



Phenome-Emphasis-Elixir: phenotyping data management and integration

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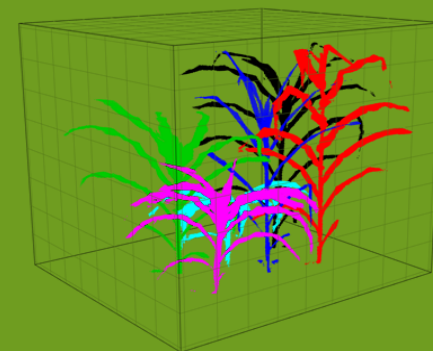
Submitted on 5 Jun 2020

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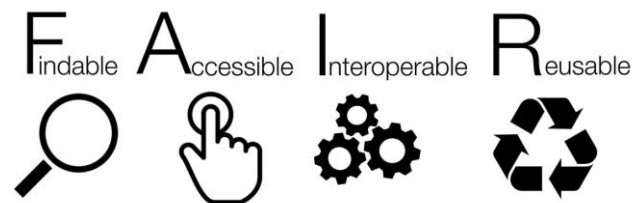
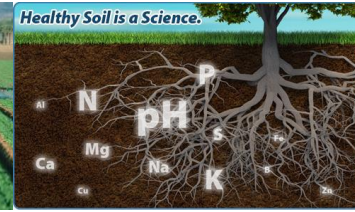
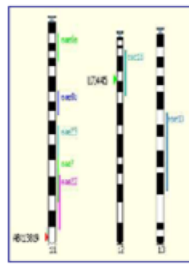
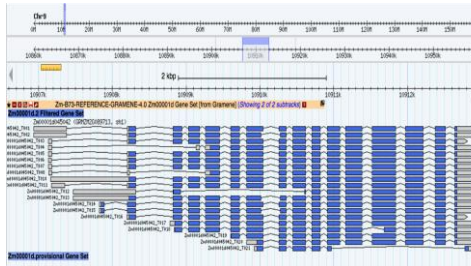
Phenome-Emphasis-Elixir: phenotyping data management and integration



A-F Adam-Blondon, C Pommier, L Cabrera-Bosquet

Grape Genetics and Breeding Symposium, Workshop on
grapevine phenotyping, France, Bordeaux, 2018 July 16-20th

