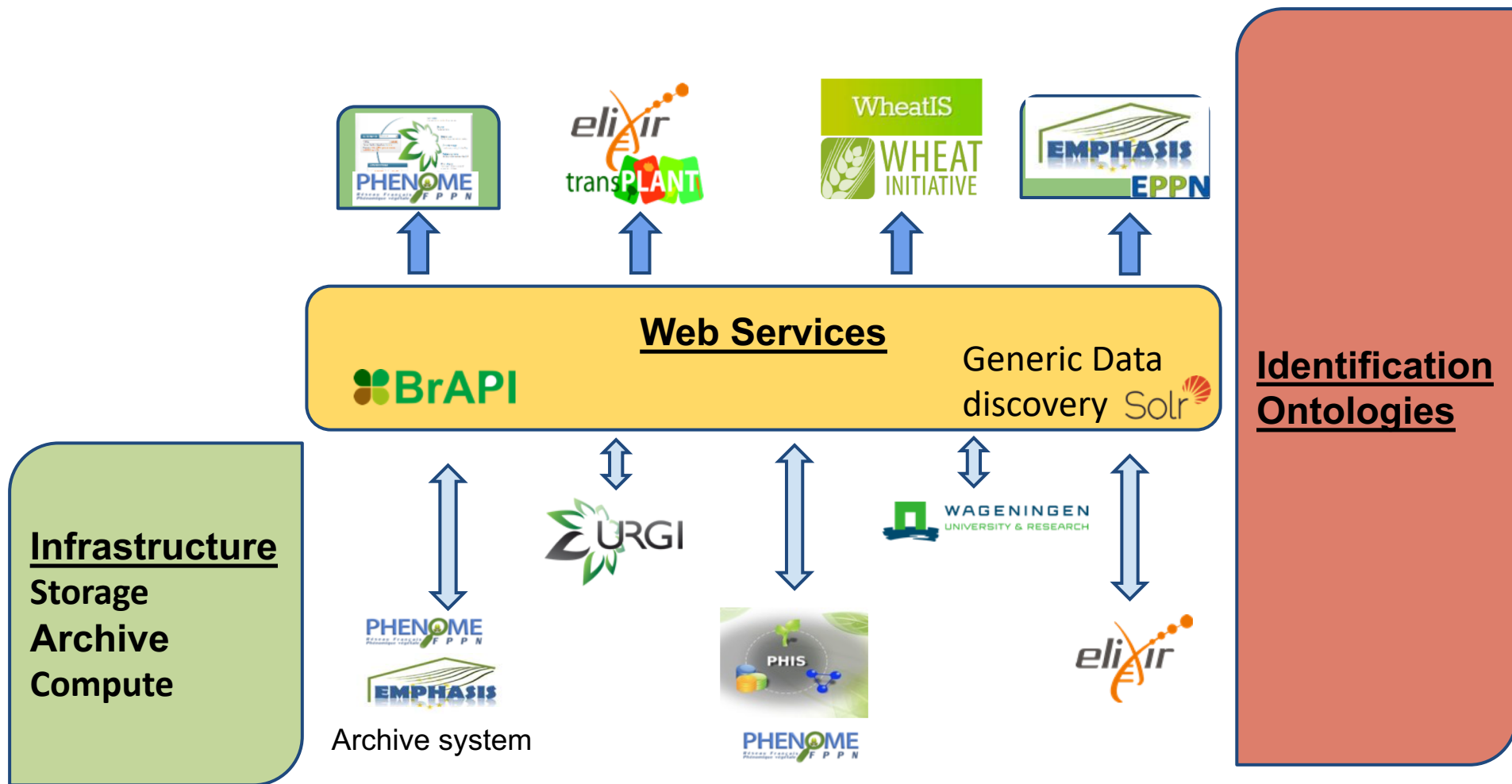
Built by CassavaBase, this is a fully BrAPI compliant tool for viewing and exploring germplasm pedigrees.

- Study Comparison tool



The screenshot shows a web browser window titled "BrAPI Study Comparison". The interface includes a header section with the text "Requires: D3, jQuery". Below this is a main heading "Study Comparison BrApp Example". The form contains several input fields and buttons: "BrAPI Server Address" (with "yamibase.org" entered), "Username" (with "John_Doe" entered), and "Password" (with masked characters). There is a "Study IDs" field with "19,20,21" entered, a "Unit Type" dropdown menu set to "Plot", and a "Group By Accession" checkbox. A blue "Load" button is positioned next to the "Group By Accession" checkbox. At the bottom, there is a "Select Variable" dropdown and a blue "Compare Variable" button.

