

# Systemes d'acquisition de donnees et chaines de traitement

5 Avril 2022, Paris

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AU SERVICE DE LA SCIENCE

ANR11-INBS-0012

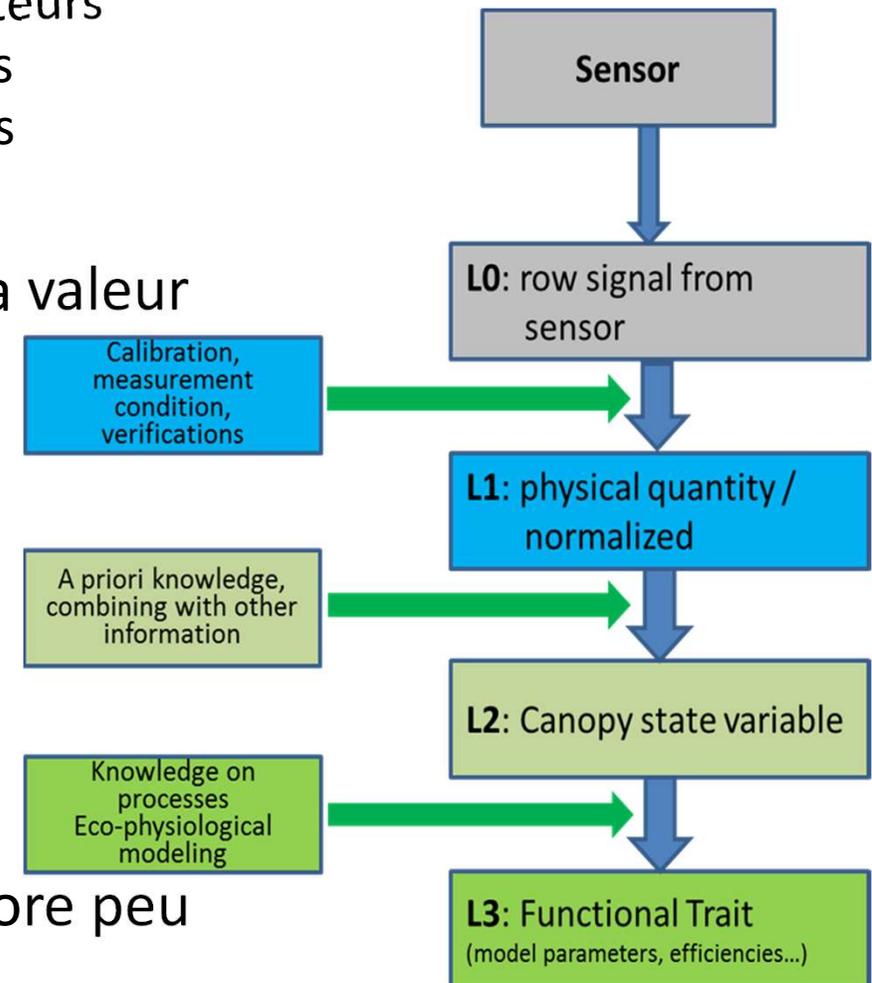
**INRAE**

**ARVALIS**  
Institut du vegetal

**Terres  
Inovia**  
l'agronomie en mouvement

- **Système d'acquisition de données**
  - Capteurs
  - plateforme portant les capteurs
  - Système de pilotage de la plateforme
  - Système et de déclenchement des capteurs
  - Système d'enregistrement des données
  - (Système de transmission) des données

- **Traitement des données:** transformer la valeur brute du capteur en variables d'intérêt: estimation de traits



Focus sur le phénotypage au champ ou encore peu de solutions commerciales sont disponibles

Mesure non-destructive, non-invasive du rayonnement réfléchi ou émis par chaque élément du couvert.

$$\textit{Trait} = f[M(x, y, z, \lambda, \Omega, t)]$$

Measurement

Scanner

Imagerie

3D imagerie

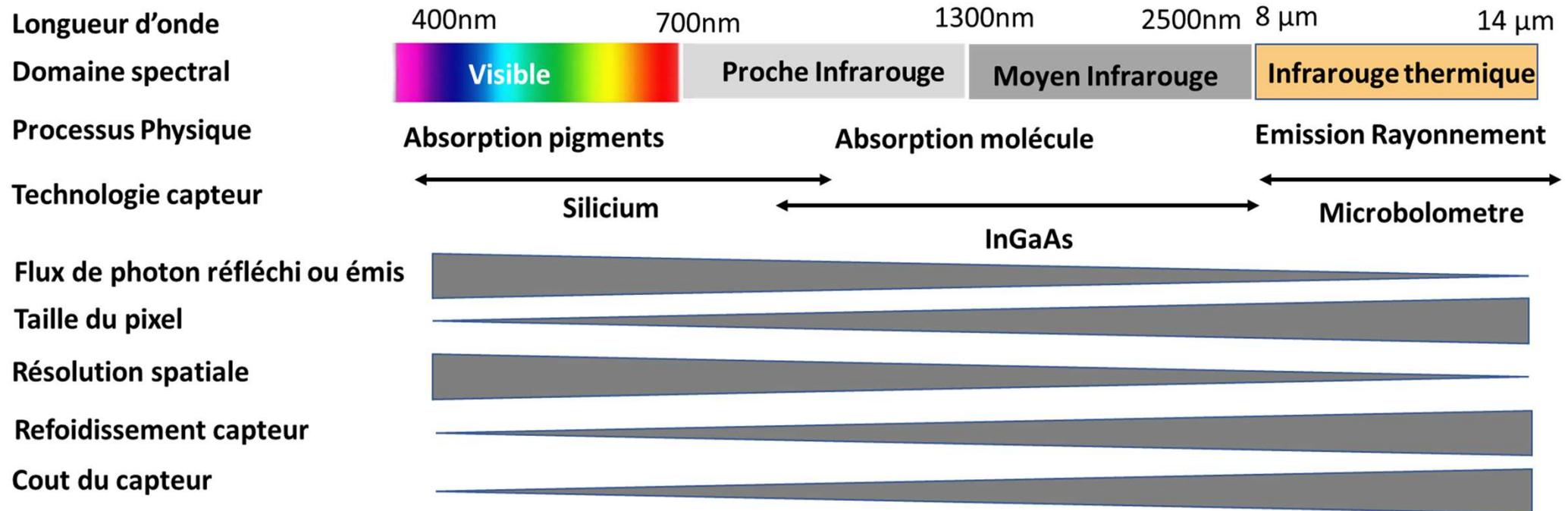
Longueur d'onde

Direction

Temps

- ***Trait d'état***
  - estimation d'une caractéristique du couvert/plante/organe à un moment donné à partir des 5 dimensions disponibles  $(x, y, z, \lambda, \Omega)$
- ***Trait fonctionnel/dynamique***
  - calcul à partir de l'évolution d'un trait d'état

# Capteurs et domaines spectraux



- Dans le domaine réflectif (400-2500 nm)
  - l'absorption détermine le niveau de réflectance/radiance: Accès à:
    - la composition biochimique
    - Identification d'objets par propriétés spectrales
    - La structure du couvert
- Dans le domaine infrarouge thermique (8-14 μm) accès à
  - la température de brillance

# Les capteurs utilisés

Capteurs	Resolution (Mpix)	Traits Structuraux /Morphologique	Traits Biochimiques	Traits Sanitaires	Traits physiologiques
 RGB camera	10-100	++++	+	+++	-
 Multi-spectral camera	0.5-2	++	+++	++	-
 Hyper-spectral Camera	0.1-0.5	+	++++	+++	++
 Thermal camera	0.1-1	++	-	++	+++
 LiDAR (scanner)	1mm-1m	+++	-	-	-

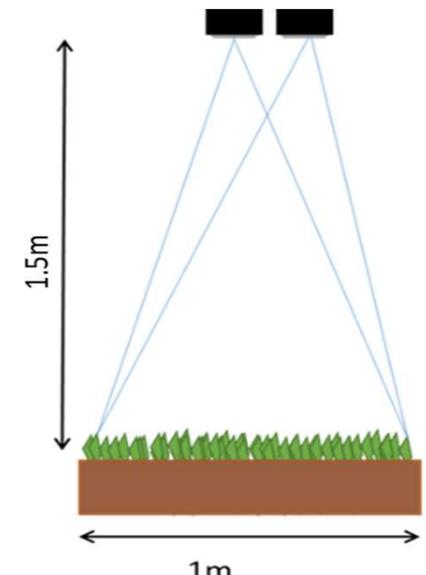
## **Camera AIRPHEN** pour drone

- Adaptation aux mesures rapprochées
- Production abandonnée car produite en trop petit nombre



## **Camera HYSTERCAM**: mesures multispectrales haute résolution stéréoscopique

- 2 cameras RGB dont une transformée
- couple stéréoscopique
- haute résolution spatiale (>12 Mpix)
- Estimation de la radiance dans toutes les bandes spectrales du visible et proche-infrarouge par reconstruction

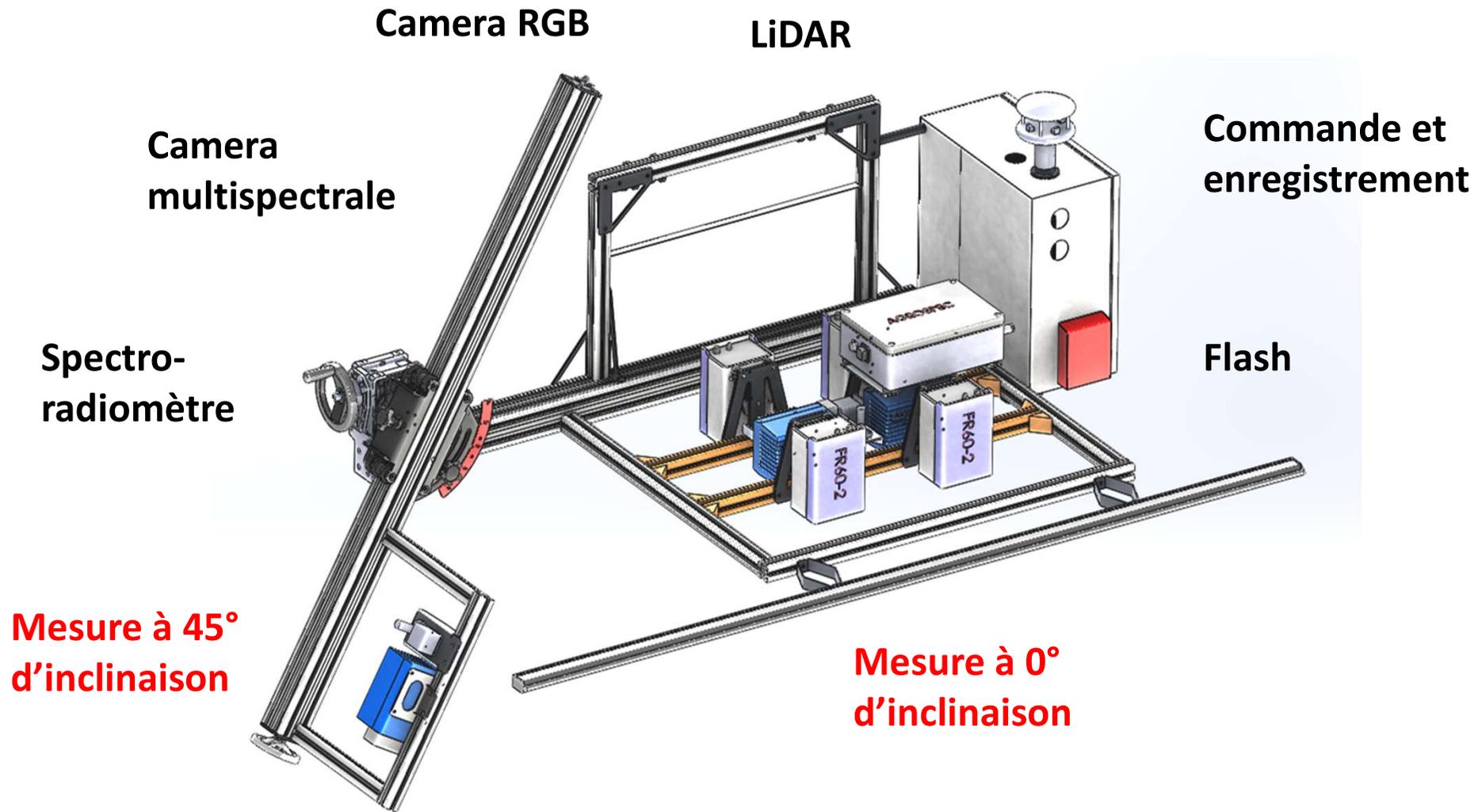




	Fixe	Porté	Tracteur	Phenomobile	Portique	Drone	Satellite
Résolution spatiale	1mm	0.2mm	0.5mm	0.5mm	0.5mm	0.5mm – 5cm	0.5m-10m
Couverture spatiale	<100m <sup>2</sup>	<1 ha	<5 ha	<5ha	<0.3ha	<15ha	>500km <sup>2</sup>
Temps de revisite	1h-1j	3j-30j	3j-30j	3j-30j	3h-30j	3h-30j	1j-10j
Directionnalité	0°    45°	0° & 45°	0°	0° & 45°	0° & 45°	0° (45°)	≈ 0°
Richesse Spectrale	RGB	RGB	RGB+Multi	RGB+Multi	RGB+Multi	RGB+Multi+IRT	Multi
3D	Non	Photo	Photo, LiDAR	Photo, LiDAR	Photo, LiDAR	Photo (LiDAR)	Non

- **L'offre DJI correspond bien aux besoins pour le drone**
- **Focus sur les systèmes terrestres avec tête de mesure polyvalente:**
  - LITERAL (porté)
  - PhiB (tracteur)
  - Phenomobile (robot)
  - Portique (PhenoField)

# Tête de mesures polyvalente



Systeme adaptable à de nombreux véhicules

# Une tête de mesures polyvalente et configurable

The screenshot displays the Pheno IHM software interface. On the left is a dark sidebar with a green header containing a back arrow, the text 'PHENO', and a gear icon. Below the header are several menu items with icons: 'Vecteurs' (highlighted in green), 'Têtes de mesure', 'Missions', 'Données géographiques', 'Enregistrer chemin', 'Lancer mission', 'Lancer mission non géo-référencée', 'Télécharger', and 'Pilotage manuel'. At the bottom of the sidebar are a 'Connexion' button and a large red 'STOP' button.