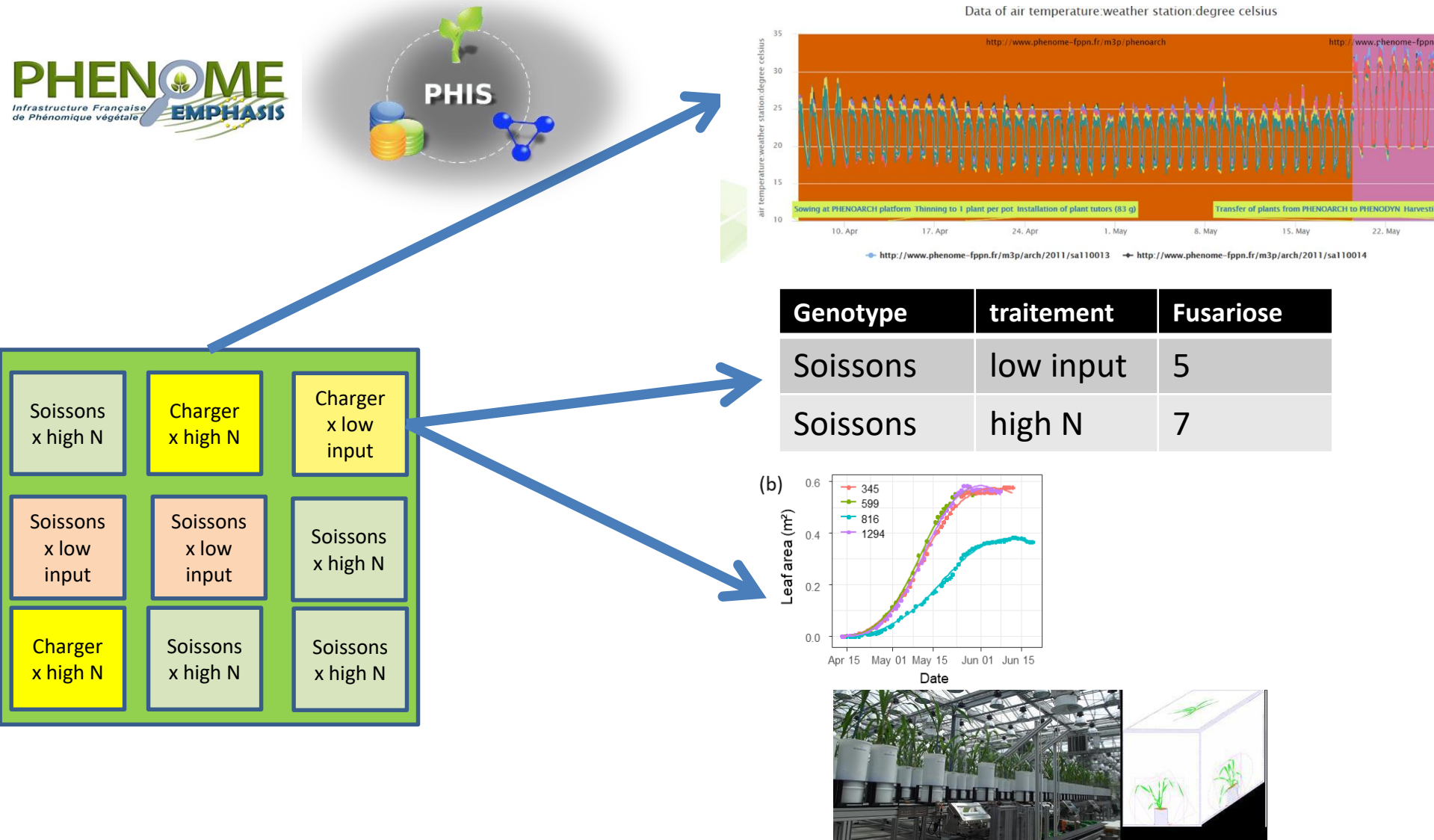
Genomic X Environment X Phenomic



- Climate change adaptation
- Variety improvement
- Cultural Practices adaptations
- ...



Phenomic multidimensional data

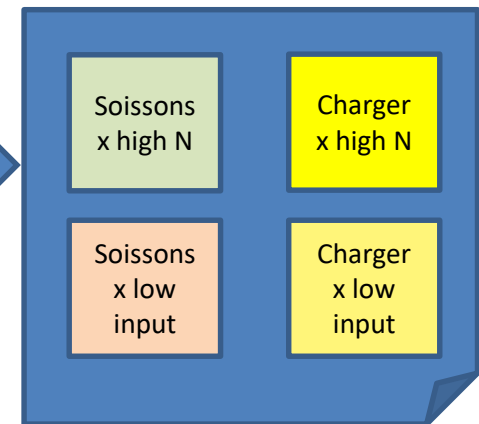
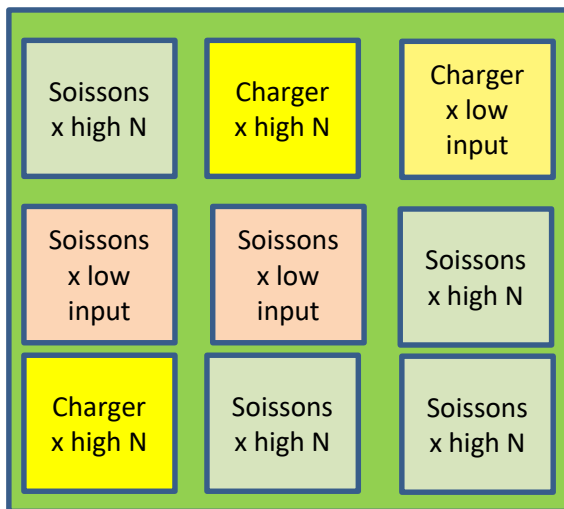