USE case WS3: Distributed Information System



Generic data discovery

- Full text
- Facets

WheatIS

Filters

Database

☐ TRITICEAE TOOLBOX (64)
 ☐ CR-EST (7)
 ☐ GNPIS (3)
 ☐ ENSEMBL PLANTS (1)
 ☐ GNPIS JBROWSE (1)
 ☐ PLANTPHENODB (1)

Type

☐ ACCESSION (42)
 ☐ PHENOTYPE (14)
 ☐ EXPERIMENT (9)
 ☐ EXPRESSED SEQUENCE TAGS (7)
 ☐ SEQUENCE FEATURE (2)
 ☐ PHENOTYPE (1)
 ☐ QTL (1)
 ☐ SEQUENCE FEATURE (1)

Species

☐ TRITICUM AESTIVUM (69)
 ☐ HORDEUM VULGARE (6)
 ☐ TRITICUM AESTIVUM L. (1)
 ☐ TRITICUM DURUM (1)

Search

About

WheatIS nodes:

transPlant-MIPS (UP):

- CrowsNest: 13324

transPlant-IPK (UP):

- CR-EST: 199220

- GEBIS: 52878

- MetaCrop: 355

fhb

1-10 of 77

10 results per page

ID	Source	Type	Taxon	Description
Traes_5DL_E12C501B4	Ensembl Plants	-	Triticum aestivum	Sequence feature, Ensembl Plants, Traes_5DL_E12C501B4, Traes_5DL_Phylla1 [Source:UniProtKB/TrEMBL;Acc:A0FHB0], Triticum aestivum, prot
HDP14M22T	CR-EST	-	Hordeum vulgare	HDP14M22T, expressed sequence tags, CR-EST, Hordeum vulgare, gi 26793073 hypothetical protein; gi 28951047 gb AAO63447.1 At2g37930
HDP20D01w	CR-EST	-	Hordeum vulgare	HDP20D01w, expressed sequence tags, CR-EST, Hordeum vulgare, gi 15501515 hypothetical protein; gi 34906406 ref NP_914550.1 [Rickettsia prowazekii str. Madrid E] SFHB ; gi 34906406 ref NP_914550.1
HDP20D01T	CR-EST	-	Hordeum vulgare	HDP20D01T, expressed sequence tags, CR-EST, Hordeum vulgare, gi 15501515 hypothetical protein; gi 34906406 ref NP_914550.1 [Rickettsia prowazekii str. Madrid E] SFHB ; gi 34906406 ref NP_914550.1
HDP21C08T	CR-EST	-	Hordeum vulgare	HDP21C08T, expressed sequence tags, CR-EST, Hordeum vulgare, gi 15501515 hypothetical protein; gi 31979237 gb AAP68831.1 [Rickettsia prowazekii str. Madrid E] SFHB ; gi 31979237 gb AAP68831.1
HDP31N10w	CR-EST	-	Hordeum vulgare	HDP31N10w, expressed sequence tags, CR-EST, Hordeum vulgare, gi 15501515 hypothetical protein; gi 34906406 ref NP_914550.1 [Rickettsia prowazekii str. Madrid E] SFHB ; gi 34906406 ref NP_914550.1
HDP35A10T	CR-EST	-	Hordeum vulgare	HDP35A10T, expressed sequence tags, CR-EST, Hordeum vulgare, gi 26793073 hypothetical protein; gi 28951047 gb AAO63447.1 At2g37930
TS034O07u	CR-EST	-	Triticum aestivum	TS034O07u, expressed sequence tags, CR-EST, Triticum aestivum, Gi 15501515 hypothetical protein; gi 7487460 pir T01820 hypo; Gi 15604676 ref NP_221194.1 SFH
HWW FHB	Triticeae Toolbox	Experiment	Triticum aestivum	Experiment, Triticeae Toolbox, HWW FHB, phenotype experiment, Include HWWFHB_2014_Fargo, Triticum aestivum, phenotype
URSN_2012_BrookingsSD	Triticeae Toolbox	Experiment	Triticum aestivum	Experiment, Triticeae Toolbox, URSN_2012_BrookingsSD, phenotype trial severity, Fusarium head blight disease index, visually scabby kernels URS

