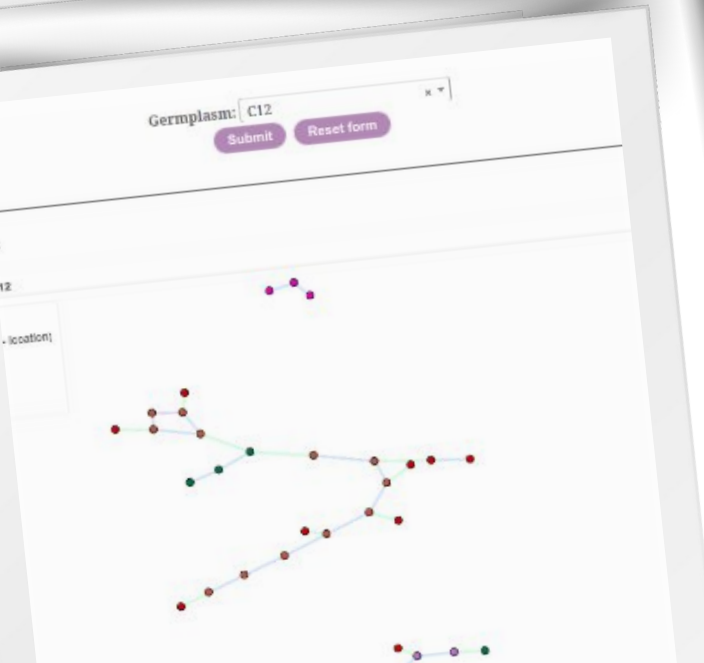


# Training in organic breeding

Module 2: Phenomics: approaches and tools for genetic resources and breeding material characterization

Unit 2.2: Intro to SHiNeMas: a web tool dedicated to Seed Lots History, Phenotyping and Cultural Practices

Authors: Yannick de Oliveira, Isabelle Goldringer



Co-funded by the European Union



Co-funded by the European Union

Funded by the European Union, the Swiss State Secretariat for Education, Research and Innovation (SERI) and UK Research and Innovation (UKRI).



UK Research and Innovation

# Training in organic breeding organized in 5 Modules

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1. **Module 1** - Plant Genetic Resources (PGRs): collection, conservation and exchange to support the increase of agrobiodiversity in farming systems
2. **Module 2** - Phenomics: approaches and tools for genetic resources and breeding material characterisation - FEBRUARY 3rd 2025, 9:00 to 17:30 CET
3. **Module 3** - Breeding methods fundamentals - FEBRUARY 13th 2025, 9:00 to 18:00 CET
4. **Module 4** - Development and application of molecular methods in organic breeding - MARCH 4th 2025, 9:00 to 18:00 CET
5. **Module 5** - Organic heterogeneous material (OHM) design and development - MARCH 7th 2025, 9:00 to 18:00 CET



**February 3rd 2025 - 9:00 to 17:30 CET**



**Unit 2.1: Main descriptors used worldwide in characterizing plant genetic resources**

- 9:00-10:30 - UPV (Adrian Rodríguez-Burruezo)
- 10:30-11:00 Break

**Unit 2.2: Intro to ShineMas: a web tool dedicated to Seed Lots History, Phenotyping and Cultural Practices<sup>1</sup>**

- 11:00-12:30 - INRAe (Yannick de Oliveira, Isabelle Goldringer)
- 12:30-14:00 Lunch Break

**Unit 2.3: Guidelines and examples of good practices in data management**

- 14:00-15:30 - INRAe (Yannick de Oliveira, Isabelle Goldringer)
- 15:30-16:00 Break

**Unit 2.4: Methods for phenotyping and selection of agronomic traits of interest in organic farming**

- 16:00-17:30 - IPC (Pedro Mendes Moreira)

**Unit 2.5: Methods for phenotyping and selection of added-value traits (e.g. taste and nutritional value)<sup>2</sup>**

ITAB (Solenne Jourden)

1 - An extra practical session to use the tool with own data is scheduled for FEB 10th (9-12h)

2 - Unit 2.5 planned for the end of March 2025. Registrants will be invited for this extra training lesson



# T1.4 Training in Organic Breeding

MODULE 2 – Phenomics: approaches and tools for genetic resources and breeding material characterisation

Unit 2.2: Introduction to SHiNeMaS

INRAE

SHiNeMaS : A web tool dedicated to seed lots history, phenotyping and cultural practices

Yannick De Oliveira  
&  
Isabelle Goldringer  
INRAE

# Outline

---

- **How this will be organized & SHiNeMaS overview (15 minutes)**
- **Basic objects manipulated (15 minutes)**
- **Administration of data (15 minutes)**
- **Explore data (15 minutes)**
- **Short quiz (10 minutes)**
- **The “Bring your own data day” (15 minutes)**

# Module 2 Unit 2 - How this will be organized ?

---

3rd of Feb. 11h00-12h30 – Introduction to SHiNeMaS, a presentation of the main features of the tool

10th of Feb. 9h00-12h00 – A “Bring your own data (half) day” (optional, priority to liveseeding partners)

# Module 2 Unit 2 - How this will be organized ?

---

**Today : A static presentation (webinar like) divided in short sessions with Q/A to make it interactive as most as possible.**

# Module 2 Unit 2 - How this will be organized ?

---

The 10th of Feb (next monday) : I will setup a demo instance of SHiNeMaS, you come (online) with your data and you play with the tool.





## **SHiNeMaS overview**

# Module 2 Unit 2 - Context and origin of SHiNeMaS

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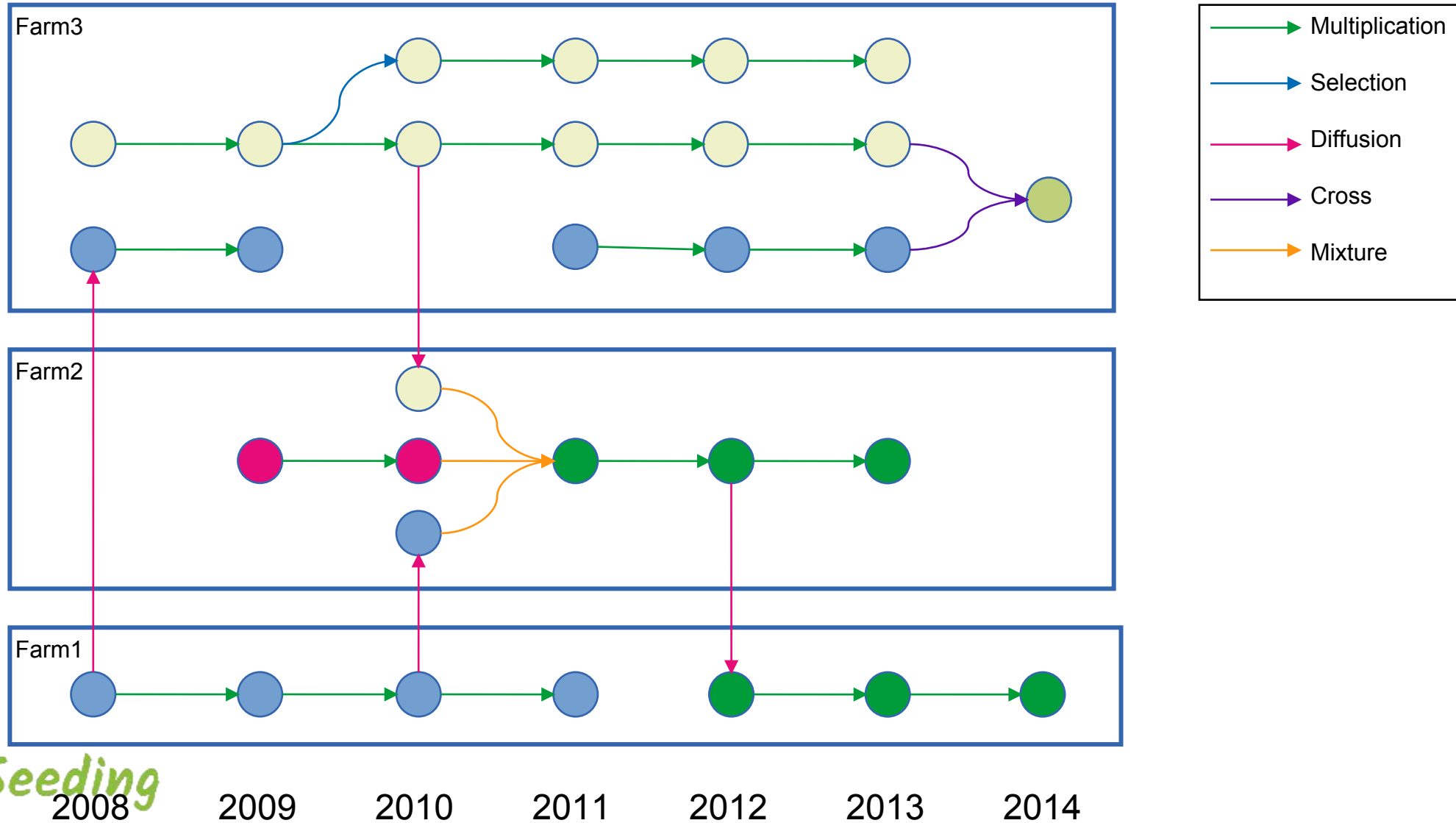
- A collaboration started in 2005 between the Réseau Semences Paysannes (RSP) and the French National Institute for Agricultural Research (INRAE, Isabelle Goldringer from GQE Lab) on wheat species
- Participatory breeding programs aims to :
  - Develop populations that fits organic farming requirement
  - Understand on farm biodiversity
- The project involved more and more farms working on 300+ varieties. Thus, requirements on data managements appears :
  - 1/ Heterogeneous data (cultural practices, phenotyping, environment) needed to be centralized
  - 2/ Seed lots needed to be tracked (stock, location, genealogy), ensuring traceability of lots in flat files is tricky