Phenotyping Data in matrix, link with other types of data



Raw data

Elaborated data



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

Genotype	treatment	LAI
Soisson	low input	6

Strategy for data management

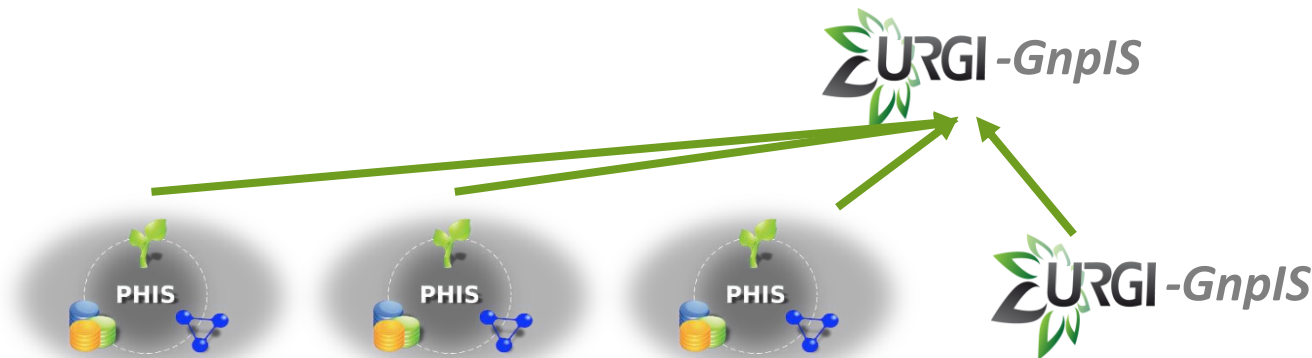
- Raw data
 - ◆ Big in High through put platforms: Terabyte by experiment
 - ◆ Difficult to obtain again and LT interest: long term storage
- No central Phenomic data archive
- Strategy: develop a federation of information system with central services
 - ◆ Need for standards to support the federation
 - ◆ Need for standard to support automatic data integration