Generic data discovery



Apache
Solr

Lucene

trans**PLANT**

Wheat Initiative



South Green[®]
bioinformatics platform



arcad

Data types

Phenotypes
Markers,
accessions,
GWAS,
Experiments
Journal articles
Seeds of
discovery data
Genomic
Features

WheatIS

Search: About

terpene

More restrictions

Show 15 entries

ID	Source	Type	Taxon	Description
80	GnPS	SEQUENCE FEATURE	Triticum aestivum	TRAE38F0911001TCF02_11 is a mRNA-GDEC of Triticum aestivum located between positions 67823747 and 67827168 on trae38pseudomolecule1 and which properties are: loc_id=TRAE38F0911001TCF02_11, Oid=443, 0111 AUGUSTUS wheat, 66336, 66405, gene_512, mRNA, 501, noncoding, function = 660373, MAIZE TRMBL, dactylar Terpene synthase 7 OS Zea mays PE 2 BY 1, locus tag=443, 0111 AUGUSTUS wheat, 66336, 66425, gene_512, bestblasthit=665173, MAIZE TRMBL, dactylar Terpene synthase 7 - 5250, 14.23 - hour: 08:52 - gene 56.33, blasthigh Confidence, function, target=665173, 23 5UT, bestp, best=443, 0111 AUGUSTUS wheat, 66336, 66450, gene_512, mRNA, 001, CDS, 58p, function, identity=14.23, source, loc=TRAE38F0911001TCF02_11, function, coverage=0.8
80	Ensembl Plants	-	Triticum urartu	TRUR3_21927
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare
80	CR-EST	-	Hordeum vulgare	Hordeum vulgare

Showing 1 to 10 of 67 entries

Previous 1 2 3 4 5 6 7 Next

rubrique < appel à projets > ci-dessous

APPEL A PROJETS

PARTENAIRES

EVENEMENTS

e!EnsemblPlants

EMBL-EBI



PLANTS DB



TGAC
The Genome Analysis Centre™

CerealsDB



UCW



Generic Search Growth

Indexing Package

- Community Building
- Indexing node deployment support
- <http://wheatis.org/Tools.php>
- <http://wheat-urgi.versailles.inra.fr/Projects/Wheat-Information-System/SolR-tool-package>

To ease the WheatIS nodes to expose their data to the [WheatIS search](#) , we developed a package to help the installation and configuration of the SolR tool.

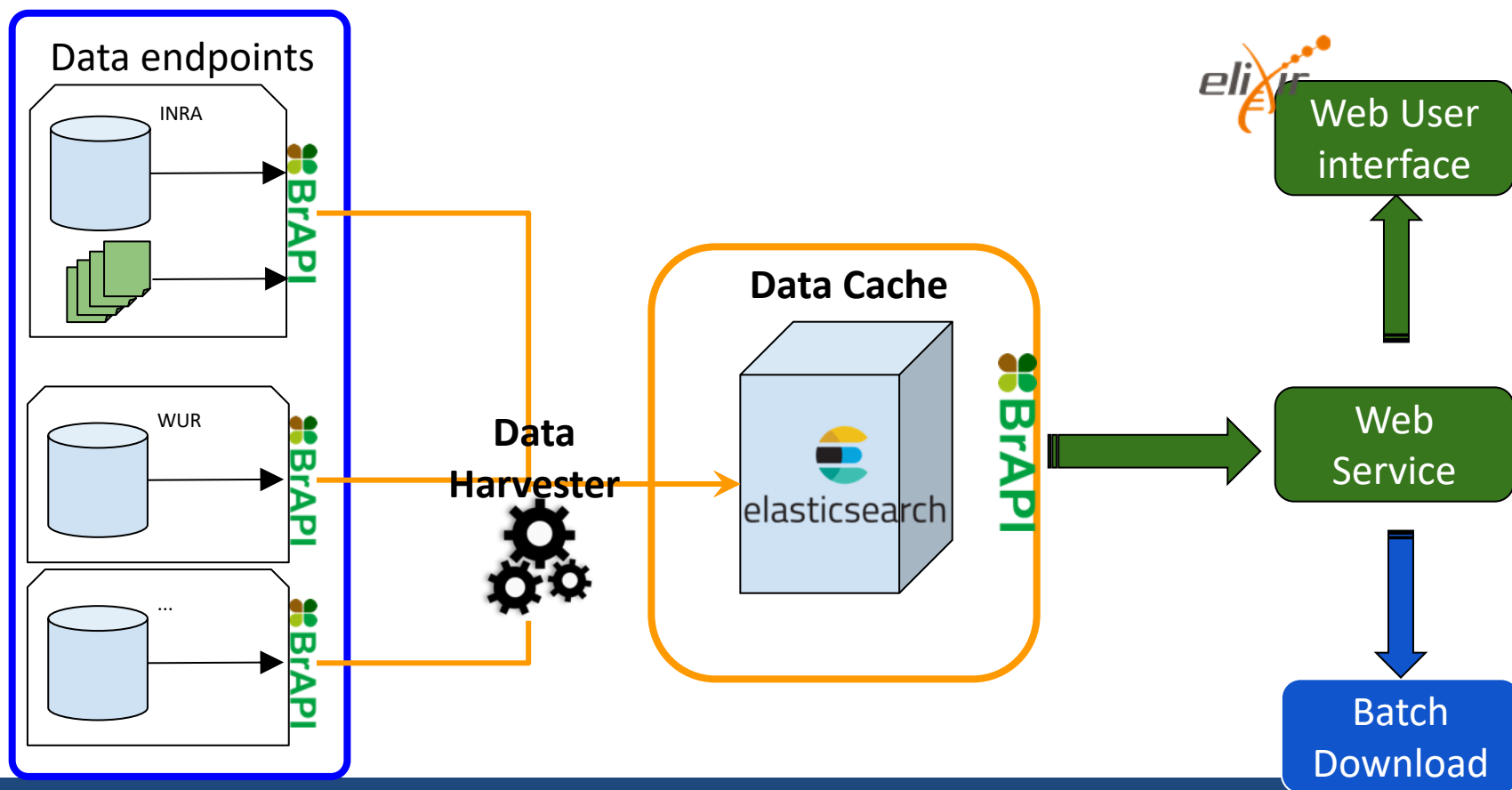
Download the package: [SolR-tool-package-WheatIS.tar.gz](#) (157.33 kB)