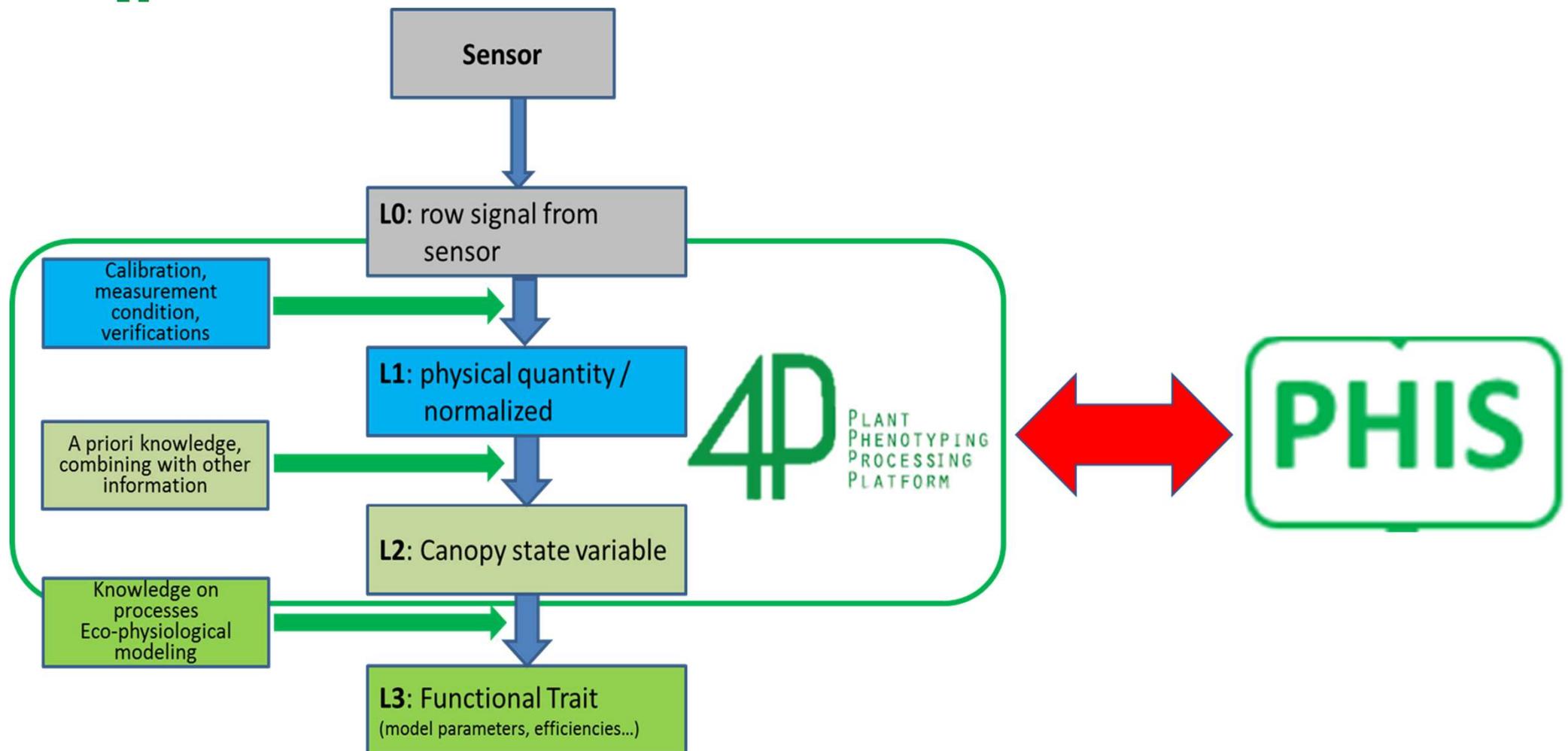
The main area is divided into two panels. The left panel, titled 'Vecteurs', shows a list of items: 'Phéno v2', 'Phéno v22', 'Phéno v2 nr3', and 'label' (highlighted in green). Below the list are trash and add (+) icons. The right panel, titled 'Caractéristiques du vecteur', contains two input fields: 'Nom' with the text 'Nouveau véhicule' and 'Type' with a dropdown menu showing 'pheno v1'. At the bottom right of the main area are checkmark and close (X) icons.

# Programmation des acquisitions

The screenshot displays the Pheno IHM software interface, divided into three main sections:

- Left Panel (Navigation):** Contains a menu with options: Vecteurs, Têtes de mesure, Missions, Données géographiques, Enregistrer chemin, Lancer mission, Lancer mission non géo-référencée, Télécharger, and Pilotage manuel. At the bottom, there are buttons for 'Connexion' and a large red 'STOP' button.
- Center Panel (Map):** Titled 'Pheno IHM', it shows a green field with a grid of red numbered rectangles representing mission points. The rectangles are arranged in three parallel diagonal rows. The top row contains rectangles numbered 13, 27, and 55. The middle row contains 12, 28, 54, 11, 29, 53, 10, 30, 52, 9, 31, 51, 8, 32, 50, 7, 33, 49, 6, 34, 48, 5, 35, 47, 4, 36, 46, 3, 37, 45, 2, 38, 44, 1, 39, 43, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83. A scale bar at the bottom indicates 0, 10, and 20 meters. The text 'Speed: 41.7 fps' is visible in the top left of the map area.
- Right Panel (Sequence Editor):** Titled 'Editeur de séquences et déclenchements', it features a table with 11 rows. Each row has an 'ID de la mi...' column and a 'Script' column with a dropdown menu. The 'Script' column contains 'script A' for all rows. Below the table are icons for deleting, adding, and saving sequences, along with buttons for 'Appliquer à la sélection' and 'Appliquer à tout'. At the bottom, there is a 'Script' dropdown menu set to 'script A', an 'Editer les scripts' button with a pencil icon, and checkmark/cancel buttons.

## 4P Plant Phenotyping Processing Platform

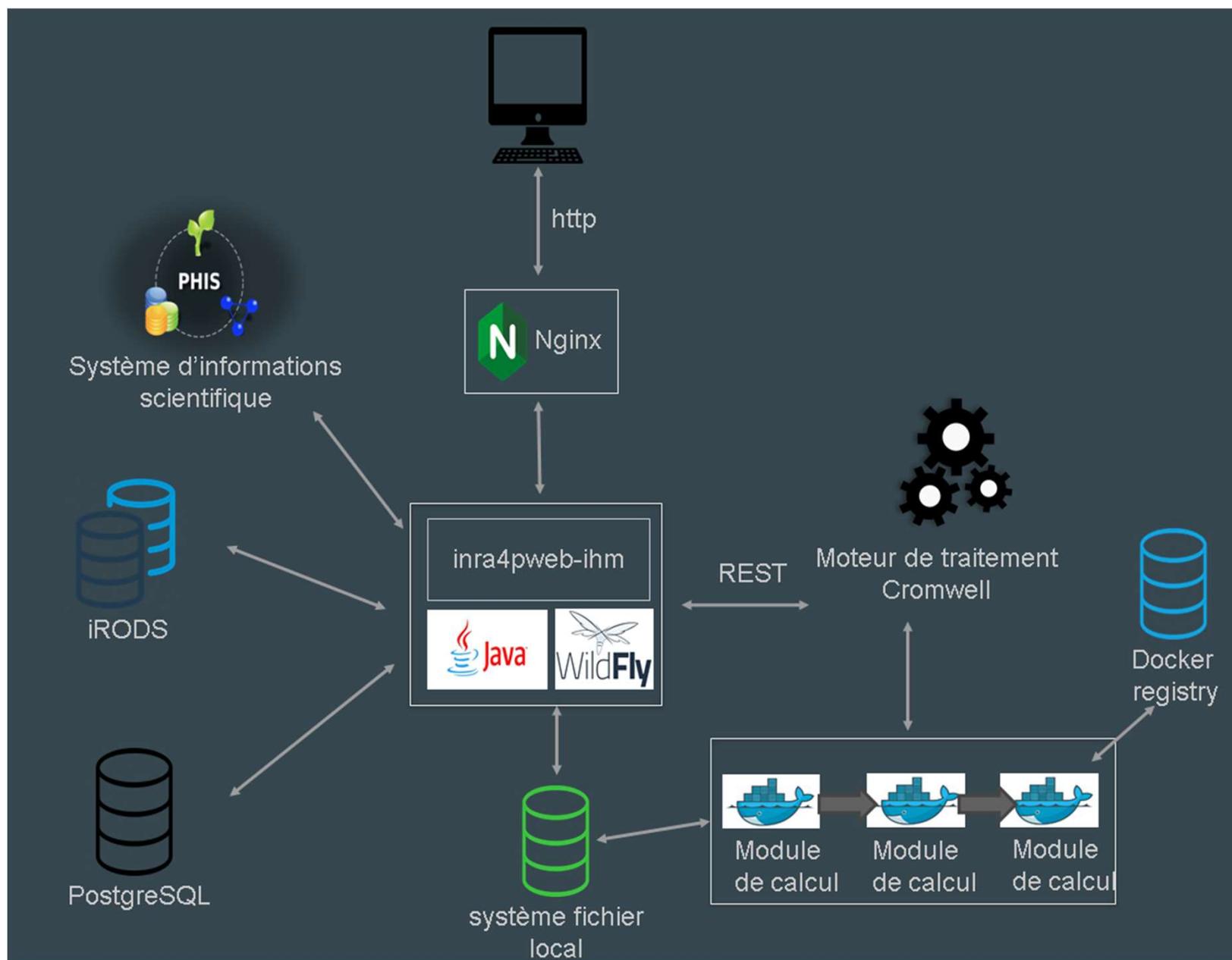


**Traitement par session:** groupe de microplots échantillonnées avec le même système d'acquisition à une date donnée

**Interfaçage avec PHIS:** échanges d'informations

# 4P: une plateforme ergonomique et conviviale

# Une architecture informatique complexe



## Drone



### 18 Modules

- Phenoscript (L0->L1)
- Inversion PROSAIL
- Calcul Hauteur Sol et Canopy  
« Validation » phenoscript

### 26 Variables

- Réflectance
- Indices de Végétation (16)
- Structure (Hauteur, GAI, ALA, fIPAR, GF, nuage de points 3D)
- Biochimie (Chlorophylle)
- Comptage grosses plantes

## Phenomobile



### 6 Modules

- Pré-traitements L0->L1  
RGB – LIDAR – AIRPHEN
- Traitement des données LiDAR
- Traitement AIRPHEN

### 12 Variables

- Structure (Hauteur, GAI, ALA, fIPAR, GF, nuage de points 3D)
- Biochimie (Chlorophylle)
- Comptage épis
- Segmentation

## LITERAL



### 3 Modules

- Pré-traitements L0->L1
- Segmentation
- Comptage épis

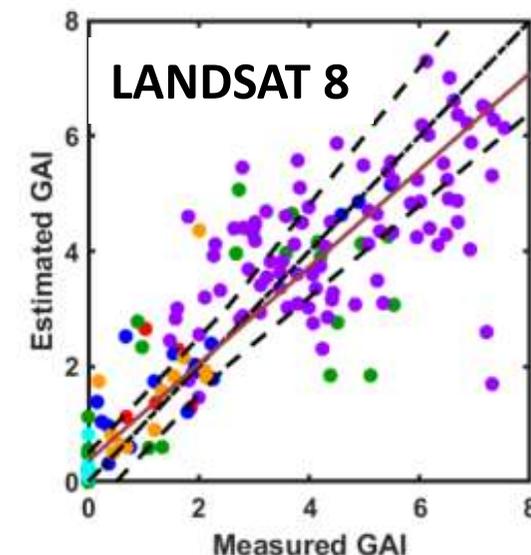
### 9 Variables

- Structure (Hauteur, GAI, ALA, fIPAR, GF, nuage de points 3D)
- Biochimie (Chlorophylle)
- Comptage épis
- Segmentation