# Module 2 Unit 2 - SHiNeMaS

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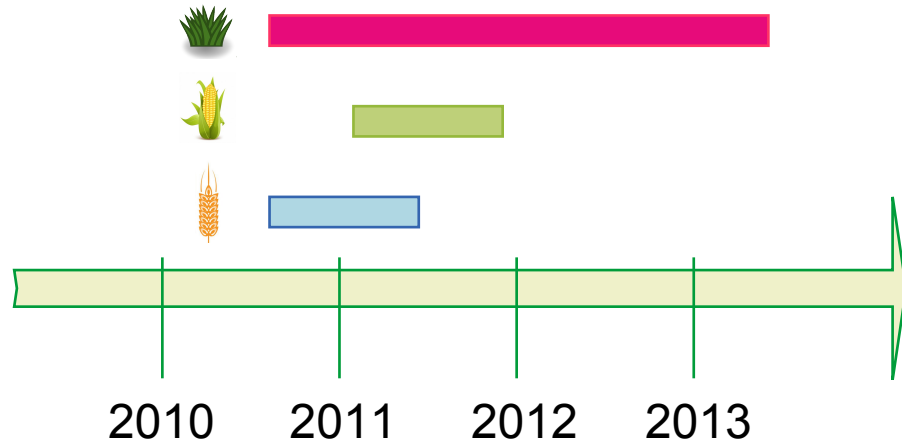
- Software development team at GQE (ABISoft) started the development of a new database tool : SHiNeMaS
- **Seeds History and Network Management System**
- **Objectives** : Create a tool that can be used by researcher and RSP facilitators, ensuring their autonomy in data management.
- This tool is a web application with a database. The tool provides interfaces both to manage and to explore data.

# Module 2 Unit 2 - Tracking seed lots





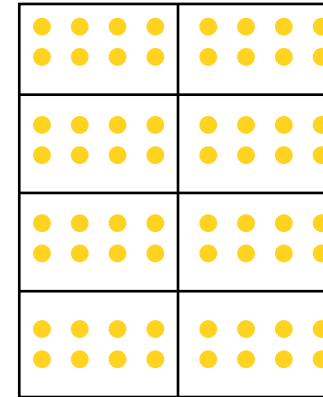
# Module 2 Unit 2 - Plot description and data collected



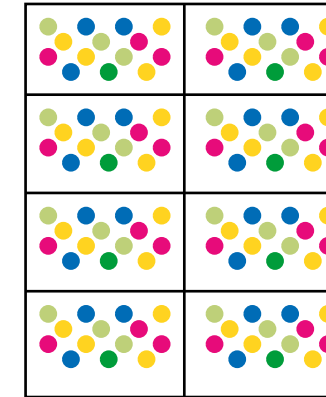
Compliant with annual species.

Also with biennial, triennial or perennial species but we have no feedback.

Same species on all microplots



Mix of species at microplot level



Data can be stored at plot level or plant level.

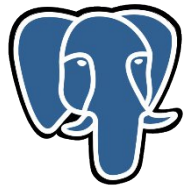
A seed lot can be sown on several plots (repetitions) but only one lot of the same species can be sown on a single plot.

Several lots of different species can be sown on the same plot.

# Module 2 Unit 2 - Technical and legal stuff

---

## Technologies



PostgreSQL

## License



## Availability

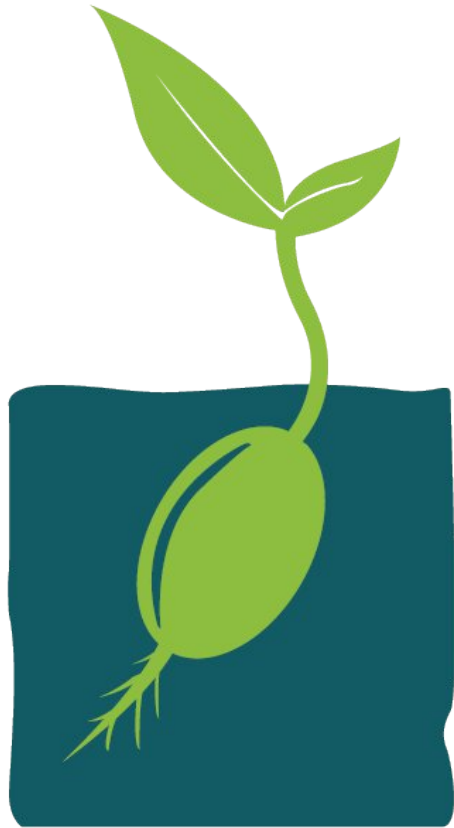


## Article :

<https://doi.org/10.1186/s13007-020-00640-2>

# Module 2 Unit 2 - SHiNeMaS overview

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Questions ?