Please [contact us](#) to have support and to add your SolR indexes to the WheatIS search.



Elixir Plant Data Lookup Service

- Phenotype & Study
- Integrated in Elixir collaboration
- Complementarity and convergence with WheatIS datadiscovery network
- Central Index
- GnpIS-Ephesis like data integration over databases network



USE CASE: MIAPPE ONTOLOGY (PPEO)



Plant Phenotyping Experiment Ontology

MIAPPE Semantic: PPEO

- Joint initiative : Elixir (Fr, NL, Pt), Emphasis, CropOntology, RDA, INRA
- MIAPPE OWL Ontology
 - ◆ First draft
 - ◆ <https://github.com/MIAPPE/MIAPPE-ontology>
- BrAPI 2 MIAPPE RDF workflow
 - ◆ <http://www.wheatis.org> data standard page
 - ◆ <http://ist.blogs.inra.fr/wdi/phenotypes-as-rdf/>
- Agroportal
 - ◆ Agronomy bioportal
 - ◆ <http://agroportal.lirmm.fr/ontologies/PPEO>
- Wheat dataset
 - ◆ <http://dx.doi.org/10.15454/1.4489666216568333E12>
 - ◆ Future Query: Impact of summer temperature on yield

Wheat Data Interoperability Guidelines

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Phenotypes as RDF

Phenotypes to Semantic web publication

The sharing and especially the reusability of complex data like phenotypes is a good use case for a publication following the semantic web principles. This page describes how to generate a Phenotype RDF dataset from a [Breeding API](#) MIAPPE compliant endpoint. The growing adoption of this API will facilitate the reusability of such a transformation process.

Recommendations

The RDF publication relies among other things on the correct identification of different resources through Permanent

Virtuoso SPARQL Query Editor

Default Data Set Name (Graph IRI)

Query Text

```
PREFIX brapi: <https://brapi.org/rdf/>
SELECT ?network ?study ?attribute ?value
FROM <urn:urgi:pheno-brapi-inra-small-grain-cereals-network>
WHERE {?study a brapi:Study;
          ?attribute ?value.
        ?trial a brapi:Trial;
              brapi:hasName ?network.}
ORDER BY ?network ?study
```

(Security restrictions of this server do not allow you to retrieve remote RDF data, see [details](#).)

Results Format:

HTML

Execution timeout:

0 milliseconds (values less than 1

Options:

☒ Strict checking of void variables ☐ Log debug info

(The result can only be sent back to browser, not saved on the server, see [details](#).)