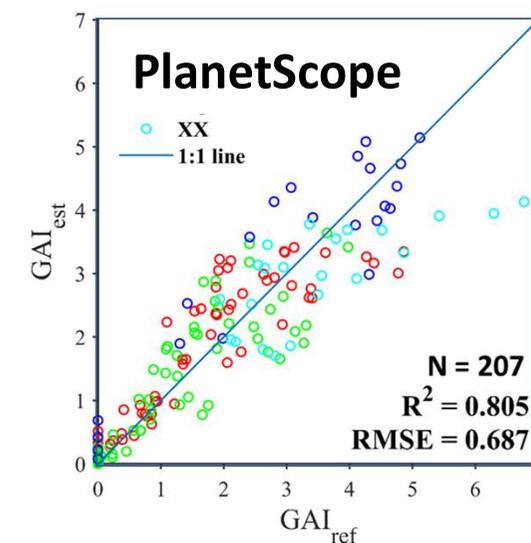
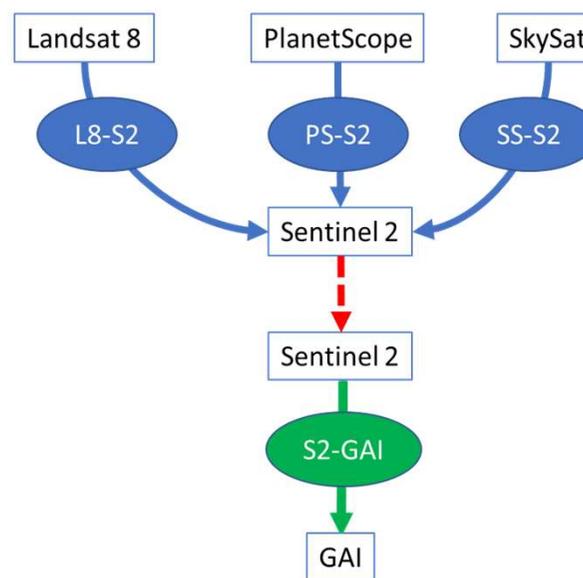
# Le satellite pour le phénotypage?



	Landsat 8	Sentinel 2	PlanetScope	SkySat
<b>Resolution</b>	30 m	10-20 m	3 m	0.5 m
<b>Nb. Sat.</b>	1	2	>100	21
<b>Revisit time</b>	16 days	3 days	1 day	program
<b>Vis</b>	3	3	3	3
<b>Red-Edge</b>		1	1	
<b>NIR</b>	1	1	1	1
<b>SWIR</b>	2	2		
<b>Cost</b>	free	free	≈1€/km <sup>2</sup> /year	≈6€/km <sup>2</sup> /image



Une approche générique multicapteurs

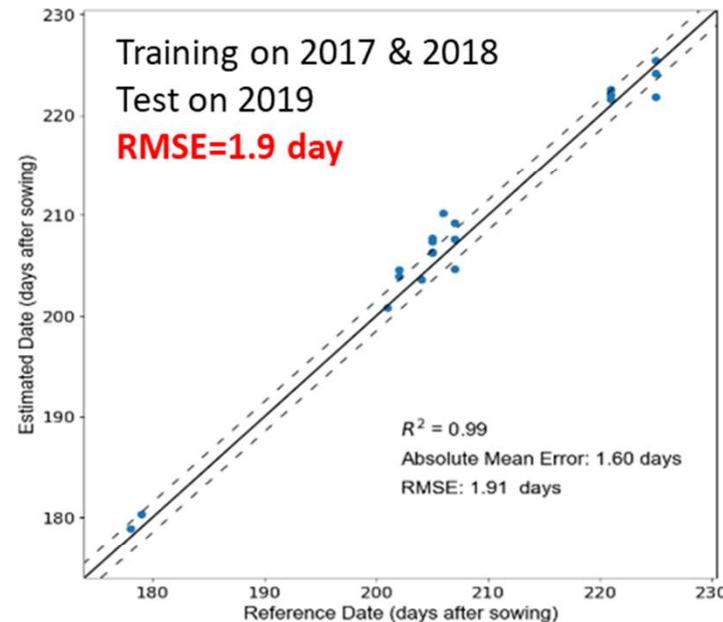


## Estimation de l'épiaison par suivi IoT



### RGB Camera

1 m above crop  
45° zenith view angle  
1 image/day @ 12:00  
Transmission by 3G



### Détection des épis dans l'image

## Comptage d'épis de blé (identification d'objets)



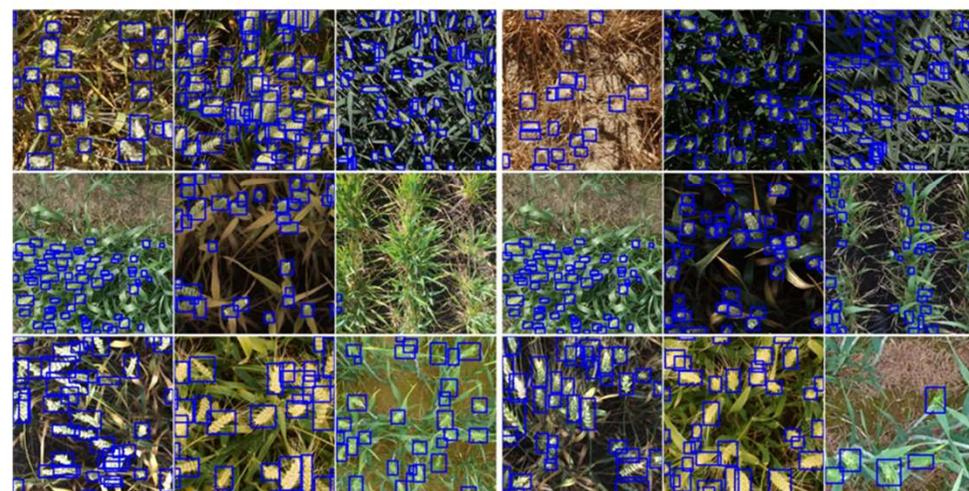
7 countries

4700 images

185.000 labeled wheat head

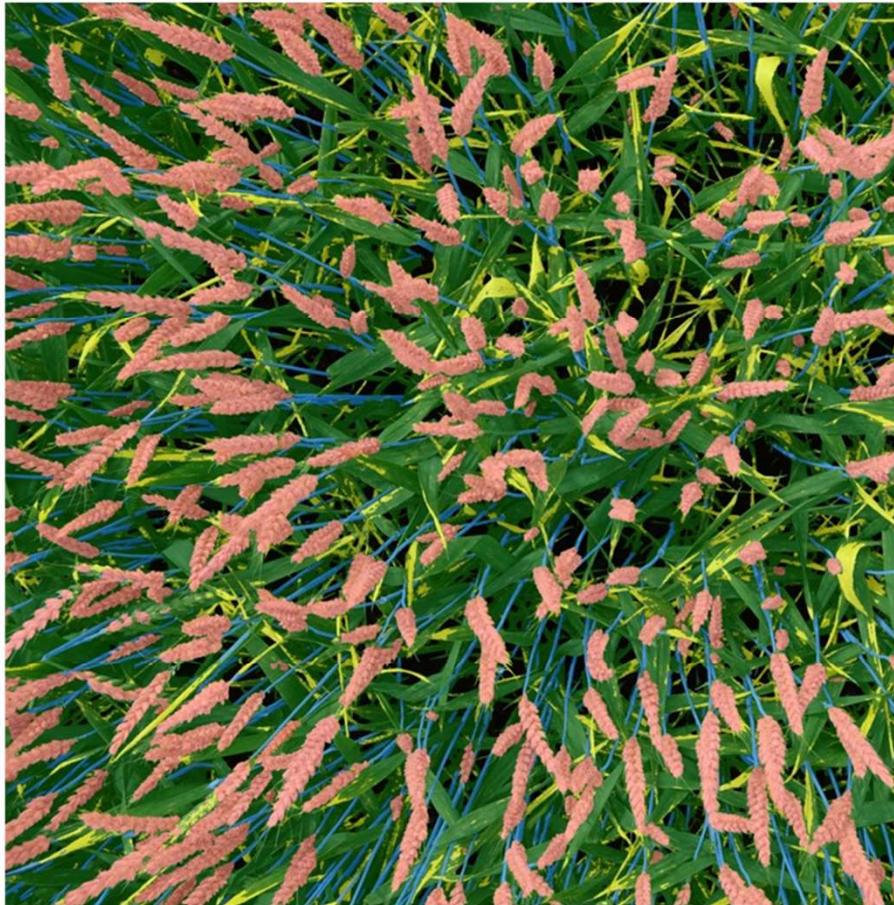


- Mai – Août 2020
- 2235 équipes participantes
- Les 3 meilleurs modèles mis à disposition

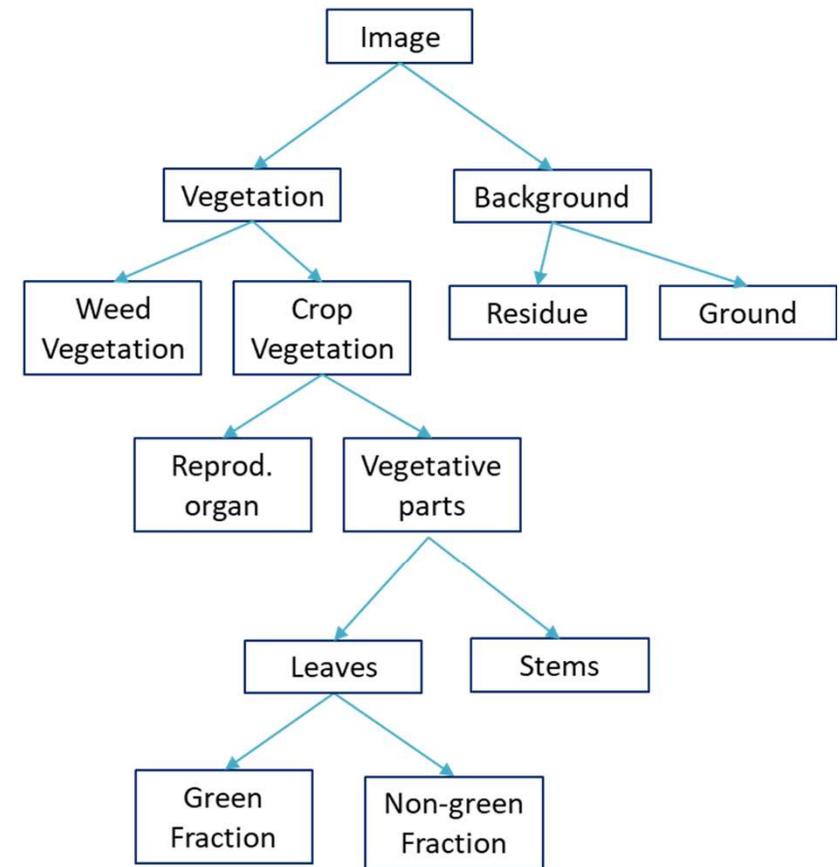


## Segmentation sémantique

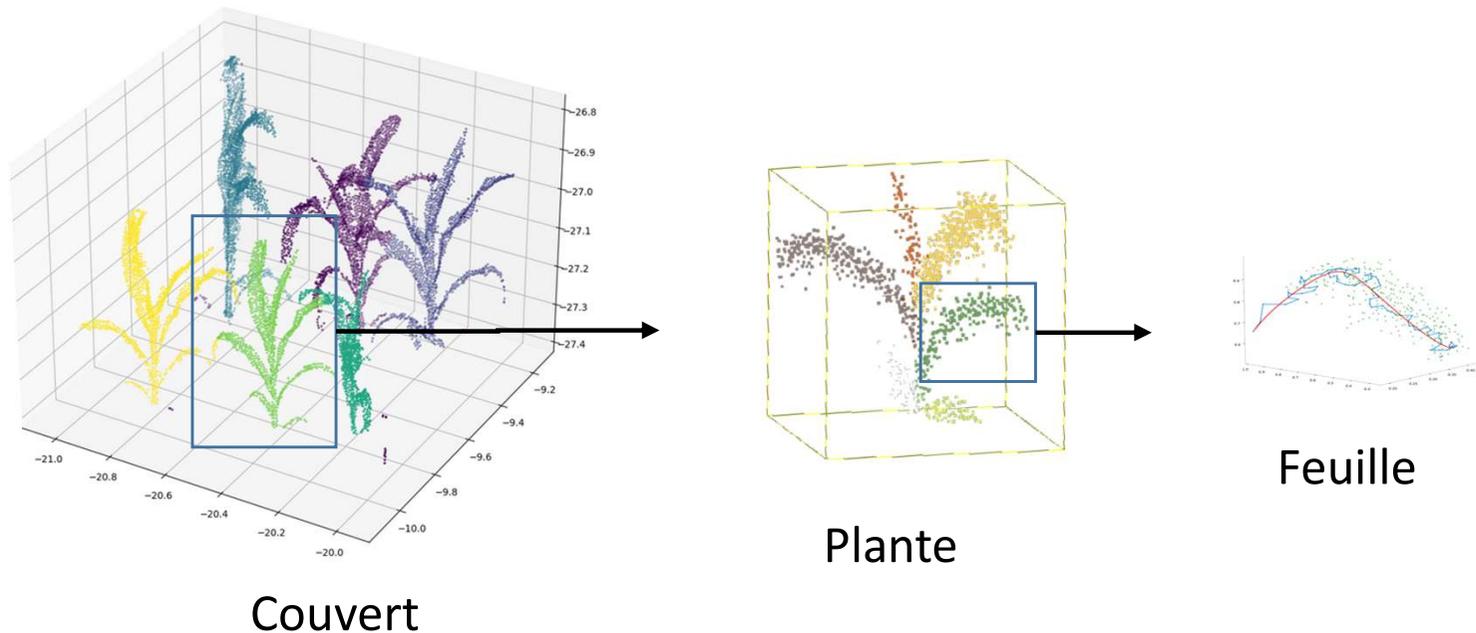
- Tiges
- Feuille saine
- Feuille malade
- Épis
- Arrière-plan