**“Objects” manipulated**



# Module 2 Unit 2 - Biological material : Germplasm

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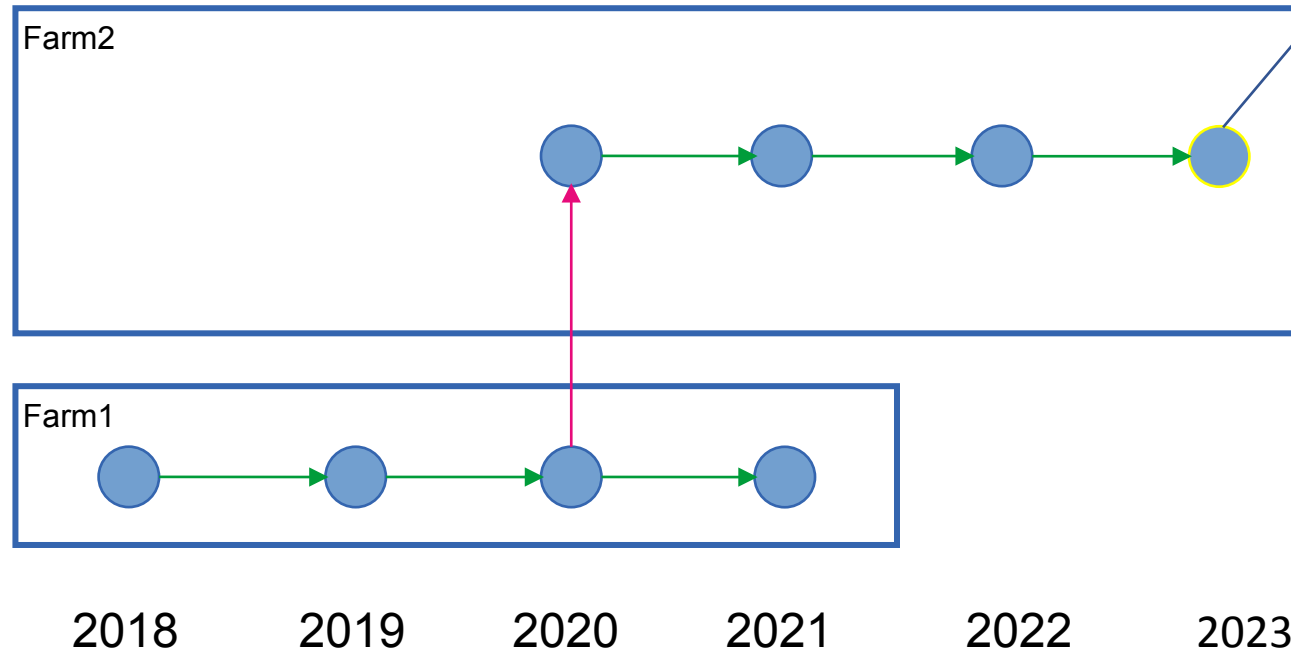
- **Germplasm are the genetics resources defined in SHiNeMaS.**
  - **A germplasm is defined by its name, a species, a type and possibly a person if you have the information of who created this germplasm.**
  - **The “germplasm type” is a way to categorized the germplasms defined. It can be a population, an OHM, but also a line etc.**

# Module 2 Unit 2 - Biological material: Seed lot

---

- **Seed lots are the “physical” instances of a genetic resource.**
  - **A seed lot is defined by its name, a germplasm, a year, a location.**
  - **Other information can define a seed lot :**
    - Storage information : quantity and devices.
    - Generation of the seed lot : how much time it have been multiplied (overall and on farm), with a confidence.
  - **The name of a seed lot is formatted as follows :**  
*germplasm\_location\_year\_num* where “num” is an incremental number ensuring uniqueness of the seed lot name.

# Module 2 Unit 2 - Focus on generation



This seed lot have been multiplied 5 time (generation=5) since 2018 but only 3 time on farm 2 (onfarm generation = 3).

The confidence on farm is "True" because we have the whole history of the lot since 2020 and the diffusion event on farm 2.

But the overall confidence is "False" because we don't know anything before 2018. The value can be set manually to "True".

# Module 2 Unit 2 - People and locations

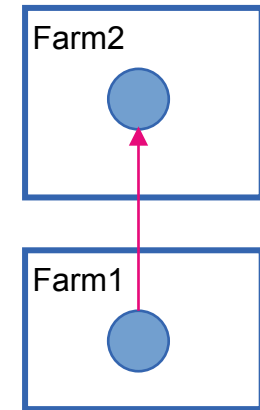
---

- A “Person” is an actor of your breeding activities. The unique information mandatory to define a person is a “short\_name”.
  - More information can be provided (first name, last name, email etc.)
- A “Location” is a farm, an experimental field or any place where a seed lot is grown. It is defined by :
  - A “short name”, latitude/longitude/elevation, an address, a type.

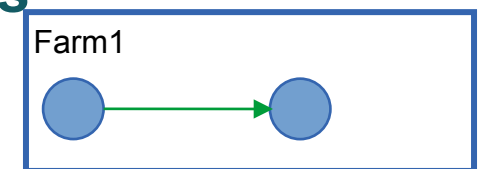


# Module 2 Unit 2 - Events (1)

- Basically, an event is a relation between 2 seed lots or a set of relations involving several seed lots. SHiNeMaS include 5 types of events : Diffusion, Multiplication, Mixture, Cross and Selection.
- A Diffusion is the action to send a seed lot from farm to another farm.
- A Multiplication is the action of reproduction of a single seed lot on a farm, a breeding method can be linked to this event. SHiNeMaS makes possible to merge seed lot from repetitions.



2018

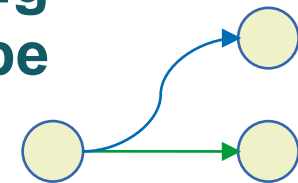
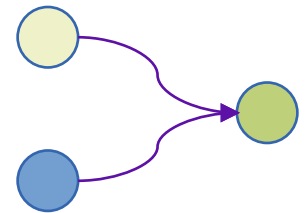
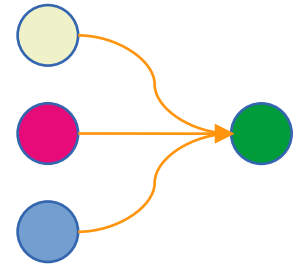


2018

2019

# Module 2 Unit 2 - Events (2)

- A Mixture is the action of blending several seed lots usually of different germplasms. This event creates a new germplasm.
- A Cross, is the action of crossing two germplasm, a breeding method can be related to this event. In that case one seed lot can be considered as a male and the other one as a female. This event create a new germplasm.
- A Selection is the action of isolation of a seed lot regarding traits of interest. In that case the selected seed lot will be named with a specific tag (selection name)