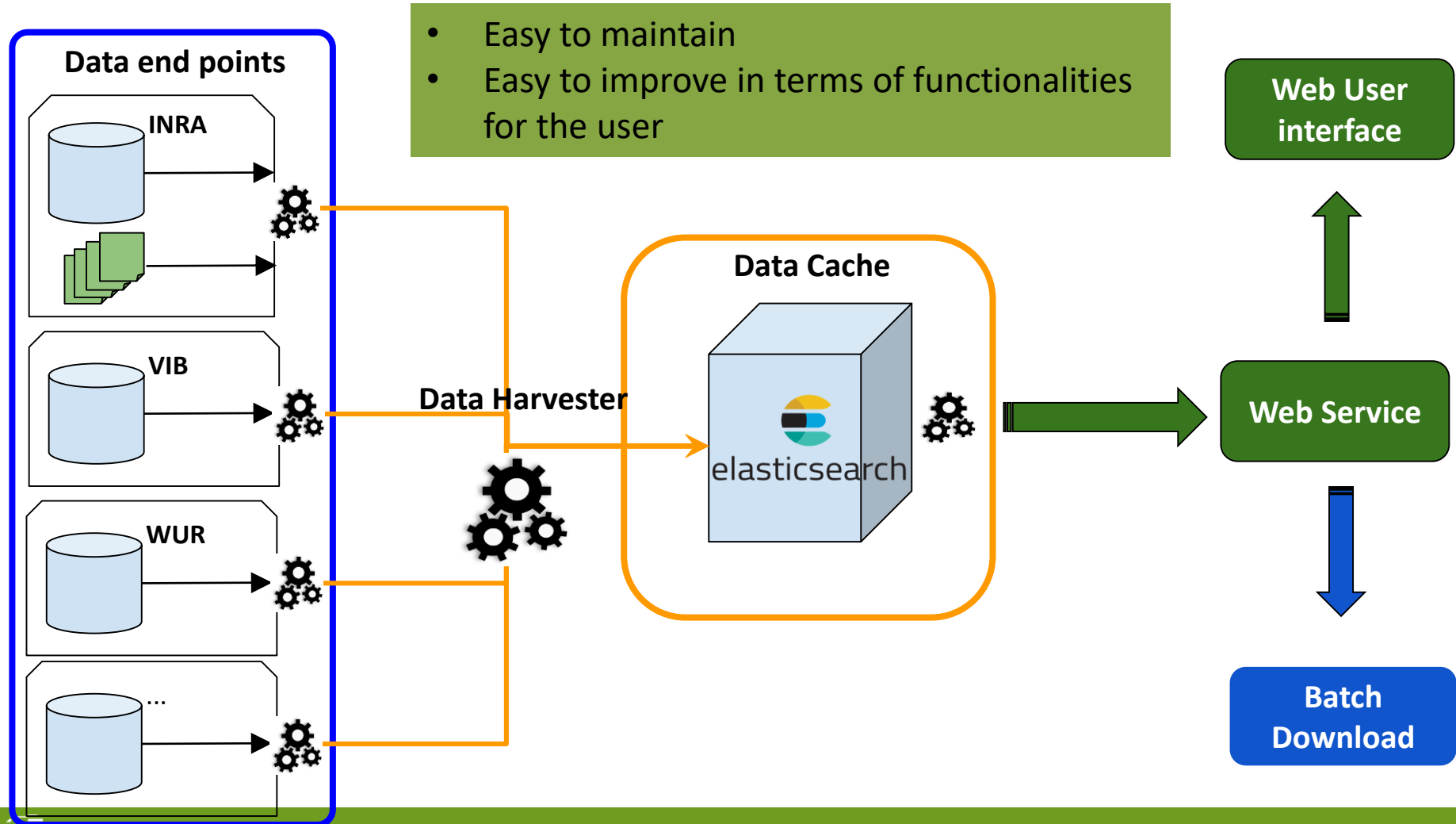
Portal

Web service

Databases



Federation of Plant phenotyping information systems



Plant Phenotyping Data Life cycle

EMPHASIS

Elixir

Following experiments



Phenotypic analysis



Data sharing and Reuse

TRAITS

- Tracking
 - objects, events, images
- Following
 - plants, sensors, cameras
- Environmental conditions Mapping/time course
- Sensor calibration

- Data cleaning
- Calculated traits
 - Time courses
 - Spatial analysis
 - Ratios (growth per ...)
- Tools for data quality
 - Reproducible?
 - Cross scale ?
 - Modelling?

- From measurements to traits
- Tools for trait quality
 - heritability
 - genetic correlations

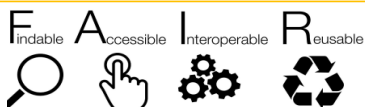
- Enable reproducible analyses (GxE, GWAS, Genomic Prediction, Evolution)
- Data integration and linking
- Data Publication
- Data discovery
- Pipeline Hosting

I Interoperable R Reusable

I Interoperable R Reusable

R Reusable

F Findable A Accessible I Interoperable



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 + 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

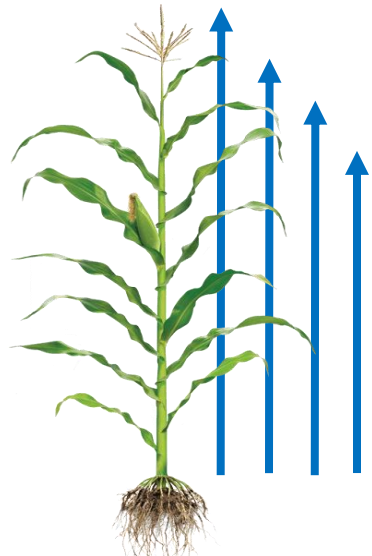
Visual scoring **METHOD**

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

Variable identification: Plant height example



T1: Plant Height



Trait

+

Method

+

Unit

M1: Total height

M2: First tassel branch

M3: Last expanded leaf

M4: Youngest growing leaf

U1: cm

U2: mm

M5: Highest pixel
corresponding to plant

U3: pixel

...Allows as many combination as needed...