L. Bernigaud, S. Madec 2021



## Description détaillée de l'architecture du couvert à partir des nuages de points 3D (LiDAR, photogrammétrie)



## ***Des systèmes d'acquisition de données opérationnels avec:***

- des niveaux d'automatisation variés
- une gamme de débits et couvertures
- ... et des coûts d'utilisation variables
- Des améliorations attendues avec HYSSTERCAM

## ***Une chaîne de traitement (4P) produisant déjà les variables essentielles***

- Importance des méthodes profondes pour l'exploitation des images 2D et 3D
- Interfaçage à PHIS
- De nouveaux modules sont attendus

# MCP 1.1 Interactions plantes micro-organismes

5 avril, Paris

David Rousseau



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ANR11-INBS-0012

**INRAE**

**ARVALIS**  
Institut du végétal

**Terres  
Inovia**  
l'agronomie en mouvement

- **Objectives**

- Characterize, detect, recognize, quantify, track, monitor biotic interactions (pathogenic and mutualistic) at all scales/ stages of plants from seed to adult including shoot and root.
- Based on state of the art imaging : RGB, LIDAR, Multispectral, NIR-SWIR, Fluorescence.
- Working under controlled or field conditions

- **Methods & Methodology**

- Generic methodological image processing tools (preprocessing, deep learning, ML-based data mining on processed images)
- Applied first on a representative set of biological use-cases already funded on phenotypic hubs (pragmatism+link with ontology in MCP2)
- Create a community of knowledge via training

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# The quest for « genericity »

Identify phenological stages, measure of size of symptoms, detect change of color, characterize change turgescence, monitor germination, determine shape of a leaf,, extract roots out of soil, count nodules on roots, quantifying amount of innoculum,, detect emergence, monitor kinetic of symptoms, ...SO MANY DIFFERENT BIOLOGICAL QUESTIONS !!!



Biologist

I don't have time to do it all since I am the only one on the platform  
please have look at the jungle of image processing tools already available on  
<https://www.quantitative-plant.org/software>



Geek1.0

# Deep learning as a generic tool

Identify phenological stages, measure of size of symptoms, detect change of color, characterize change turgescence, monitor germination, determine shape of a leaf,, extract roots out of soil, count nodules on roots, quantifying amount of inoculum,, detect emergence, monitor kinetic of symptoms, ...



Biologist

From a computer perspective all of these can be sorted in classification, segmentation, tracking and addressed with a very limited number of available neural networks : ResNet, Unet, CNN-LSTM, with help of Phenome I propose make them available in a didactic way on 4P and train all geeks and tech minded biologist to use these tools



Computer scientist

# Exemple de pipeline

## maladies sur feuilles de grandes cultures (Arvalis)

Step 1  
image acquisition



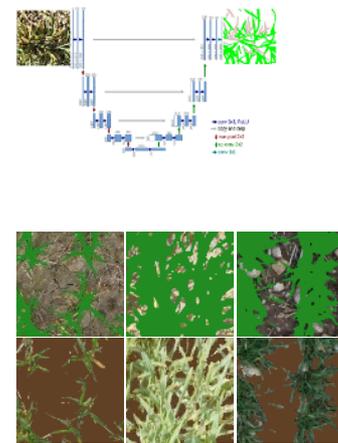
from past and future funded experiments

Step 2  
annotation



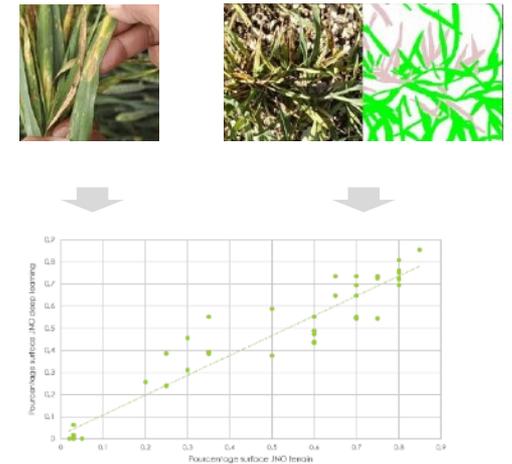
from collaborative platform

Step 3  
Deep learning



from didactic version of U-Net

Step 4  
Data analysis



Comparison with ground truth  
Automatic cluster of types of errors

## • Objectives

- Characterize, detect, recognize, quantify, track, monitor biotic interactions (pathogenic and mutualistic) at all scales/ stages of plants from seed to adult including shoot and root.
- Based on state of the art imaging : RGB, LIDAR, Multispectral, NIR-SWIR, Fluorescence.
- Working under controlled or field conditions

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- Generic methodological image processing tools (preprocessing, deep learning, ML-based data mining on processed images)
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- Create a community of knowledge via training

## • Partners

	Phenotic Angers	PhenoToul Agro-Helia	4PMI Dijon	Arvalis	Terres Inovia
Generic methodological image processing tools	✓	✓	▪	✓	▪
Quantifying Biotic stress on shoot of major crops	✓	▪	▪	✓	▪
Quantifying Biotic stress on seeds and seedlings of horticultural species of major interest	✓	✓	▪	▪	▪
Quantifying Biotic interactions on root of adult major crop	✓	✓	✓	▪	▪
Characterizing insects in situ	✓	▪	▪	▪	✓



## • Partners

Generic methodological image processing tools

Quantifying Biotic stress on shoot of major crops

Quantifying Biotic stress on seeds and seedlings of horticultural species of major interest

Quantifying Biotic interactions on root of adult major crop

Characterizing insects in situ

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Generic methodological image processing tools	✓	✓	▪	✓	▪
Quantifying Biotic stress on shoot of major crops	✓	▪	▪	✓	▪
Quantifying Biotic stress on seeds and seedlings of horticultural species of major interest	✓	✓	▪	▪	▪
Quantifying Biotic interactions on root of adult major crop	✓	✓	✓	▪	▪
Characterizing insects in situ	✓	▪	▪	▪	✓



# Interactions plante-microbiote

## PPR Sucseed



Essential in crop establishment



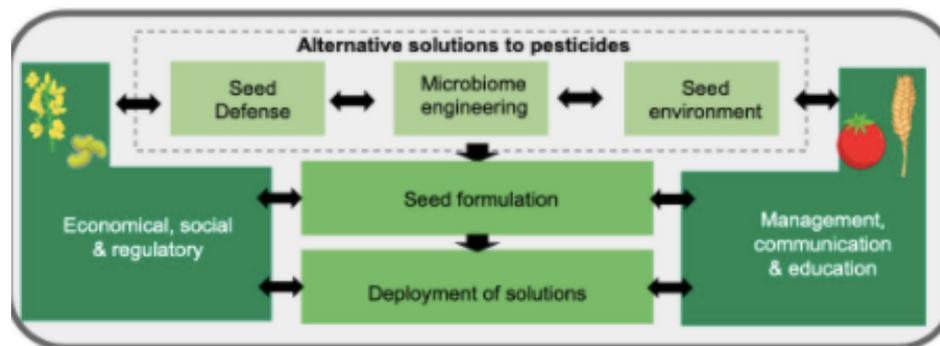
France, world leader of seed export



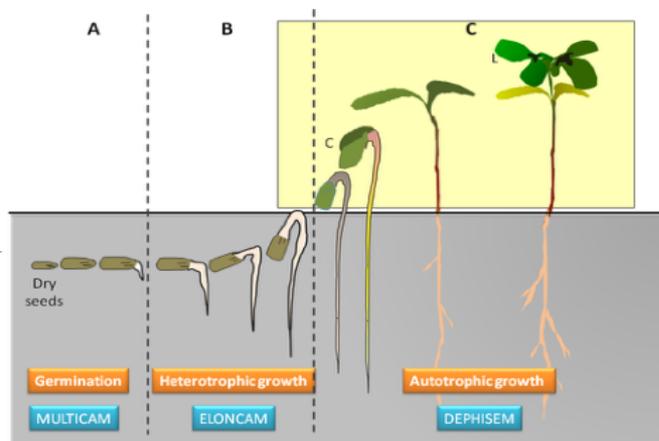
Carrier of plant pathogens



Secure quality through seed treatment



Synthetic microbiota



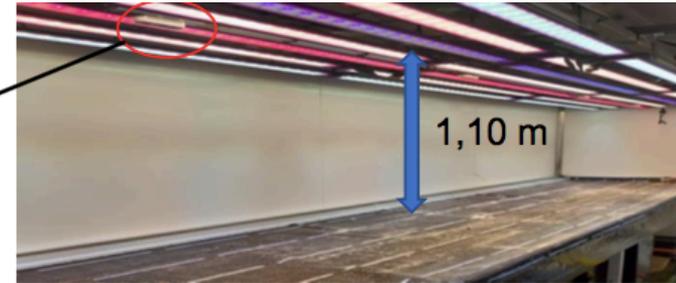
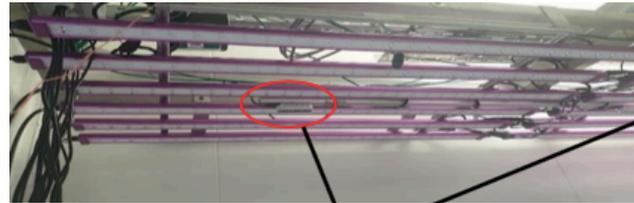
Need of high throughput Analysis

# Nouveau Capteur RGB-Depth

Garbougé, H., Rasti, P., & Rousseau, D. (2021). Enhancing the Tracking of Seedling Growth Using RGB-Depth Fusion and Deep Learning. *Sensors*, 21(24), 8425.