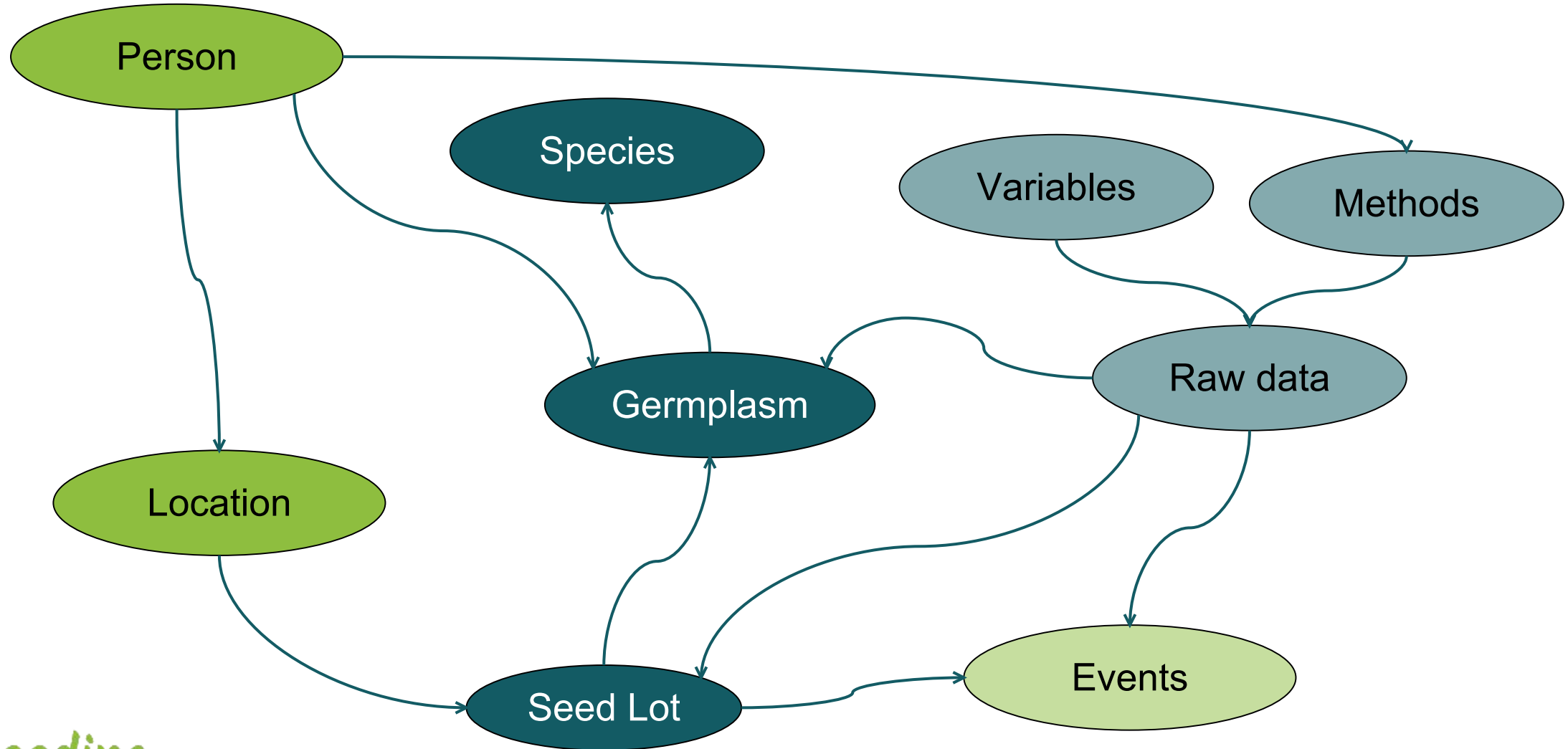


# Module 2 Unit 2 - Raw Data

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- **A Variable is the basic descriptor of a data, it can be a trait, a practice etc. It is defined by :**
  - **A name, a type, a source (some variable can be collected from other databases)**
- **A Method defines how the data have been measured. It is defined by :**
  - **Its name, a description, a unit, and a person**
- **A RawData is a value measured on an individual, a plot, a seed lot or a germplasm. It is defined by a variable, a method and a date. SHiNeMaS track information on data such as the user who submitted the data, submission date and modification date.**

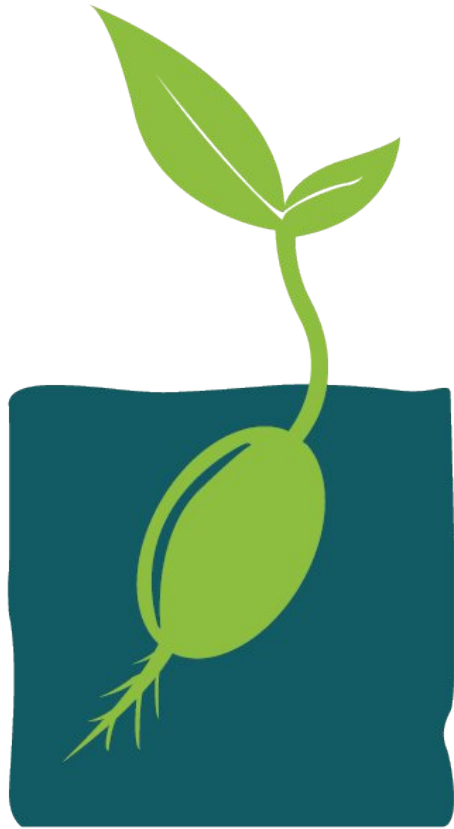
# Module 2 Unit 2 - Summary





# Module 2 Unit 2 - “Objects” manipulated

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Questions ?



**Manage information with  
SHiNeMaS**

# Module 2 Unit 2 - How data are managed ?

- SHiNeMaS provides two way to manage data :
  - Management with forms that makes possible to create/edit one object at a time
  - Management with files (text, csv or tsv) that makes possible to create several objects at the same time (events, germplasm, seedlot)

## Create Germplasm

**Germplasm information**

Name:

Idgermplasm:

Germplasm type:

Person:

Species:

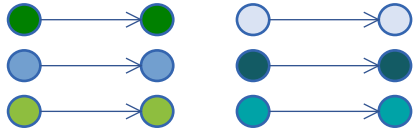
**Germplasm data**

Variable	Raw data	Method	Date	Delete
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="checkbox"/>

[Back](#) [Update](#) [Update and continue](#)

# Module 2 Unit 2 - Events “life cycle” with files

Step 0 – define initial objects (person, locations, methods, variables, species, germplasms etc.) and create your first seed lots.



Step 3 – Submit your file in SHiNeMaS. When the file is submitted events and harvested seed lots are automatically created.



Step 1 - export **pre-filled file** with :  
- sowed seeds lots list (previous harvested seeds lots)  
- sowing/harvesting year  
*Example with multiplication file*



Step 2 – fill exported file with:  
- plot location  
- quantity  
- field evaluation data



# Module 2 Unit 2 - Germplasm management

Single form to create/update one germplasm

Update a Germplasm

**Germplasm information**

Name:

Idgermplasm:

Germplasm type:

Person:

Species:

**Germplasm data**

Variable	Raw data	Method	Date	Delete
quality	<input type="text" value="good"/>	quality	<input type="text"/>	<input type="checkbox"/>
disease	<input type="text" value="resistante"/>	disease	<input type="text"/>	<input type="checkbox"/>
protein	<input type="text" value="good"/>	protein	<input type="text"/>	<input type="checkbox"/>

Germplasm list

Add germplasm

Name:  Germplasm type:

Species:  Person:

Page 1 of 1.

Action on selected germplasm :

	Name	IDGermplasm	Germplasm Type	Species	Person
<input type="checkbox"/>	C14	C14	Cross	Blé-tendre	JFB
<input type="checkbox"/>	C140 1	C140-1	Cross	Blé-tendre	MLN
<input type="checkbox"/>	C140 2	C140-2	Cross	Blé-tendre	MLN
<input type="checkbox"/>	C140 3	C140-3	Cross	Blé-tendre	MLN
<input type="checkbox"/>	C14+C174	C14+C174		Blé-tendre	None
<input type="checkbox"/>	C14 sélection massale	C14-sélection-massale		Blé-tendre	ADP
<input type="checkbox"/>	C14sP C174sA	C14sP-C174sA	Mixture	Blé-tendre	None
<input type="checkbox"/>	M2(Vilmorin Blé de Nuissement+C14+Bon Moulin)	M2(Vilmorin-Blé-de-Nuissement+C14+Bon-Moulin)		Blé-tendre	ADP
<input type="checkbox"/>	M(C139+C140)	M(C139+C140)		Blé-tendre	ROW
<input type="checkbox"/>	M(C14 C16)	M(C14-C16)		Blé-tendre	RIH
<input type="checkbox"/>	M(C14+C46)	M(C14+C46)	Mixture	Blé-tendre	RIH
<input type="checkbox"/>	M(C14 C46)	M(C14-C46)		Blé-tendre	RIH
<input type="checkbox"/>	M(C16+C14)	M(C16+C14)	Mixture	Blé-tendre	RIH
<input type="checkbox"/>	M(C37 C46 C88 C83 C14 C42)	M(C37-C46-C88-C83-C14-C42)		Blé-tendre	RIH

File to create multiple germplasms

	A	B	C	D	E
1	name	idgermplasm	type	species	person
2	Germplasm1	gp1	OHM	wheat	ISG
3	A germplasm with spaces	Gp-with-spaces	OHM	wheat	ISG
4					
5					

SHiNeMaS also provides a tool to prepare/export a file with a list of germplasm and a list of variables to describe these germplasms.

This file can also be imported here.

**Submit a file**

File:  Aucun fichier sélectionné.

Mode:  Create  Add data



# Module 2 Unit 2 - Seed lot management

Create seed lots or add data linked to seed lots works exactly the same way than germplasms.

## Seedlot list

Page 1 of 3. [next](#) [last](#) »

Action on selected seedlot :

<input type="checkbox"/>	Name	Location	Germplasm	Date	Storage
<input type="checkbox"/>	<a href="#">C14#C_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#D_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#E_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#F_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#G_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#H_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#I_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#J_MLN_2012_0001</a>	MLN	C14	2012	None
<input type="checkbox"/>	<a href="#">C14#J_MLN_2011_0001</a>	MLN	C14	2011	None
<input type="checkbox"/>	<a href="#">C14#K_MLN_2011_0001</a>	MLN	C14	2011	None

But update a seed lot is something a bit tricky, and basic information can't be changed.

## Update a Seedlot

**Seedlot information**

Name:

Quantity ini:

Location: MLN

Germplasm: C14

Date: 2009



# Module 2 Unit 2 - Event management

## Generate reproduction file

Search seed lots

Filters :

Creation year: 2012

Location: MLN

Projects: -----

Species: -----

Search

[download template file](#)

Wizards tools are available to prepare files for any type of events : diffusion, mixture, cross, multiplication, selection, individual data.

Only headers will be different from a file to another.