...Each trait, method and unit has to be identified

Object identification (URIs)

URIs (Uniform Resource Identifiers)

⇒ standardized, unique, unambiguous identification of objects



Prefix m3p: `<http://phenome-fppn.fr/m3p>`

(a)

URI of plant

`<m3p:arch/2017/c17000118>`

URI of pot:

`<m3p:arch/2013/pc13001542>`

URI of cart:

`<m3p:arch/2013/ct1300123>`

URI of cabin:

`<m3p:arch/2018/ac180015>`

URI of camera:

`<m3p:arch/2018/ac180019>`



URI of image:

`<m3p:arch/2017/ic17002295855>`

Prefix diaphen: `<http://phenome-fppn.fr/diaphen>`

(b)

URI of plot

`<diaphen:2017/o1700029>`

URI of plant:

`<diaphen:2017/17000147>`

URI of leaf:

`<diaphen:2017/117000590>`

URI of camera:

`<diaphen:2018/ac180002>`

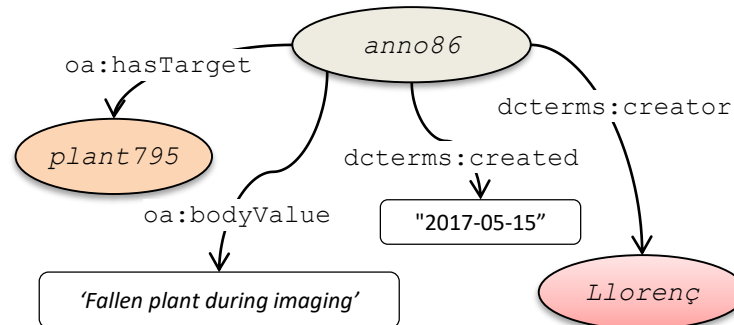
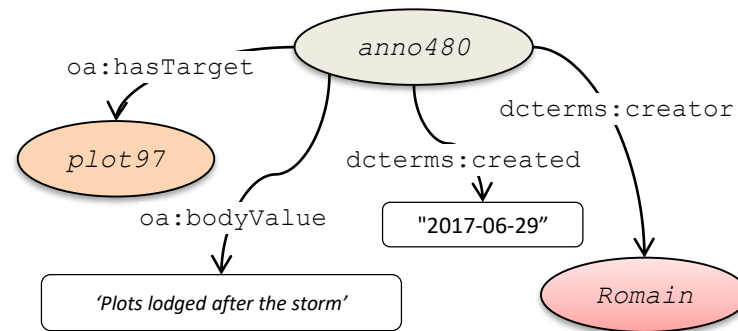


URI of image:

`<diaphen:2017/ic14001480237>`

The same applies to infrastructure, sensors, people, variables...

Annotation of events: plot and plant accidents



Events or follow the [Web Annotation Data Model](#) that allows assigning motivation and purpose attributes to annotations (e.g. `oa:describing`, `oa:identifying`, `oa:linking`, `oa:replying`, etc.). [Dublin Core](#) properties such as `dcterms:created` or `dcterms:creator` are also used.

Minimum Information About Plant Phenotyping Experiment

- Standard for metadata : data about the data set
- www.miappe.org
- Recently improved: detailed specification of the checklist and alignment with other existing standards, include needs of the forest trees community, ...

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 Frohberg, 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