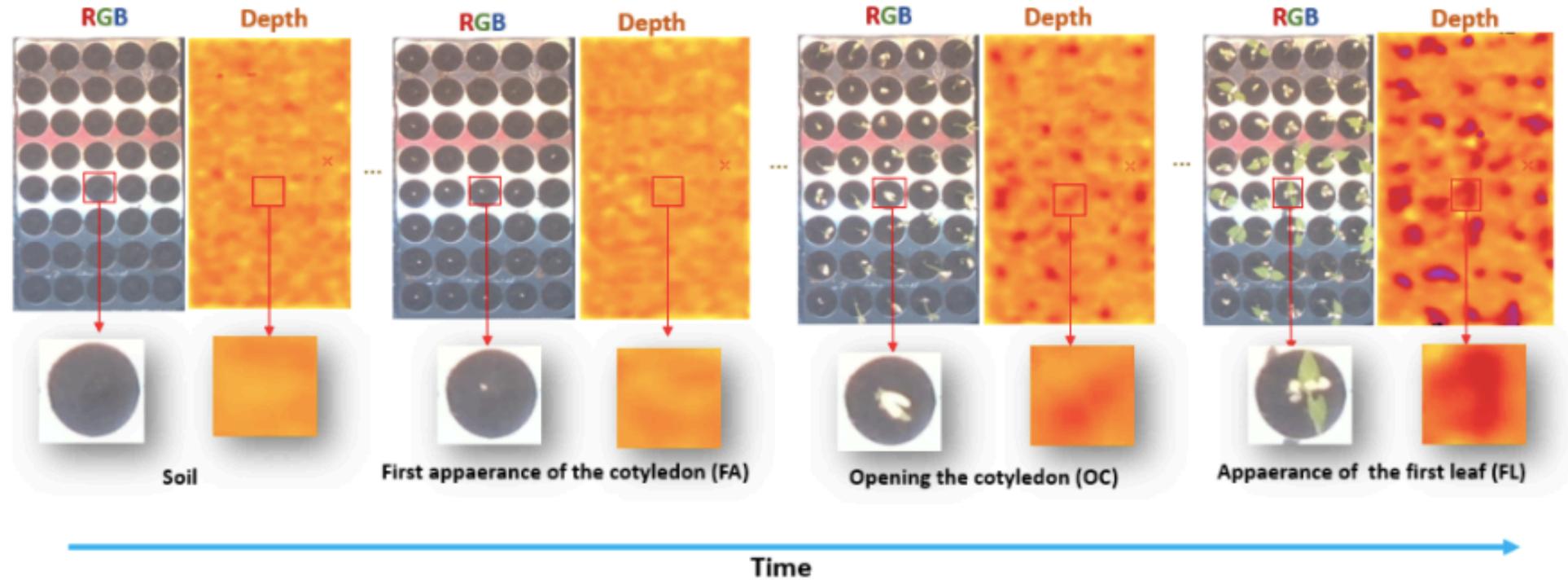


300 euros



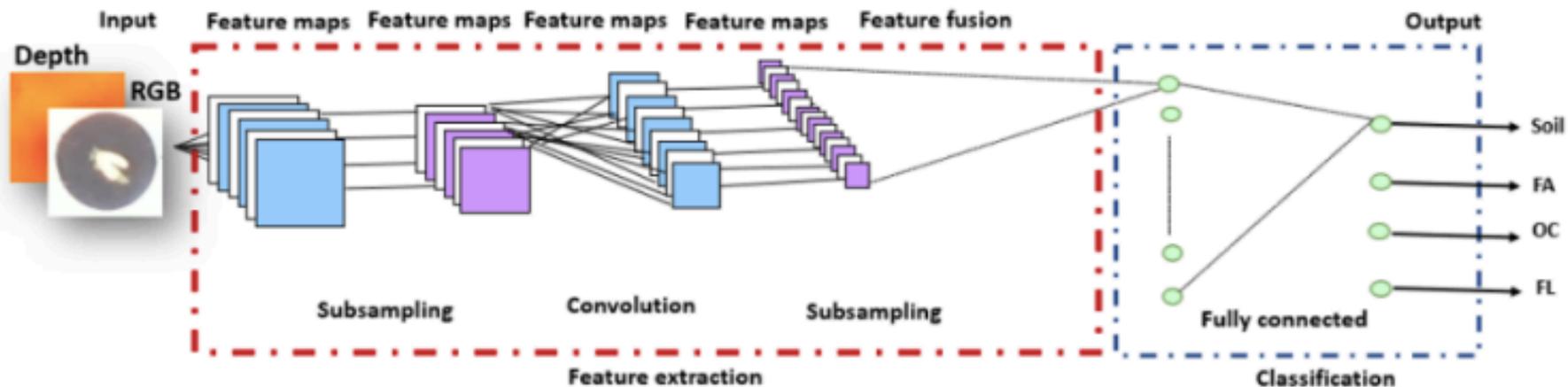
PHENOTIC  
SEMENCES & PLANTES

# Plant microbiota interactions

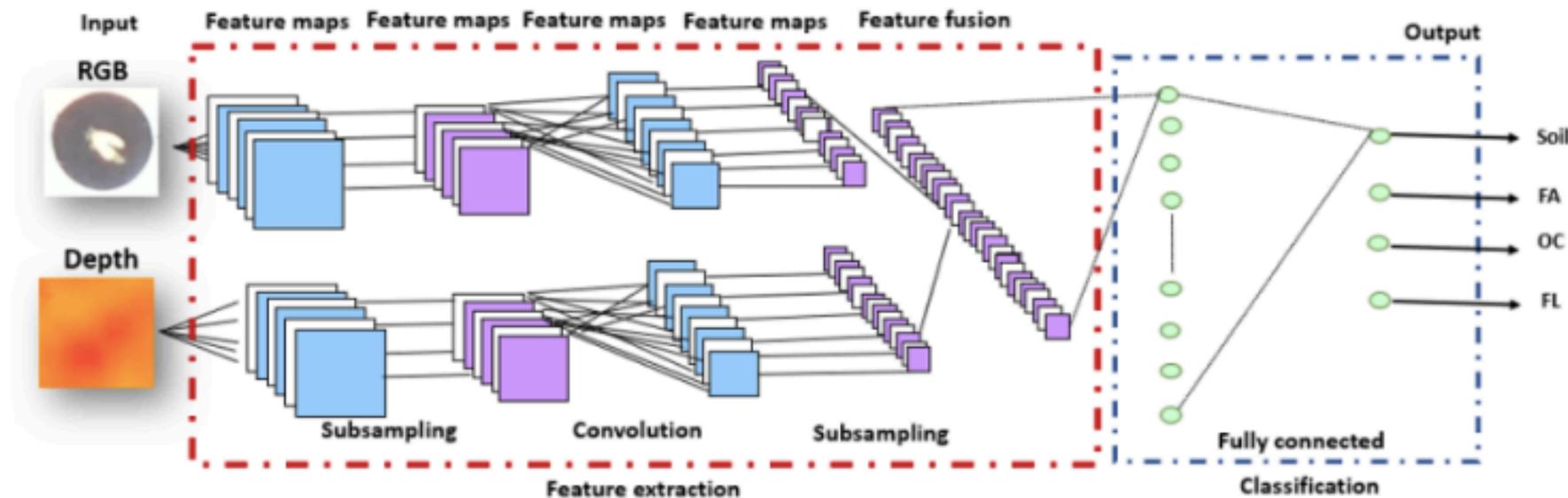


H. Garbougé 2022, Sensors

# Interactions plante-microbiote



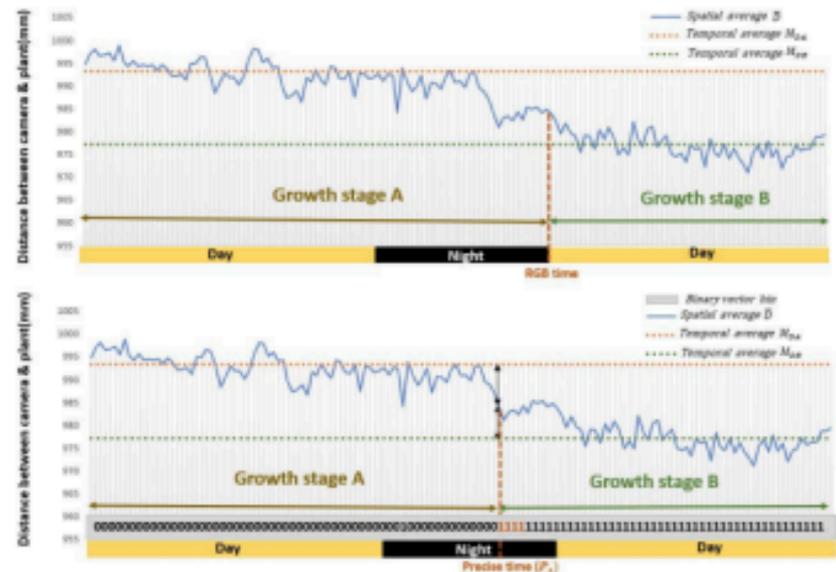
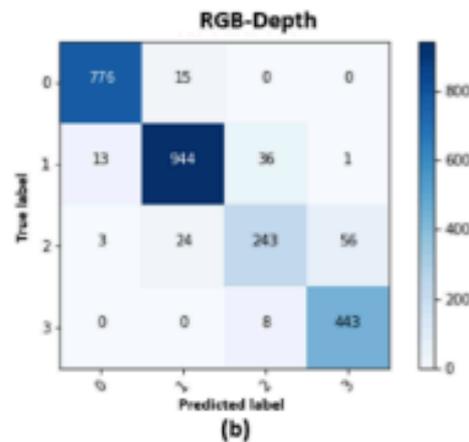
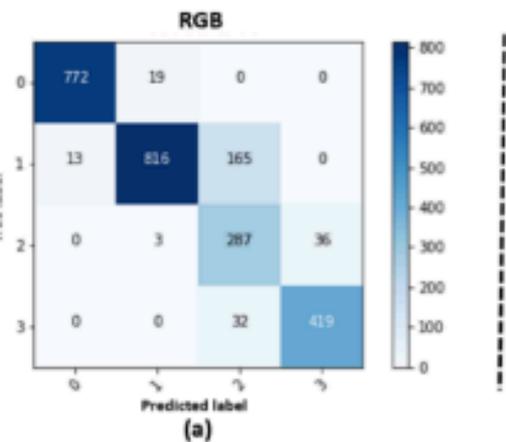
(a)



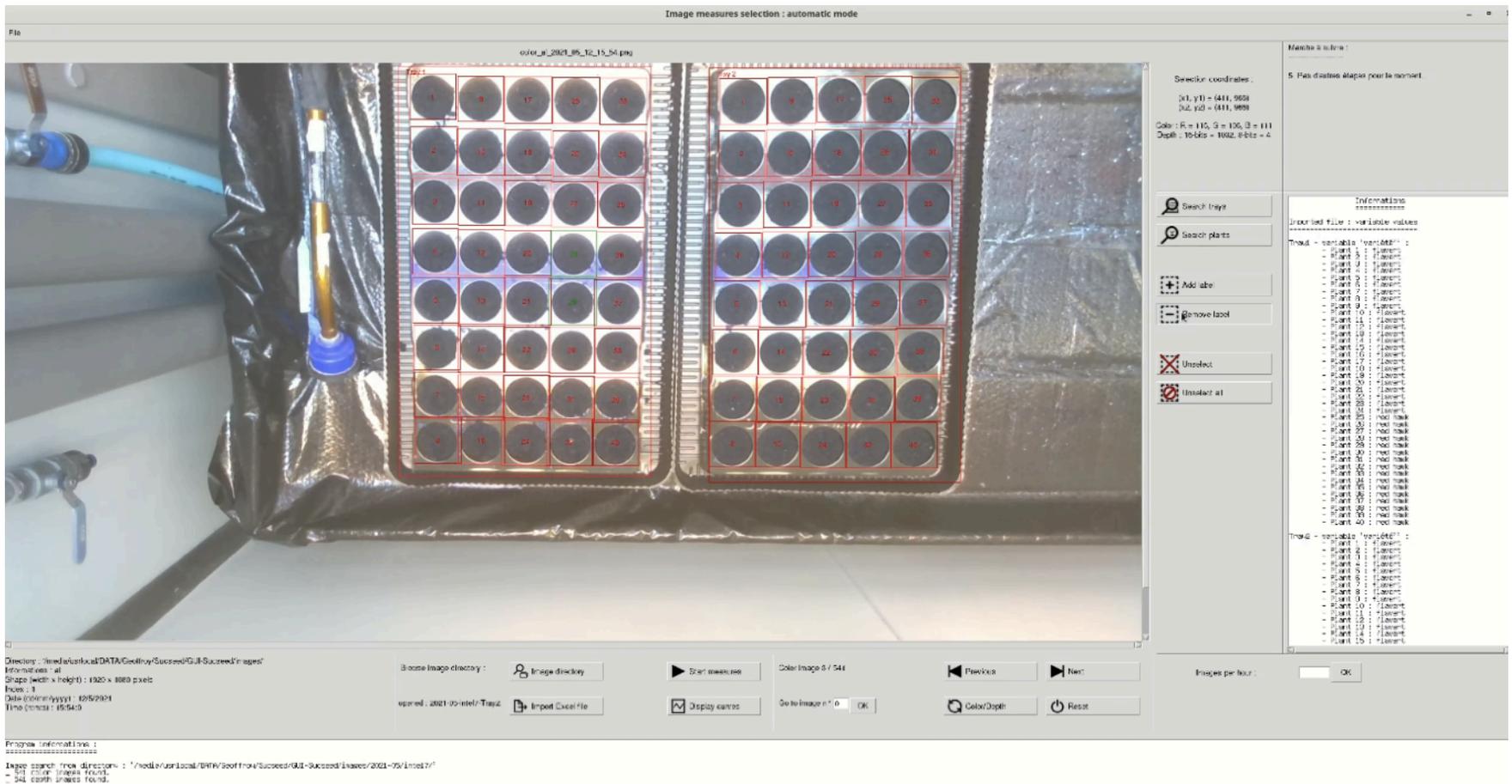
(b)

# Interactions plante-microbiote

	Training	Validation	Test
<b>RGB</b>	$0.95 \pm 0.02$	$0.91 \pm 0.03$	$0.88 \pm 0.05$
<b>Image fusion RGB-Depth</b>	$0.97 \pm 0.02$	$0.95 \pm 0.02$	$0.94 \pm 0.04$
<b>Features fusion RGB-Depth</b>	$0.97 \pm 0.01$	$0.96 \pm 0.01$	$0.94 \pm 0.01$