### Seed lot found for your query :

- Add all seed lots
- 144epi-C-JFB\_MLN\_2012\_0001
- 144epi-C-JFB\_MLN\_2012\_0002
- 144epi-P-JFB#B\_MLN\_2012\_0001
- 144epi-P-JFB\_MLN\_2012\_0001
- 144epi-P-JFB\_MLN\_2012\_0002
- 144epi-P-JFB\_MLN\_2012\_0003
- 144epi-P-JFB\_MLN\_2012\_0004
- 144epi-P-JFB\_MLN\_2012\_0005
- 144epi-P-JFB\_MLN\_2012\_0006
- 144epi-P-JFB\_MLN\_2012\_0007
- 144epi-P-JFB\_MLN\_2012\_0008
- 144epi-P-JFB\_MLN\_2012\_0009
- 144epi-P-JFB\_MLN\_2012\_0010
- 144epi-P-JFB\_MLN\_2012\_0011

**Selected seed lot :**

- 21x3\_MLN\_2012\_0004
- 21x3\_MLN\_2012\_0007
- BB\_MLN\_2012\_0001
- C13\_MLN\_2012\_0007
- C14\_MLN\_2012\_0002

Projects: PPB Splited: Yes

Sowing year: 2015 Harvesting year: 2016

Export file

Submitting an event file will create the event itself but will also run other actions :

- create the output seed lot with initial quantity
- update quantity (if filled)
- create raw data (if data are filled)

	A	B	C	D	E	F	G	H	I	J	K	L
1	project	sown year	harvested year	id seed lot sown	intra selection name	etiquette	split	quantity sown	quantity harvested	block	X	Y
2	PPB	2015	2016	21x3_MLN_2012_0004			1			1		
3	PPB	2015	2016	21x3_MLN_2012_0007			1			1		
4	PPB	2015	2016	BB_MLN_2012_0001			1			1		
5	PPB	2015	2016	C13_MLN_2012_0007			1			1		
6	PPB	2015	2016	C14_MLN_2012_0002			1			1		
7												
8												
9												



# Module 2 Unit 2 - Quantity and storage management

---

SHiNeMaS makes possible to manage storage and quantity information of a seed lot.

- **Quantities :**

- When a seed lot is created an **initial quantity** can be set.
- Each time the seed lot is used in an event the **quantity used** is recorded.
- **Remaining quantity** is computed.
- At any time an **update of the quantity** can be done
- The **remaining quantity** will be then computed regarding all updates that have been done.

- **Storage devices :**

- It is possible to **create** storage devices on a location.
- Any **seed lot can be stored** in a storage device.
- The **location** of the seed lot must be **consistent** with the location of the storage device.

# Module 2 Unit 2 - Storage devices management

Step 1 : Create storage devices on the location.  
Storage devices can be defined with 4 nested levels.

## Storage devices

Search for Location :

Search

MLN [add](#) [view](#)

- Cold room 1
  - Cold room 1 > chamber 1
  - Cold room 1 > chamber 2
  - Cold room 1 > chamber 3
- Cold room 2
  - Cold room 2 > chamber 1
  - Cold room 2 > chamber 2
  - Cold room 2 > chamber 3

Step 2 : Submit a file to store your seed lot

	A	B	C	D	E
1	seedlot	level1	level2	level3	level4
2	21x3_MLN_2009_0001	Cold room 1	chamber 1		
3	21x3_MLN_2009_0002	Cold room 2	chamber 1		
4	21x3_MLN_2010_0001	Cold room 1	chamber 1		
5	21x3_MLN_2010_0002	Cold room 2	chamber 1		
6	21x3_MLN_2010_0003	Cold room 1	chamber 1		
7	21x3_MLN_2010_0004	Cold room 2	chamber 1		
8	21x3_MLN_2010_0005	Cold room 1	chamber 1		
9	21x3_MLN_2010_0006	Cold room 2	chamber 1		
10	21x3_MLN_2010_0007	Cold room 1	chamber 1		
11	21x3_MLN_2011_0001	Cold room 2	chamber 1		
12					


# Module 2 Unit 2 - Quantities management

SHiNeMaS makes possible to update remaining quantity of a seed lot at any time

**Stock information**

Storage device : Cold room 1 > chamber 1

Seed lot still available ? Yes


Remaining quantity : 350.0 g 

**Stock evolution :**  
Initial quantity : 550.0 g  
100.0 g used in this relation : 21x3\_MLN\_2009\_0001 --> 21x3\_MLN\_2010\_0001  
100.0 g used in this relation : 21x3\_MLN\_2009\_0001 --> 21x3\_FLM\_2015\_0001

**Stock information**

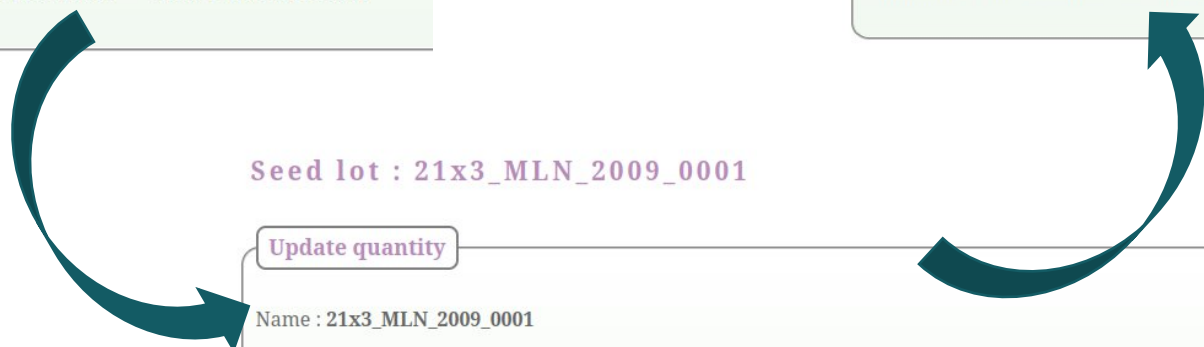
Storage device : Cold room 1 > chamber 1

Seed lot still available ? Yes

Remaining quantity : 300.0 g 

**Stock evolution :**  
Initial quantity : 550.0 g  
100.0 g used in this relation : 21x3\_MLN\_2009\_0001 --> 21x3\_MLN\_2010\_0001  
100.0 g used in this relation : 21x3\_MLN\_2009\_0001 --> 21x3\_FLM\_2015\_0001

An update of the stock has been done (Jan. 29, 2025, 10:37 a.m.): 300.0 g is the new stock quantity (Annual inventory)



**Seed lot : 21x3\_MLN\_2009\_0001**

**Update quantity**

Name : 21x3\_MLN\_2009\_0001


Current quantity : 350.0 g

New quantity :  Comment :

# Module 2 Unit 2 - Images management

Link image(s) to entities

Image : C21.jpg



Germplasms:


Relations:

Seed lots:

Date:

Comment:

Image : C22.jpg



Germplasms:

Relations:

Seed lots:

- Submit a set of images and choose the material to link with (germplasm, seeds lots, events)
- Visible in the card of the related material or event

# Module 2 Unit 2 - Weather data

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Weather data can be managed by two way :

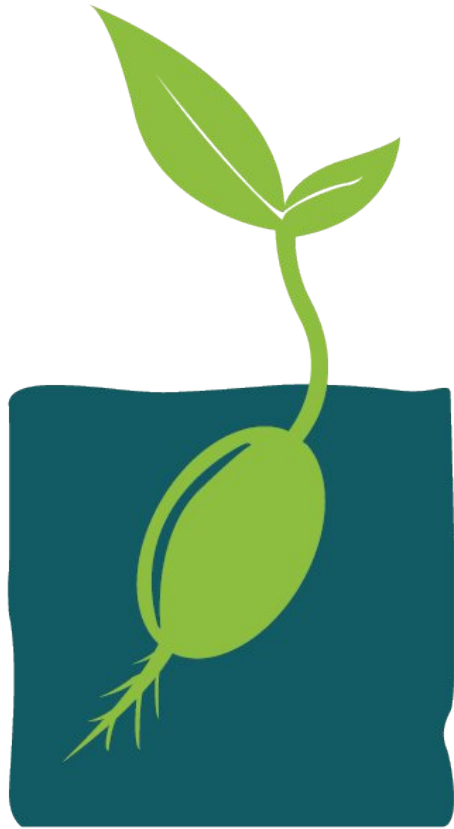
- Manage weather stations and variables in SHiNeMaS and submit data files in the database.
- Use available web services from weather databases. Stations and variables are automatically updated in SHiNeMaS from the web service, data aren't stored in SHiNeMaS but queries are possible.
  - Currently SHiNeMaS is connected to Climatik INRAE service but data access is restricted.
  - Point of improvement : connect SHiNeMaS to other service and if possible with free access to data





# Module 2 Unit 2 - Manage data with SHiNeMaS

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Questions ?