Run Query

Reset

MIAPPE STATUS AND PERSPECTIVES



Adoption

- Plant community involved
 - ◆ Elixir (European bioinformatic infrastructure)
 - ◆ Emphasis (European Phenotyping infrastructure)
 - ◆ Bioversity international CGIAR
- Breeding API is Elixir official Phenotyping standard web service
- MIAPPE and BrAPI high collaboration
 - ◆ adoption and compliance
- Data repositories and management tools
 - ◆ GnpIS <https://urgi.versailles.inra.fr/gnpis/>
 - ◆ eDale <https://edal.ipk-gatersleben.de/>
 - ◆ PlantPhenoDB at IPGPAS <http://cropnet.pl/plantphenodb/>
 - ◆ In progress: COPO, Elixir plant databases (iBet, WUR, VIB, ...), Brassica Information Portal, ...



Perspectives

- Version 2 : Emphasis, Elixir, ...
 - ◆ Environment
 - ◆ Sensor traceability
 - ◆ Phenoharmonis Workshop Montpellier may 2018
- Elixir data lookup service, MIAPPE enabled.
 - ◆ Data discovery
 - ◆ Elixir
 - ◆ WheatIS & Emphasis ?
 - ◆ Open source software
- Dataset Validation
 - ◆ Elixir
 - ◆ File archive (ISA Tab) and BrAPI based



Perspectives: Emphasis Ontology & MIAPPE

- Emphasis Ontology in construction
 - ◆ High level organization of phenotyping infrastructures
 - ◆ Complementary of MIAPPE
 - ◆ For instance: Installation $\approx$ Assay
 - elementary level for data acquisition
 - Set of sensor + vectors

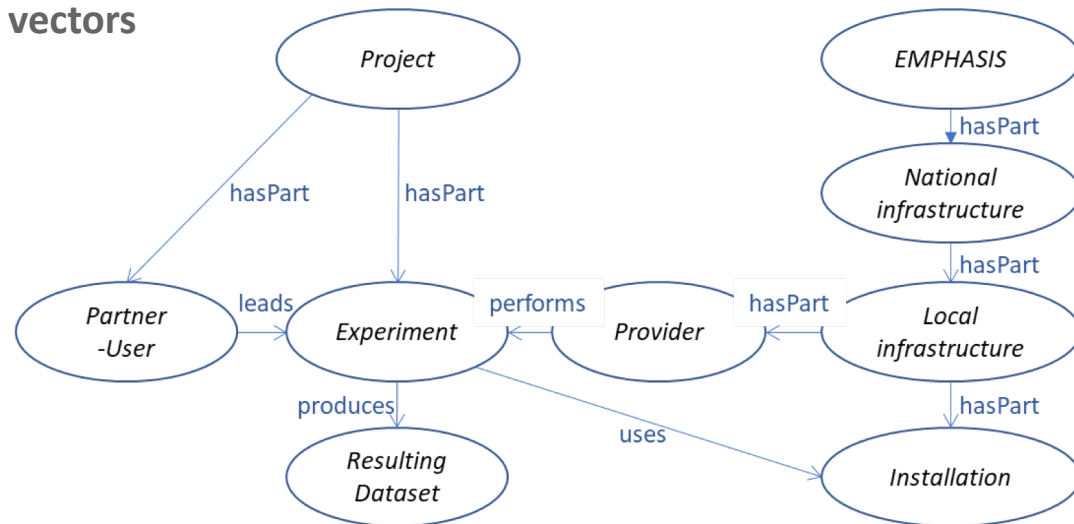


Fig. 1. Main terms used in this document and their functional relationships. Each instance has its own attributes, not represented here for better legibility. *Provider*: group of people involved in a *local infrastructure*, usually involving subgroups at *installation* level. *Project*: any project, (e.g. UE or national) that involves *partners* that perform experiments, themselves part of the *project*. The terms *Partner* (in a project) and *User* (in a phenotyping infrastructure) map to each other. All these terms are implemented in the information system.

Plant Phenotyping Data & FAIR

- FAIR allows handling big data on the long term (decades)
 - ◆ **Findability**
 - in a lot of datasets
 - With different approaches
 - Without relying on any Archive logic/Folder mechanisms
 - ◆ **Accessibility**
 - Avoid storing high volumes for nothing
 - ◆ **Interoperability**
 - Processing lot of data
 - Aggregating several datasets into new ones
 - ◆ **Reusability**
 - Understandability of the data
 - Reducing data format heterogeneity

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