# Nouveau logiciel

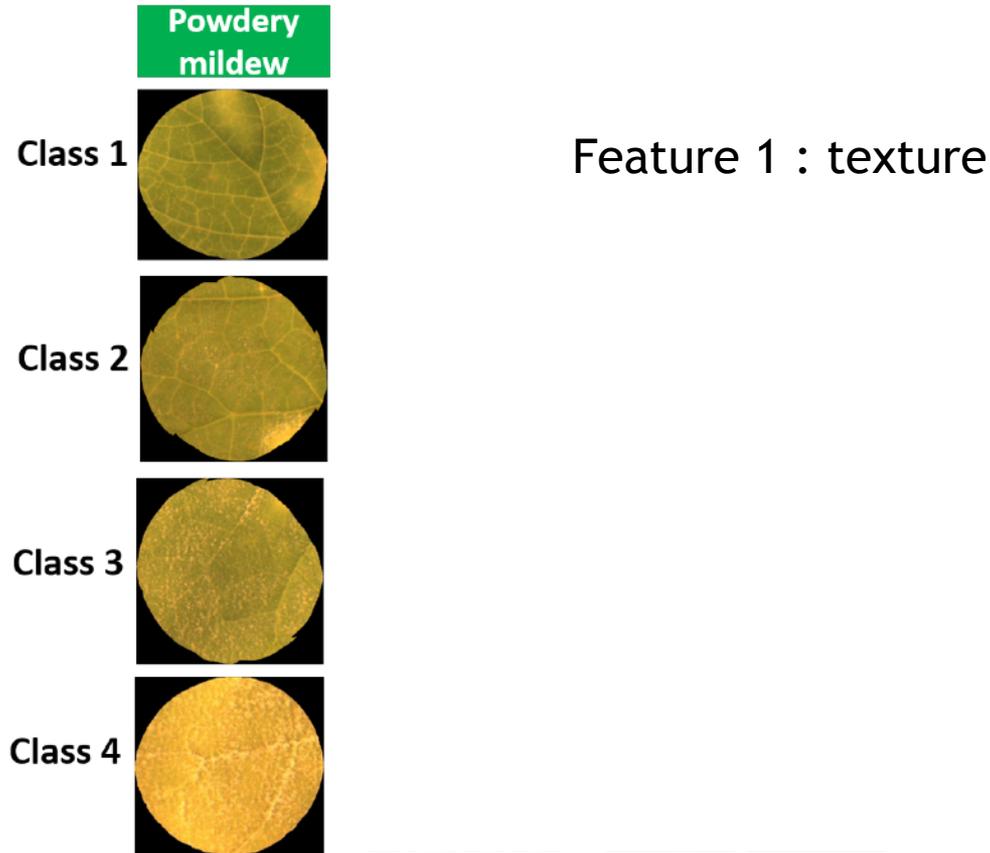


Garbuge, H., Couasnet G, & Rousseau, D. et al (2022). *SoftwareX*, en préparation

## Les maladies ...des données ordinales

Exemple sur données ordinales

Proposition de caractéristiques pour classer ces images

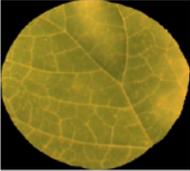


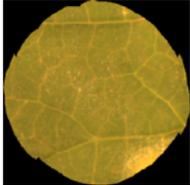
## Les maladies ...des données ordinales

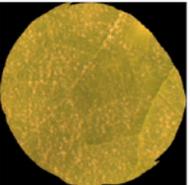
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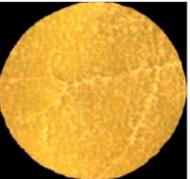
Proposition de caractéristiques pour classer ces images

**Powdery mildew**

Class 1 

Class 2 

Class 3 

Class 4 

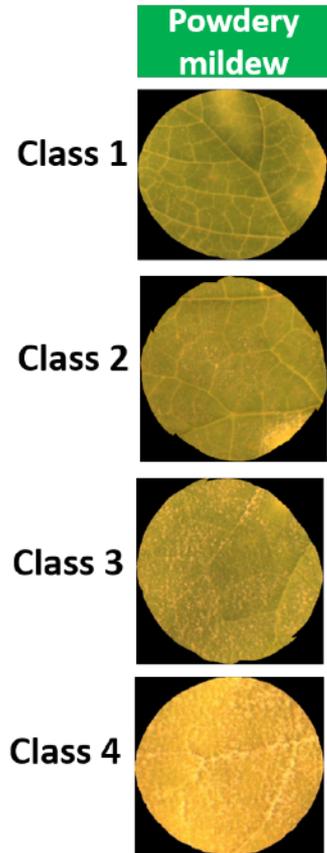
Feature 1 : texture  
Feature 2 : couleur

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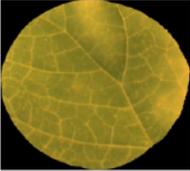
Feature 1 : texture  
Feature 2 : couleur  
Feature 3 : surface de spore

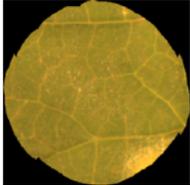
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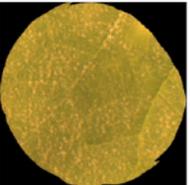
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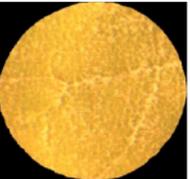
Proposition de caractéristiques pour classer ces images

**Powdery mildew**

Class 1 

Class 2 

Class 3 

Class 4 

Feature 1 : texture  
Feature 2 : couleur  
Feature 3 : surface de spore  
Feature 4 : intensité

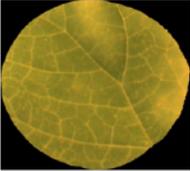
-----

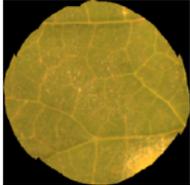
## Les maladies ...des données ordinales

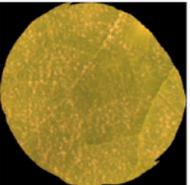
Exemple sur données ordinales

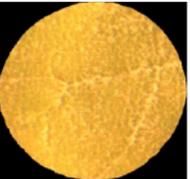
Proposition de caractéristiques pour classer ces images

**Powdery mildew**

Class 1 

Class 2 

Class 3 

Class 4 

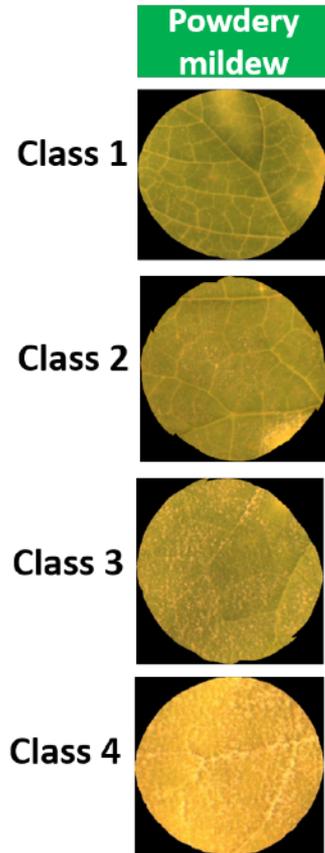
Feature 1 : texture  
Feature 2 : couleur  
Feature 3 : surface de spore  
Feature 4 : intensité  
Feature 5 : ...  
...

-----

## Les maladies ...des données ordinales

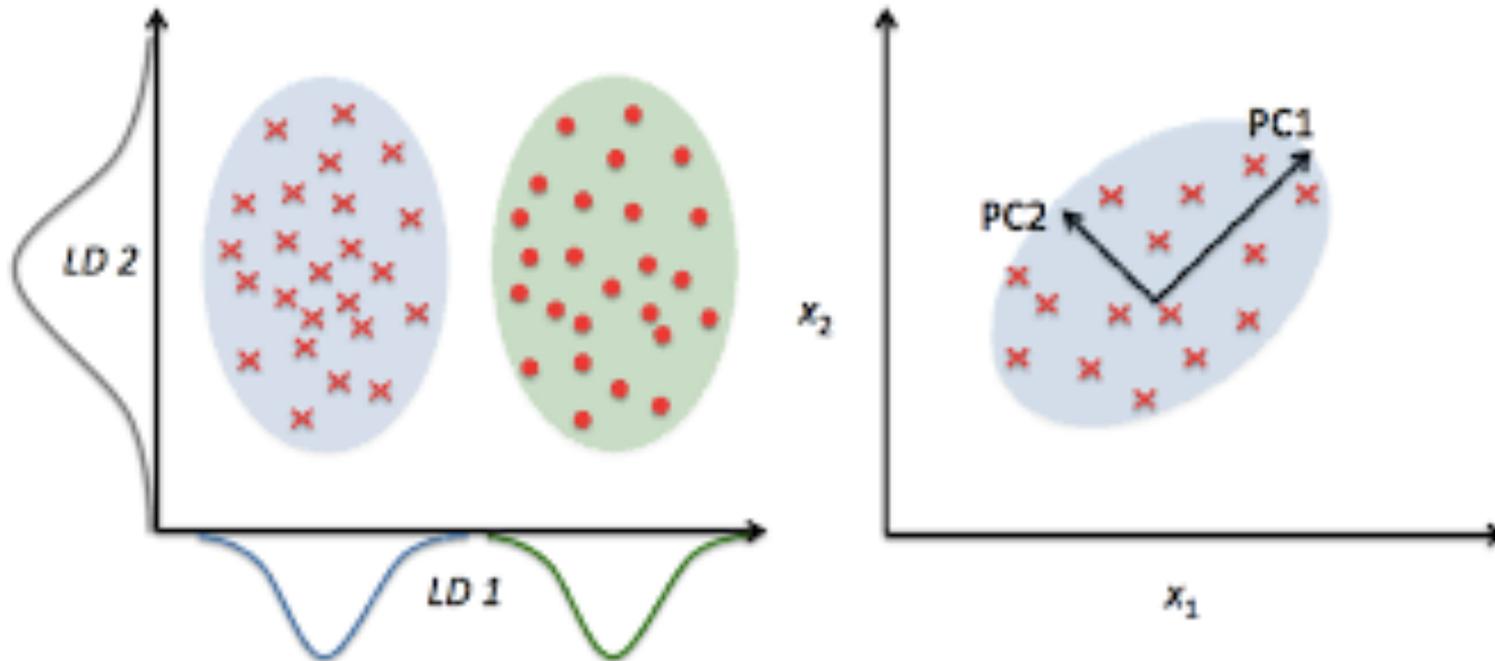
Exemple sur données ordinales

Proposition de caractéristiques pour classer ces images



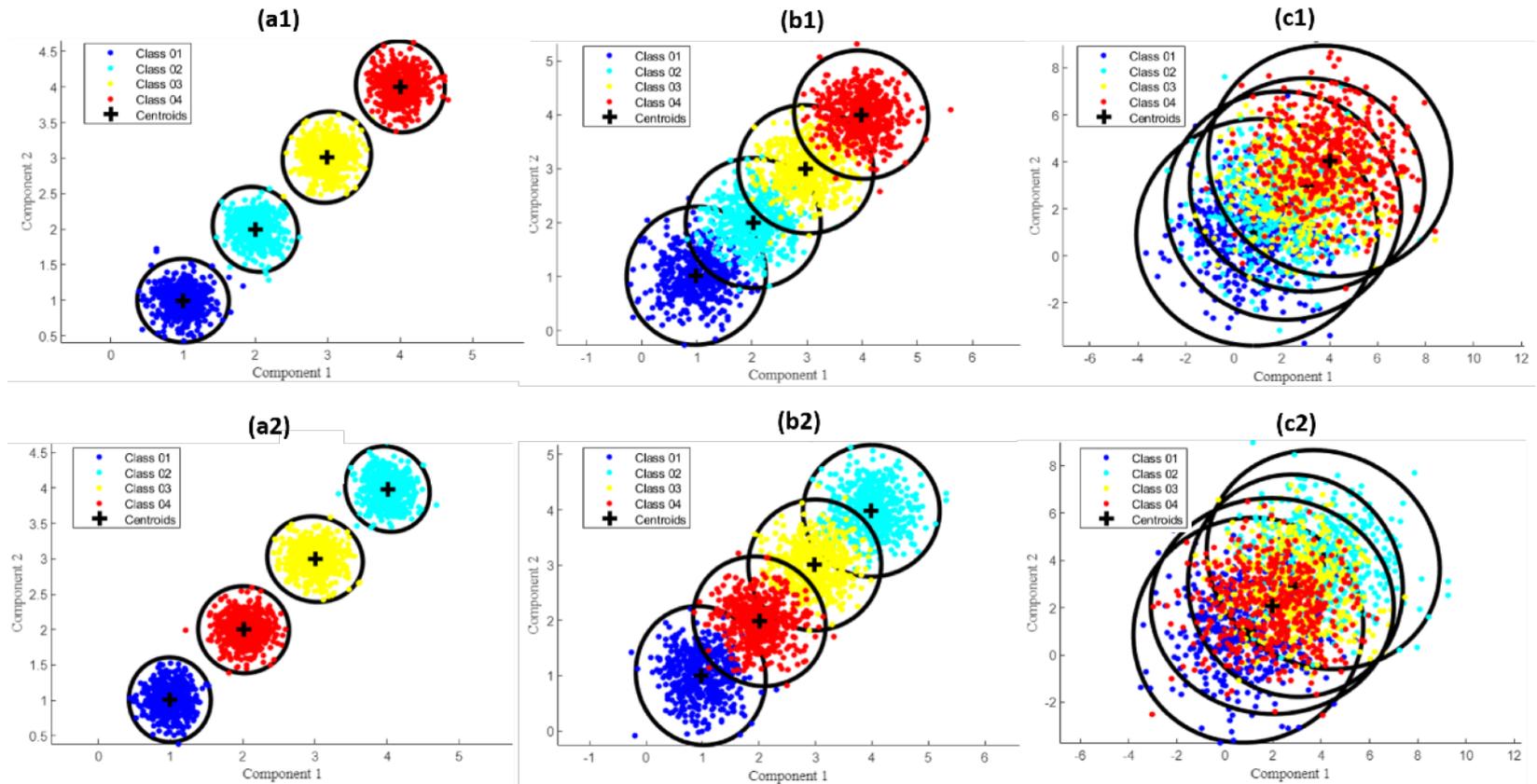
- Feature 1 : texture
- Feature 2 : couleur
- Feature 3 : surface de spore
- Feature 4 : intensité
- Feature 5 : ...
- ...