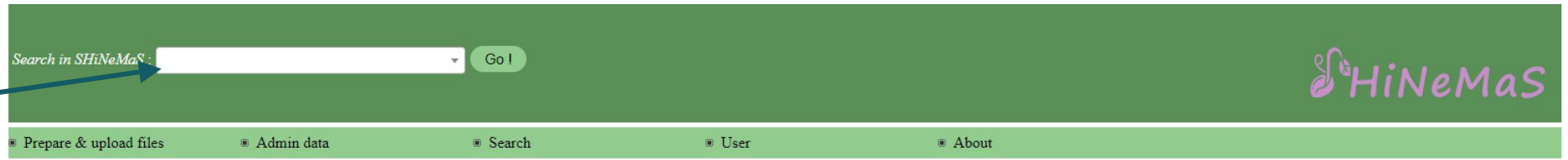




**Explore data with SHiNeMaS**

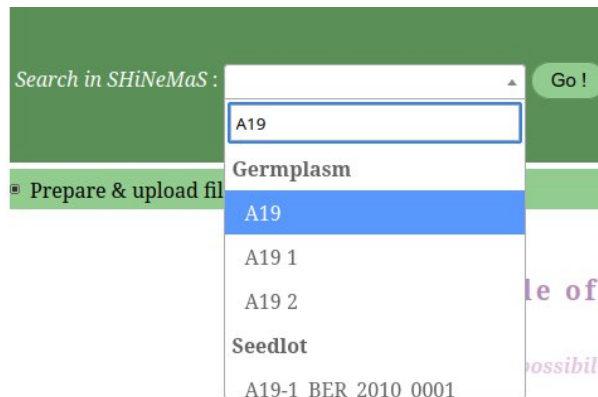
# Module 2 Unit 2 - Global search bar

Global search bar to access cards.



This bar is available on each interface of the web application.

The auto-completion feature search in seed lot, germplasm and relations



# Module 2 Unit 2 - Germplasm card

Germplasm profil : C14

## Germplasm informations

Name : C14

Species : **Blé-tendre**

Person (creator) : JFB

Germplasm type : **Cross**

Creation year : 2006

Germplasm parents : **Alauda, Poncheau-selection-fermier,**

## Germplasm data

quality : **good (quality)**

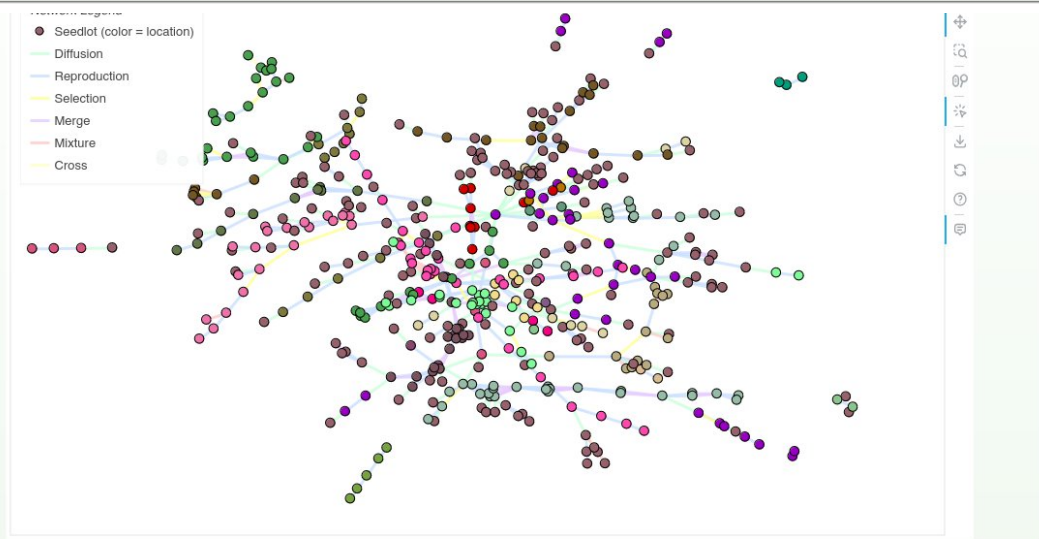
disease : **resistante (disease)**

protein : **good (protein)**

## Germplasm images [Show images](#)



## Map of seedlot location



# Module 2 Unit 2 - Seedlot card

Seed lot profil : 21x3\_MLN\_2009\_0001

## Seed lot informations

Name : 21x3\_MLN\_2009\_0001  
Species : [Blé-tendre](#)  
Germplasm : [21x3 \(Cross\)](#)  
Owner : MLN  
Creation year : 2009  
Projects involved in : PPB,

## Seed lot history

Creation history :  
[21x3\\_FLM\\_2009\\_0001](#) ⇒ 21x3\_MLN\_2009\_0001 in a Diffusion event  
Use history :  
[21x3\\_MLN\\_2009\\_0001](#) ⇒ [21x3\\_MLN\\_2010\\_0001](#)  
[21x3\\_MLN\\_2009\\_0001](#) ⇒ [21x3\\_FLM\\_2015\\_0001](#)

Links to navigate in seed lot history

## Seed lot data

tkw (tkw) : 110  
color (spring\_color) : brown

Data related to this seed lot

## Stock information

Storage device : Cold room 1 > chamber 1

Seed lot still available ? Yes

Remaining quantity : 300.0 g 

Storage and quantity information

### Stock evolution :

Initial quantity : 550.0 g

100.0 g used in this relation : 21x3\_MLN\_2009\_0001 -> 21x3\_MLN\_2010\_0001

100.0 g used in this relation : 21x3\_MLN\_2009\_0001 -> 21x3\_FLM\_2015\_0001

An update of the stock has been done (Jan. 29, 2025, 10:37 a.m.): 300.0 g is the new stock quantity (Annual inventory)



# Module 2 Unit 2 - Relation card: information

Relation profil : C21#ficelle-rouge\_JFB\_2009\_0001 --> C21#ficelle-rouge\_JFB\_2010\_0001

## Relation information

Relation type : **Reproduction**  
Quantity used : **None g**  
Split : **None**

X : E  
Y : 10  
Block : 1  
Description : **reproduction**  
Kernel number : **None**  
Realised : **None**  
Start date : **2009**  
End date : **2010**  
Reproduction method name :  
Description :

Other relations :

## Relation cross references

### Seedlots :

[C21#ficelle-rouge\\_JFB\\_2009\\_0001](#)  
[C21#ficelle-rouge\\_JFB\\_2010\\_0001](#)

### Previous relations :

C21\_JFB\_2008\_0001 → C21#ficelle-rouge\_JFB\_2009\_0001

### Next relations :

C21#ficelle-rouge\_JFB\_2010\_0001 → C21#ficelle-rouge\_MLN\_2010\_0001

### Other relations of the Reproduction event :

C21#ficelle-rouge\_JFB\_2009\_0001 → C21#ficelle-rouge-s2010\_JFB\_2010\_0001

Cross references for this relation :  
– seed lots  
– other related relations

information on  
the relation

## Relation images

No images for this relation.