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transPLANT

PHENOME
Infrastructure Française
de Phénotypage végétal

European
Plant
Phenotyping
Network
EPPN *accelerate*

INRA
SCIENCE & IMPACT

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

 Author Affiliations

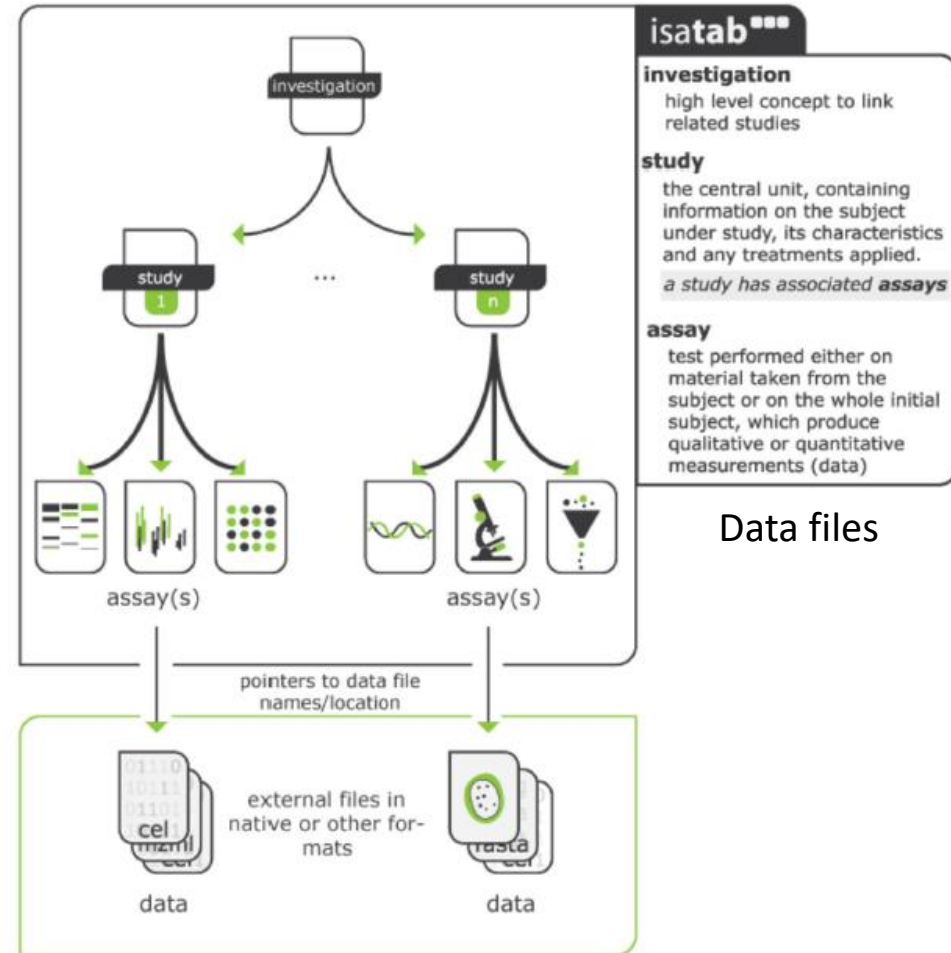
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J. Exp. Bot. (2015) 66 (18): 5417-5427.
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MIAPPE implementation: File Archive standard format

- ISA Tab for Phenotyping
 - ◆ Investigation/Study/Assay
 - ◆ Zip Archive
 - MIAPPE Metadata
 - Raw data
 - Elaborated data
 - Linked data / Metadata / Discovery data



MIAPPE implementation: Web Service

- Breeding API: International collaboration
- Servers implementations => **standard data exports**
 - ◆ CGIARs international network: Integrated Breeding Platform
 - ◆ Elixir Plant Community (GnpIS, CIRAD, ...)
 - ◆ Emphasis Plant Community: (+PHIS, ...)
 - ◆ Germinate (James Hutton Institute, UK)
- Clients implementations => **functionalities for users**
 - ◆ Flapjack (JHI, UK): genotyping data visualization
 - ◆ Search data in federations (URGI, EU)
 - ◆ R analysis pipelines (CIP, Peru)
 - ◆ Ontology Widget (URGI, FR)
 - ◆ Diverse BrAPI Apps (USA) currently being developed for data visualisation
- Tools => **functionalities for data managers**
 - ◆ BRAVA (IPK, D): validator of a BrAPI server implementation
 - ◆ BrAPI to ISA-TAB; Batch downloads (ELIXIR, EU)