**Problème pour visualiser les données**

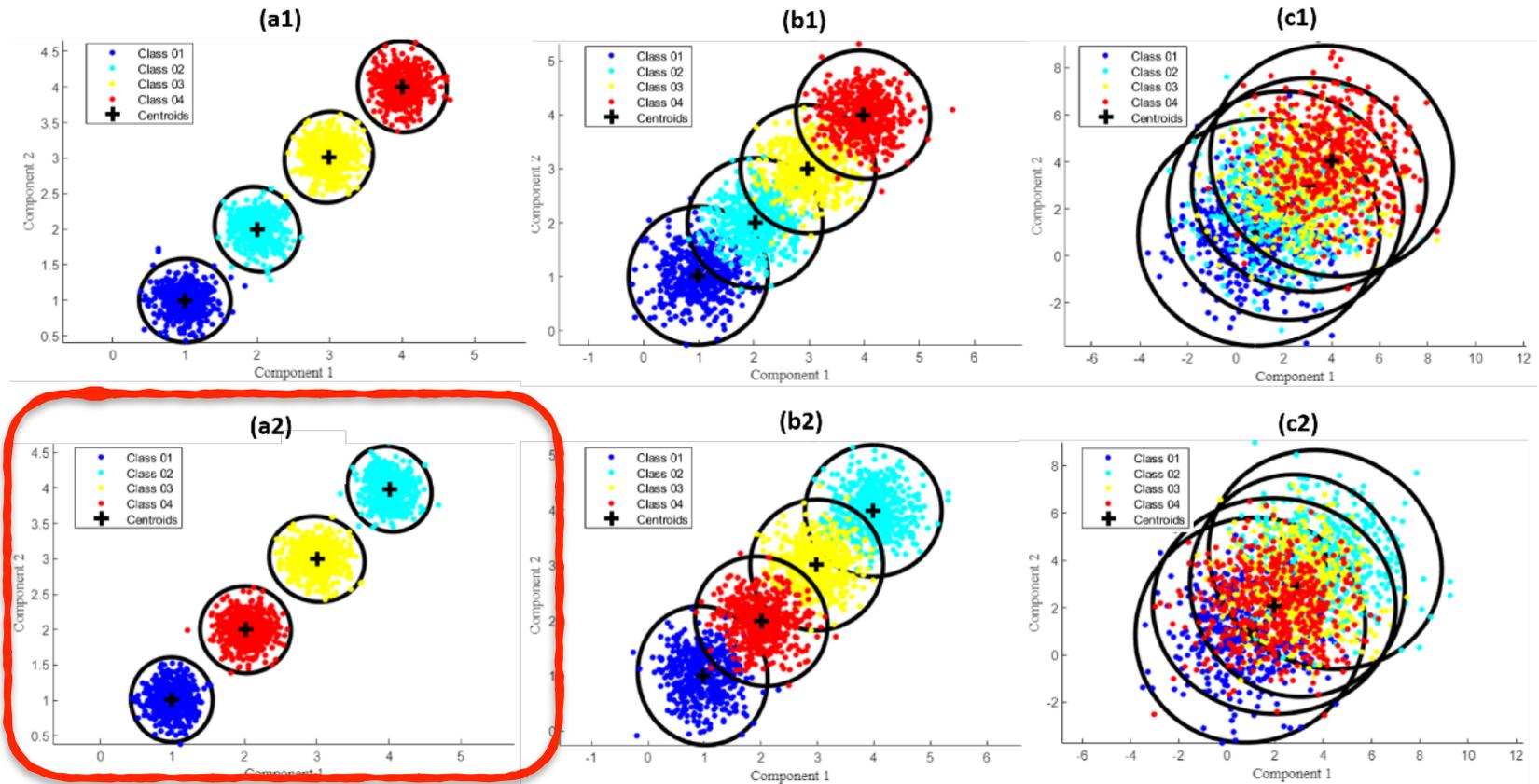


Pour compresser les données  
Pour identifier les variables clés  
Pour visualiser les données si  $> 3$

# ... après réduction de dimension



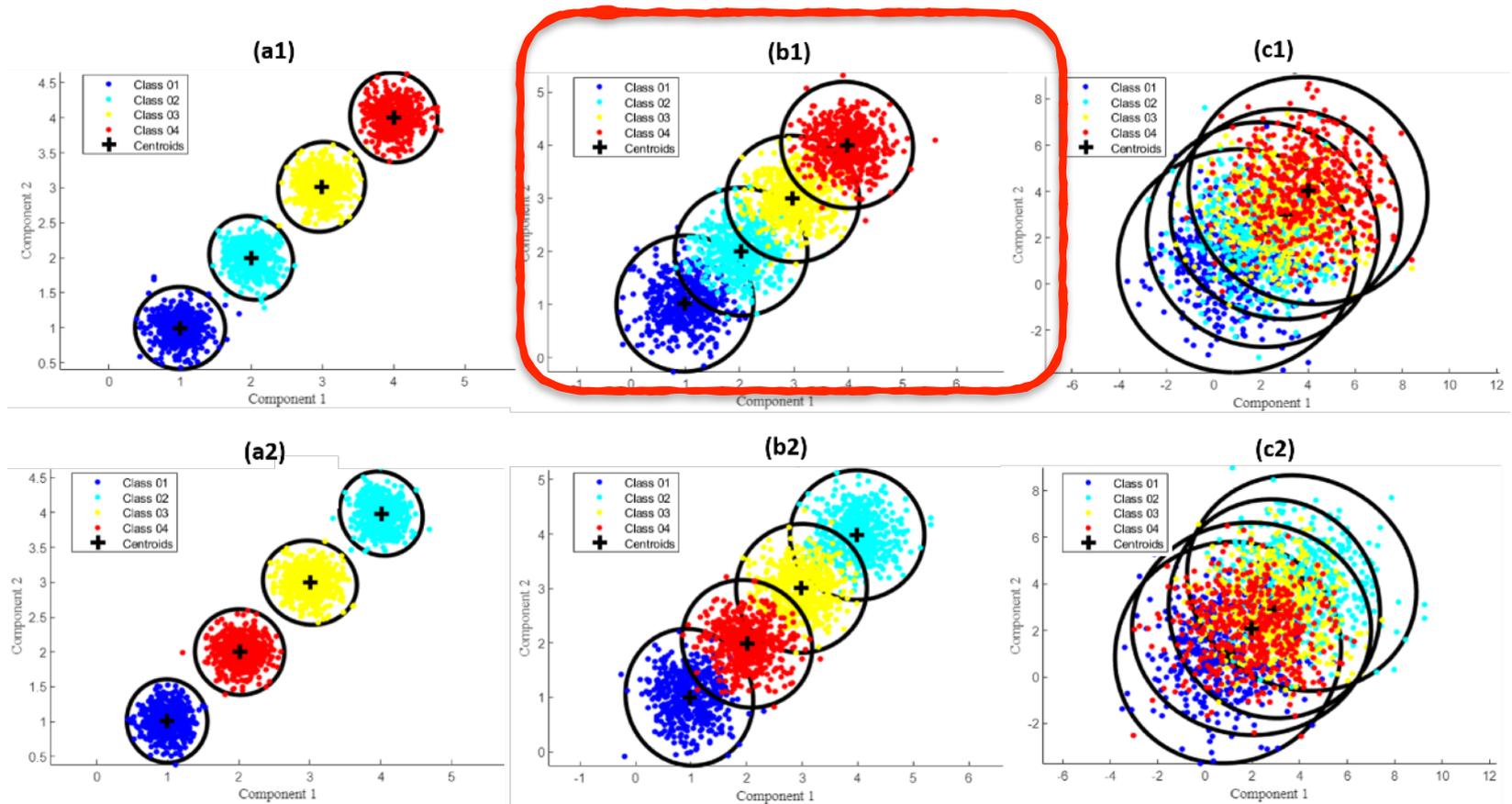
# ... après réduction de dimension



Bonne classification mais Mauvaise interprétabilité

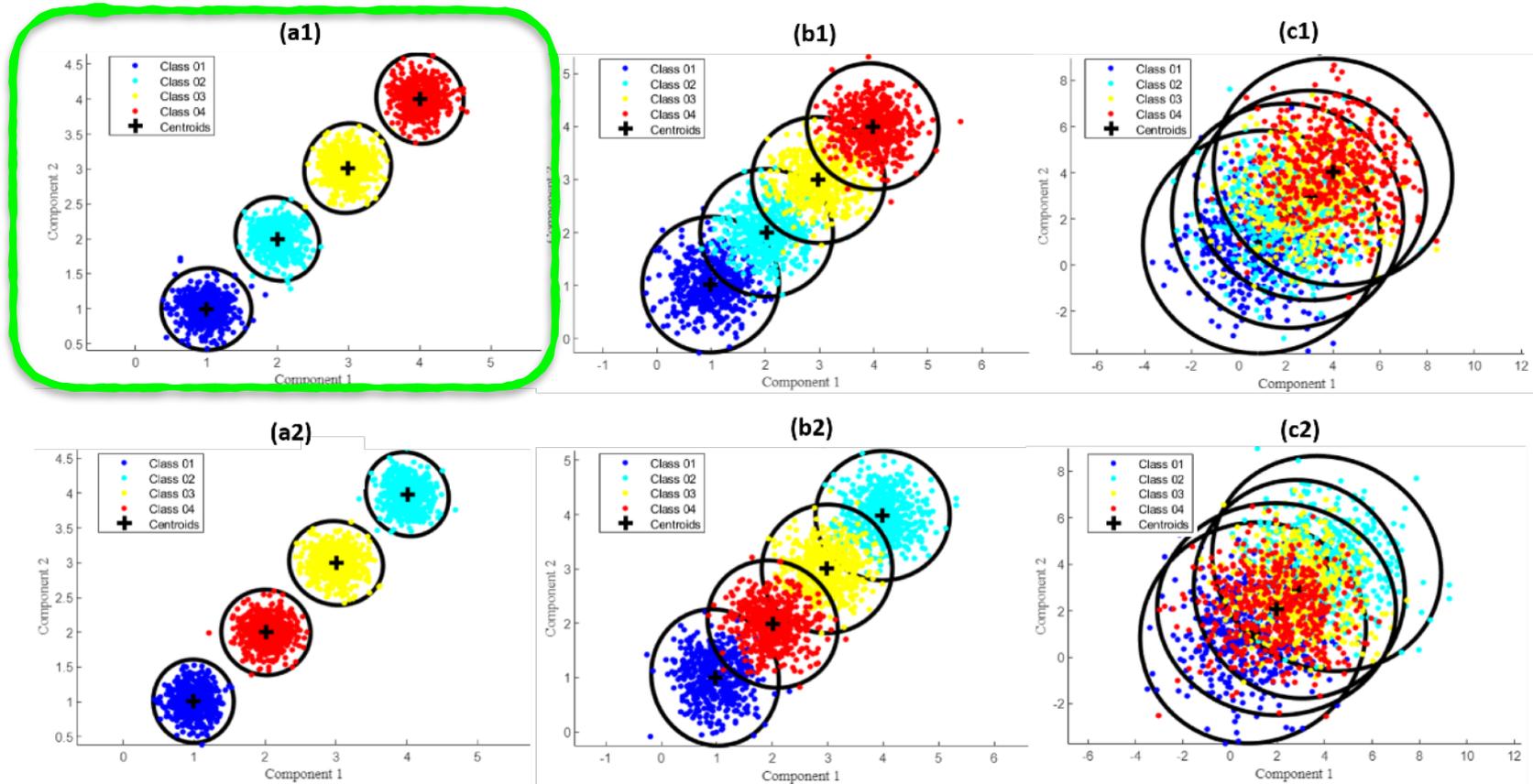
# ... après réduction de dimension

Bonne interprétabilité mais un peu de bruit



# ... après réduction de dimension

## Bons features





## Dimensionality Reduction for Ordinal Classification

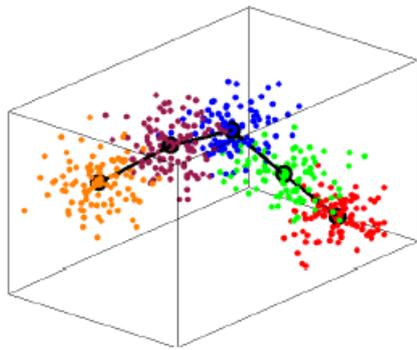
Mouad Zine-El-Abidine  
*LARIS*  
*Université d'Angers*  
Angers, France  
zine\_mouadaix@hotmail.fr

Helin Dutagaci  
*Electrical-Electronics Engineering*  
*Eskisehir Osmangazi University*  
Eskisehir, Turkey  
hdutagaci@ogu.edu.tr

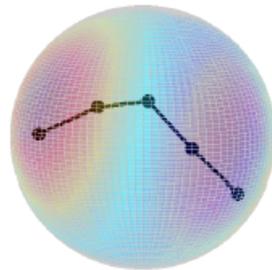
David Rousseau  
*LARIS*  
*Université d'Angers*  
Angers, France  
david.rousseau@univ-angers.fr

# Méthode proposée : Best View Projection (BVP)

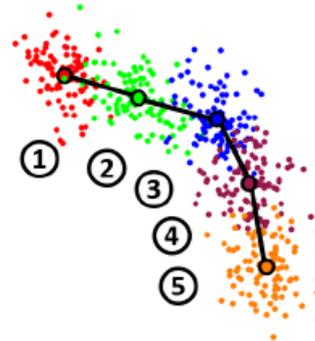
**Objective:** determine the optimal viewpoint via maximization of the squared distances between centers of adjacent classes in the projected space. The dimensionality is reduced by one from  $N$  to  $N-1$  by projecting the features to the lower dimensional space defined by the optimum viewpoint. The process is repeated until the desired dimensionality is achieved.