# Module 2 Unit 2 - Relation card: data

Data

- Individual data
- Global data

Variable	Value	Date	Method
enherbement	1	-	enherbement_jud
heterogeneite	5	-	heterogeneite_jud
curve	het	-	port_epi_jud
summer_globale	1	-	globale_jud
disease	2	-	disease
biomass	1	-	biomass_jud
verse	0	-	verse_jud
dens-epis	2	-	dens_epi_jud

Data tables :

- plot level at the top
- on the right, individual data

Individual data

Individual	awns	awns\$date	awns\$method	color	color\$date	color\$method	curve	curve\$date	curve\$method
1	2	-	awns_M	0	-	color_M	0	-	
2	2	-	awns_M	0	-	color_F	2	-	
3	2	-	awns_F	0	-	color_F	2	-	
4	2	-	awns_M	1	-	color_F	1	-	
5	2	-	awns_F	1	-	color_F	1	-	
6	2	-	awns_M	0	-	color_F	2	-	
7	2	-	awns_F	1	-	color_F	2	-	
8	2	-	awns_F	2	-	color_F	0	-	
9	2	-	awns_M	1	-	color_M	1	-	
10	2	-	awns_M	0	-	color_F	1	-	
11	2	-	awns_F	1	-	color_F	0	-	
12	2	-	awns_M	1	-	color_F	0	-	
13	2	-	awns_M	0	-	color_M	2	-	
14	2	-	awns_M	1	-	color_M	2	-	
15	2	-	awns_M	0	-	color_F	2	-	
16	2	-	awns_M	0	-	color_F	1	-	
17	2	-	awns_F	0	-	color_F	2	-	
18	2	-	awns_F	1	-	color_F	2	-	
19	2	-	awns_F	2	-	color_F	2	-	
20	2	-	awns_F	2	-	color_F	2	-	
21	2	-	awns_F	0	-	color_F	1	-	
22	2	-	awns_F	0	-	color_F	1	-	
23	2	-	awns_F	0	-	color_F	2	-	
24	2	-	awns_F	0	-	color_F	2	-	
25	2	-	awns_F	0	-	color_F	1	-	

# Module 2 Unit 2 - Relation card: weather data

**Meteorologic search**

Start Date :

End Date :

Period :  ▾

Choosing climatic variables :

Choosing weather stations in order of preference:

Station 1 :

Station 2 :

Station 3 :

Bourran - INRAE - Climatik ( 1991-01-01 - ... )

Mauvezin-sur-Gupie - METEO-FRANCE - Climatik ( 2013-12-09 - ... )

**Estillac - METEO-FRANCE - Climatik ( 1940-01-01 - ... )**

Prignonrieux - INRAE - Climatik ( 2021-06-01 - ... )

Data tables : weather data can be collected from the closest stations of the trial location.



# Module 2 Unit 2 - Advanced query

## Search seed lots

Search seed lots

**Filters :**

Creation year :  ▾

Projects :  Not  ▾      Relation type :  Not  ▾

Location :  Not  ▾      Germplasm :  Not  ▾

Only seed lots with images :

**Select query mode :**

Classic  Generations  Measures

Will change with v2.2 of SHiNeMaS.

3 distinct advanced query :

- Germplasm
- Seedlot
- Relations

169 Results :

Download data

Seed lot name	Relation	Parents names	Grandparents Relation
<a href="#">C21#AA_MLN_2012_0001</a>	Diffusion	C21#AA_CHD_2012_0001	Selection
<a href="#">C21#a_MLN_2011_0001</a>	Diffusion	C21#a_JFB_2011_0001	Reproduction
<a href="#">C21#b_MLN_2011_0001</a>	Diffusion	C21#b_JFB_2011_0001	Reproduction
<a href="#">C21#b_MLN_2012_0001</a>	Reproduction	C21#b_MLN_2011_0001	Diffusion
<a href="#">C21#b_MLN_2012_0002</a>	Reproduction	C21#b_MLN_2011_0001	Diffusion
<a href="#">C21#b_MLN_2012_0003</a>	Merge	C21#b_MLN_2012_0001; C21#b_MLN_2012_0002	Reproduction; Reproduction
<a href="#">C21#b_MLN_2012_0004</a>	Reproduction	C21#b_MLN_2011_0001	Diffusion
<a href="#">C21#b_MLN_2012_0005</a>	Diffusion	C21#b_JFB_2012_0001	Reproduction
<a href="#">C21#c_MLN_2011_0001</a>	Diffusion	C21#c_BRE_2011_0001	Selection
<a href="#">C21#c_MLN_2012_0001</a>	Diffusion	C21#c_EUK_2012_0001	Reproduction
<a href="#">C21#c_MLN_2012_0002</a>	Diffusion	C21#c_EUK_2012_0002	Reproduction
<a href="#">C21#c_MLN_2012_0003</a>	Diffusion	C21#c_EUK_2012_0003	Reproduction
<a href="#">C21#dansFR_MLN_2011_0001</a>	Diffusion	C21#dansFR_JFB_2011_0001	Reproduction
<a href="#">C21#dansFR_MLN_2012_0001</a>	Reproduction	C21#dansFR_MLN_2011_0001	Diffusion
<a href="#">C21#dansFR_MLN_2012_0002</a>	Reproduction	C21#dansFR_MLN_2011_0001	Diffusion
<a href="#">C21#dansFR_MLN_2012_0003</a>	Merge	C21#dansFR_MLN_2012_0002; C21#dansFR_MLN_2012_0001	Reproduction; Reproduction
<a href="#">C21#dansFR_MLN_2012_0004</a>	Diffusion	C21#dansFR_JFB_2012_0001	Reproduction
<a href="#">C21#D_MLN_2011_0001</a>	Diffusion	C21#D_BRE_2011_0001	Selection
<a href="#">C21#E_MLN_2011_0001</a>	Diffusion	C21#E_OLR_2011_0001	Selection
<a href="#">C21#ficelle-rouge_MLN_2010_0001</a>	Diffusion	C21#ficelle-rouge_JFB_2010_0001	Reproduction

# Module 2 Unit 2 - Explore germplasm network

Germplasm: C12

**Graph**  
Graph of relation of seedlot :

Seedlot network for C12

Network Legend

- Seedlot (color = location)
- Merge
- Reproduction
- Diffusion

**Graph**  
Graph of relation of seedlot :

Seedlot network for C12

Network Legend

- Seedlot (color = location)
- Merge
- Reproduction
- Diffusion

To the seed lot card

Name: C12\_BEN\_2012\_001

# Module 2 Unit 2 - Explore weather data

**Climatic data form**

Start Date :

End Date :

Period :  ▾

Choosing climatic variables :

Choosing location :  ▾

Choosing weather stations in order of preference:

Station 1 :

Station 2 :

Station 3 :

Gif-sur-Yvette - INRAE - Climatik ( 2020-01-01 - ... )  
**Versailles - INRAE - Climatik ( 2001-02-15 - ... )**  
Trappes - METEO-FRANCE - Climatik ( 1904-09-01 - ... )  
Thiverval-Grignon - INRAE - Climatik ( 1992-05-06 - ... )

SHiNeMaS also provide an independant query interface for weather data.

This will show the closest stations from your location. You can choose 3 ordered stations. Order is important as all stations do not measures the same variables.