Bill & Melinda Gates Foundation

CassavaBase

T3

IBP

JHI

Bioversity

CIRAD

INRA

IRRI

GOBII

Wageningen

CIP

DaRT

Cornell

iPlant

BILL & MELINDA
GATES foundation



The James
Hutton
Institute



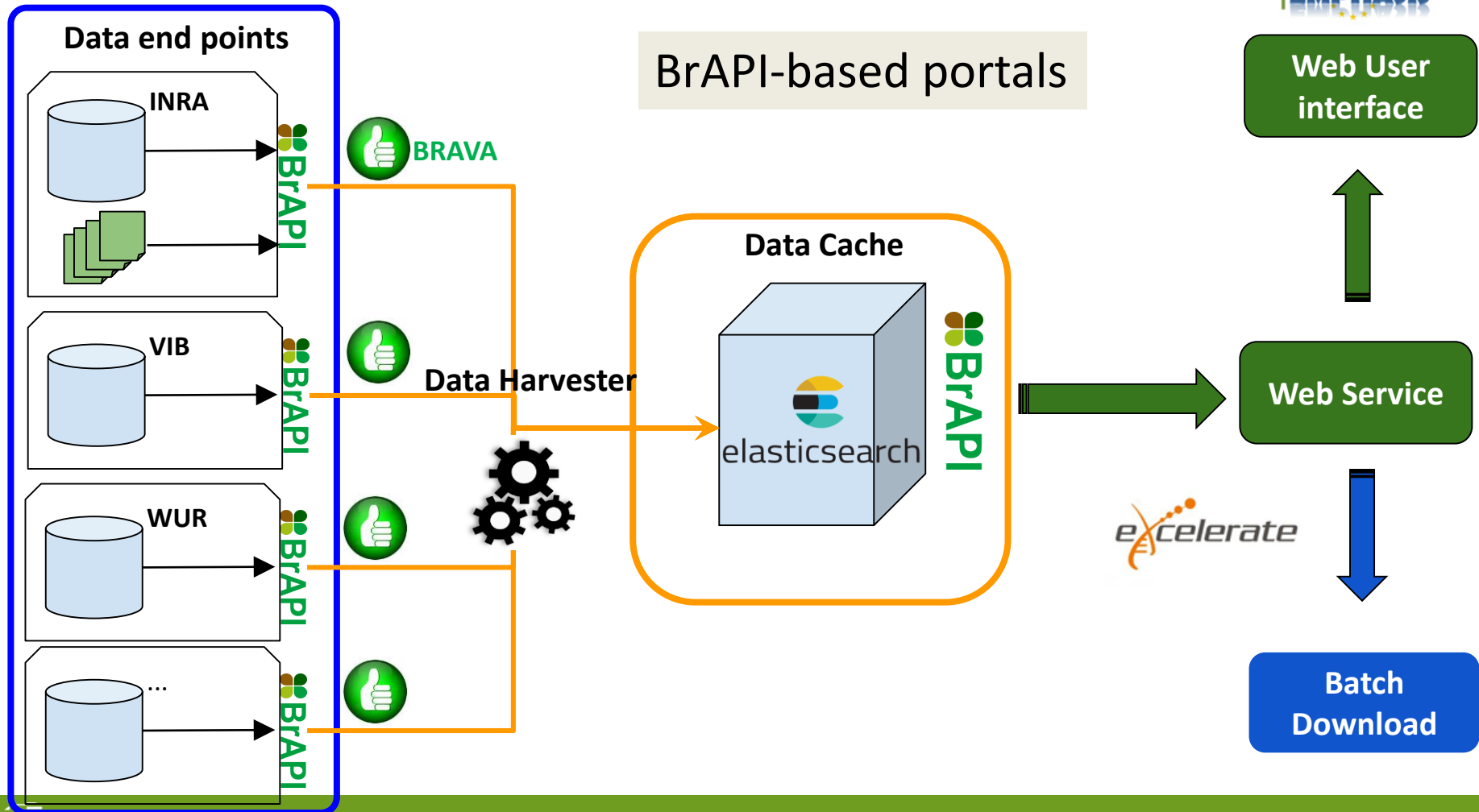
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SCIENCE & IMPACT



WAGENINGEN
UNIVERSITY & RESEARCH

www.brapi.org

Federation(s) of Plant Information systems



Acknowledgment & Questions