- Station 1 is requested first for all variables
- For variables without any data station 2
- Then station 3

# Module 2 Unit 2 - Advanced usage: API

## api

GET	/api/locations/
GET	/api/variables/
GET	/api/germplasm/
GET	/api/germplasm_types/
GET	/api/projects/
GET	/api/species/

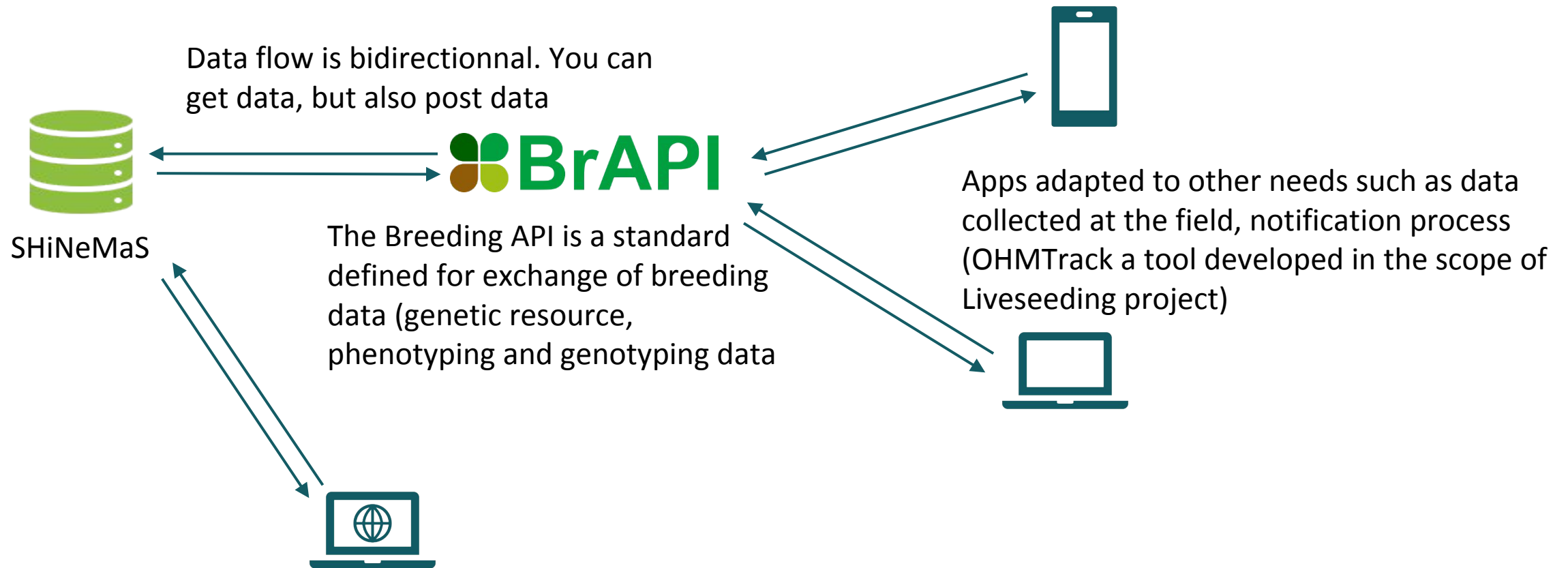
Query material in SHiNeMaS, retrieve list of objects

## SHiNeMaS' API

GET	/api/data_agro/
GET	/api/data_network_unipart_seed_lots/
GET	/api/data_agro_sr/
GET	/api/data_agro_ha/
GET	/api/data_agro_mixture/

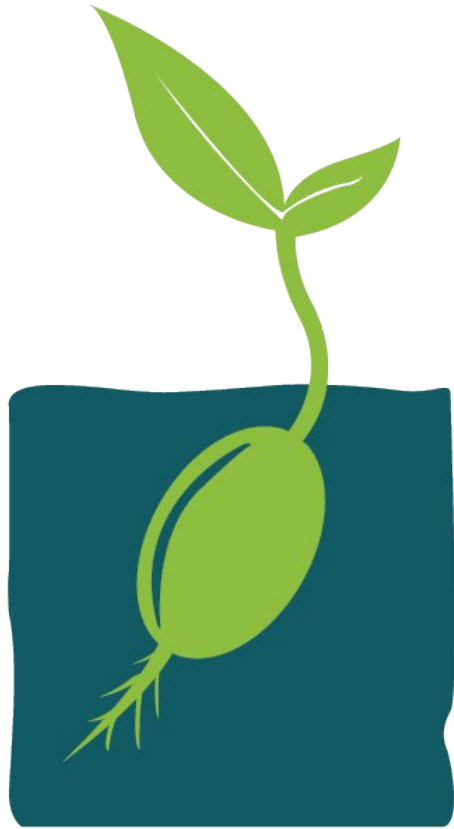
Specific agronomic queries (answer to selection, answer to environment, mixture etc.)

# Module 2 Unit 2 – Interoperability with BrAPI



# Module 2 Unit 2 - Explore data with SHiNeMaS

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Questions ?

# Module 2 Unit 2 – Short quiz

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Download the quiz :

<https://tinyurl.com/4xh66uxx>

And send it to [yannick.de-oliveira@inrae.fr](mailto:yannick.de-oliveira@inrae.fr)





**BYOD day**

# Module 2 Unit 2 - Outline of a BYOD day

---

**What is a “Bring your own data” day ?**

**The concept of a BYOD day is to test a tool with your own data.**

**The objectives is to give you a better overview of a tool in a context that is relevant and comfortable for you as you use your own data.**

# Module 2 Unit 2 - When and how ?

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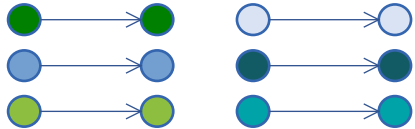
Today is a general presentation of SHiNeMaS. The main concepts have been presented.

Next monday (the 10th of February) it's your turn to work !

I will provide an instance of SHiNeMaS and you will get an individual account to access this "demo" instance of the tool.

# Module 2 Unit 2 - Remember this step by step data management ?

Step 0 – define initial objects (person, locations, methods, variables, species, germplasms etc.) and create your first seed lots.



Step 3 – Submit your file in SHiNeMaS. When the file is submitted events and harvested seed lots are automatically created.



Step 1 - export **pre-filled file** with :  
- sowed seeds lots list (previous harvested seeds lots)  
- sowing/harvesting year  
*Example with multiplication file*



Step 2 – fill exported file with:  
- plot location  
- quantity  
- field evaluation data



# Module 2 Unit 2 - What you will do ?

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- The objective is to create your first set of seed lot regarding information you will provide before the training.
- And start to build your seed lot history step by step.
- For this you can explore the different way to submit data in SHiNeMaS (forms, files). Using forms on little datasets can be a good start.
- And, of course, use the different interfaces to explore your data and see your network growing
- To do this you can use the supports available : this presentation, SHiNeMaS' documentation and me of course, I will be online to help you as much as possible.

# What do you need to provide exactly ?

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- The species you work with (and a nice picture depicting this species if you have one)
- A list of person involved in your data management (this can be virtual name if you do not want to provide real names)
- A list of locations where you lead trials
- A list of variables for which you have some data
- A list of methods related to your data (and variables)
- A list of germplasms you want to test in SHiNeMaS

# Module 2 Unit 2 - Tips for the BYOD day

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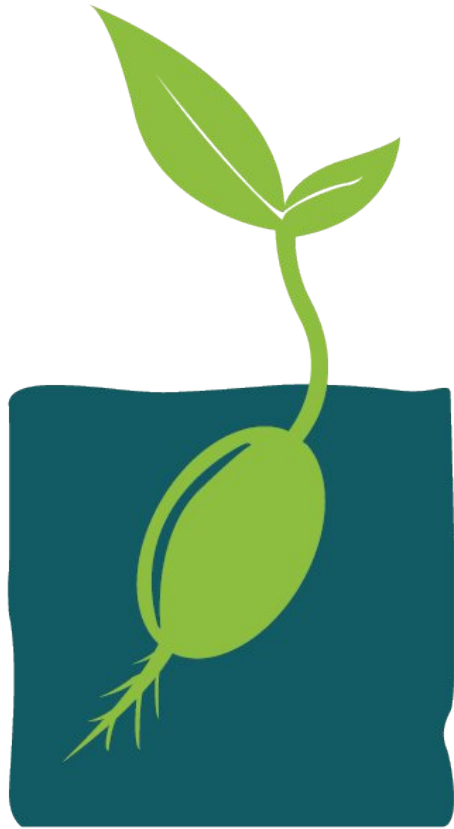
**1- You don't need huge list for each "object" : The most important is to provide consistent information.**

**2- Be aware that you will work on a demo instance of SHiNeMaS, every trainees will see data of other trainees : do not provide data that are mostly sensitive, all data will be deleted after the training**



# Module 2 Unit 2 - Bring your own data day

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Questions ?

# What we learned today

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- **SHiNeMaS is a tool useful to track breeding activities, especially if you work with OHM**
- **You can**
  - **Manage biological material (GR, seed lots) with their quantity/storage devices**
  - **Collect/store data at different levels**
  - **Use third party tool through web services (BrAPI)**





# **LiveSeeding**

**Thank you !**