(a) 3D input data



(b) View sphere



(c) Projected data

---

**Algorithm 1:** Find the optimum viewpoint

---

**Data:** Class centers:  $c_k, k = 1, 2, \dots, K$

**Result:** Optimum viewpoint:  $v^*$

Initialize  $v_0$  randomly such that  $\|v_0\| = 1$ ;

MaxIter = 100;  $\epsilon = 10^{-5}$ ;  $\gamma_0 = 0.05$ ;

**while**  $j < \text{Maxiter}$  **do**

    Calculate  $\nabla F(v_j)$  using 5 and 6;

**if**  $j > 0$  **then**

        Calculate  $\gamma_j$  using 7;

**end**

$\hat{v}_j = v_j - \gamma_j \nabla F(v_j)$ ;

$v_{j+1} = \frac{\hat{v}_j}{\|\hat{v}_j\|}$ ;

**if**  $\cos^{-1}(v_{j+1}^T v_j) < \epsilon$  **then**

$v^* = v_{j+1}$ ;

**break**;

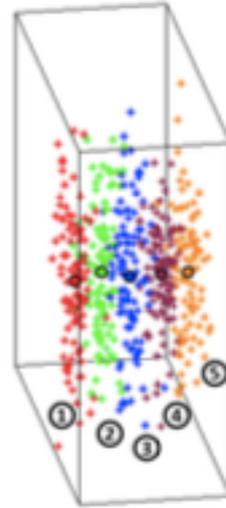
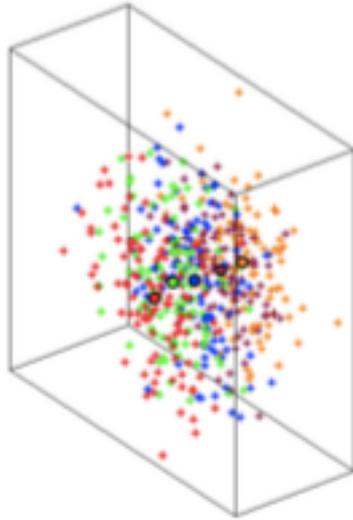
**end**

$j \leftarrow j + 1$

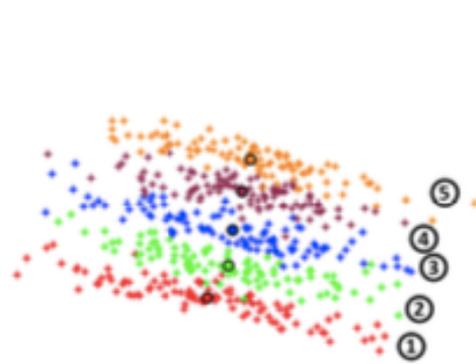
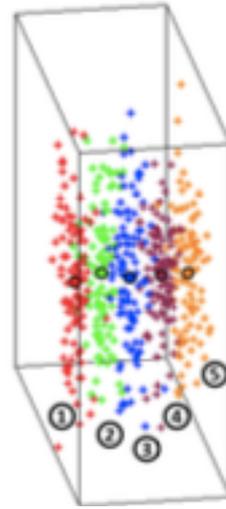
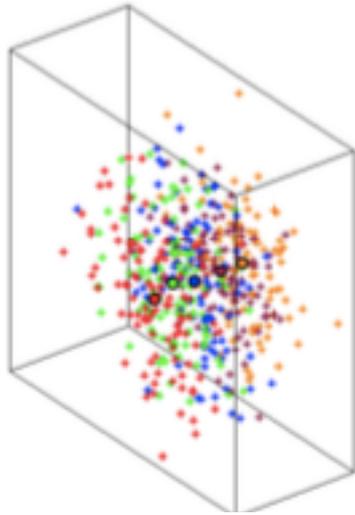
**end**

---

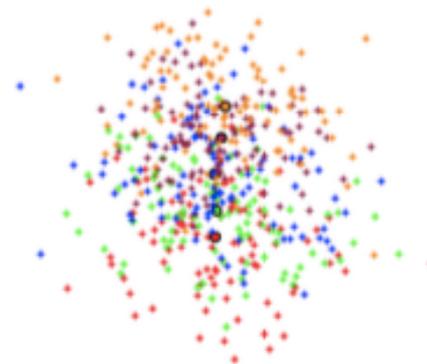
$$G(v) = \sum_{k=1}^{K-1} \|\bar{c}_{k+1}(v) - \bar{c}_k(v)\|^2$$



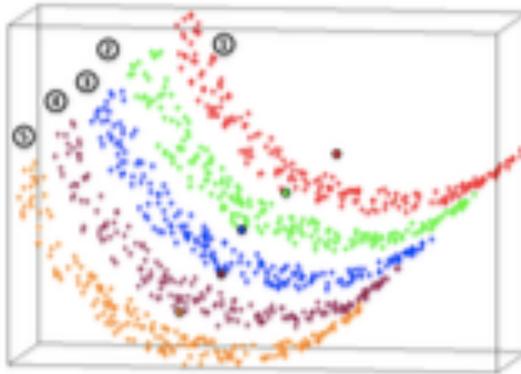
# Illustrations 3D => 2D



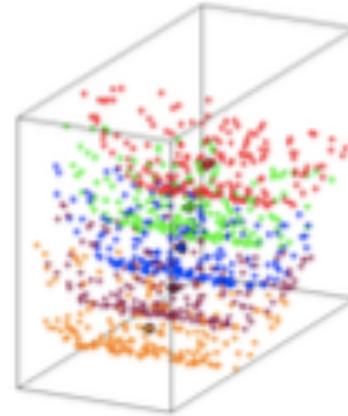
(c) BVP



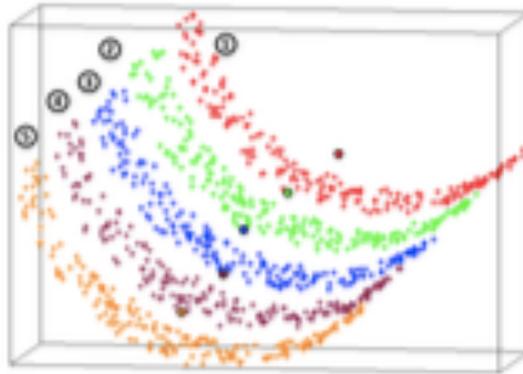
(d) PCA



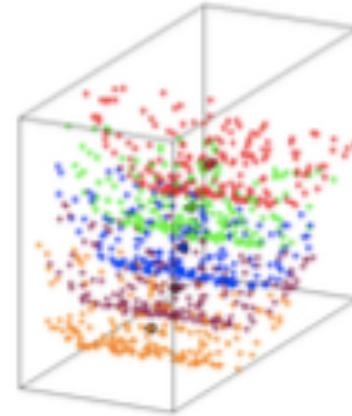
(a) 3D input data



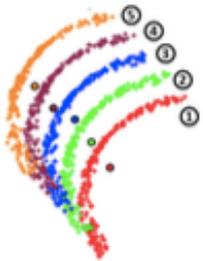
(b) 3D input data



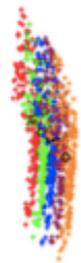
(a) 3D input data



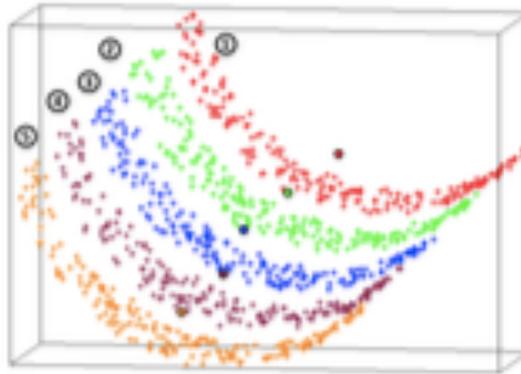
(b) 3D input data



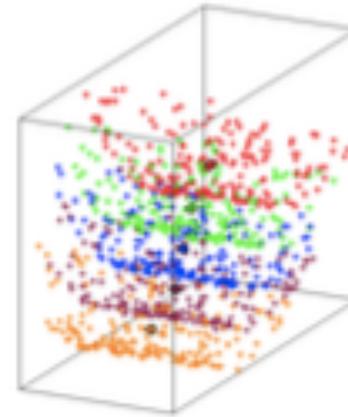
(c) BVP



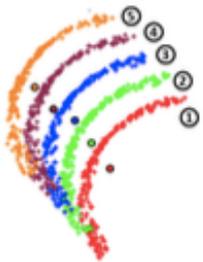
(d) PCA



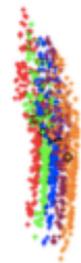
(a) 3D input data



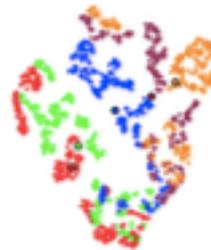
(b) 3D input data



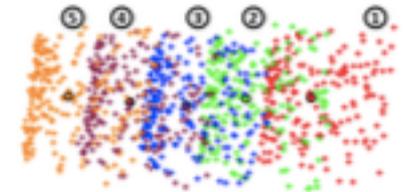
(c) BVP



(d) PCA



(f) t-SNE



(g) LDA

TABLE I: Real ordinal datasets used for the experiments [18], [19] ( $I$  is the total number of instances,  $Q$  is the dimensionality of the original data and  $K$  is the number of classes).

<b>Dataset</b>	$I$	$Q$	$K$	<b>Class Distribution</b>
contact-lenses	24	6	3	(15,5,4)
pasture	36	25	3	(12,12,12)
squash-stored	52	51	3	(23,21,8)
newthyroid	215	5	3	(30,150,35)
car	1728	21	4	(1210,384,69,65)
bondrate	57	37	5	(6,33,12,5,1)

J. Sanchez-Monedero, P. A. Gutierrez, and M. Pérez-Ortiz, “Orca: A matlab/octave toolbox for ordinal regression,” *Journal of Machine Learning Research*, vol. 20, no. 125, pp. 1–5, 2019. Available: <http://jmlr.org/papers/v20/18-349.html>

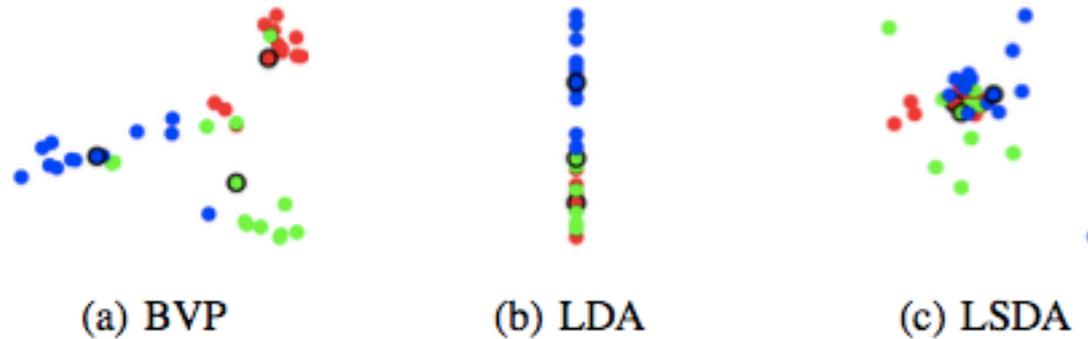


Fig. 5: 2D visualization of the dataset pasture

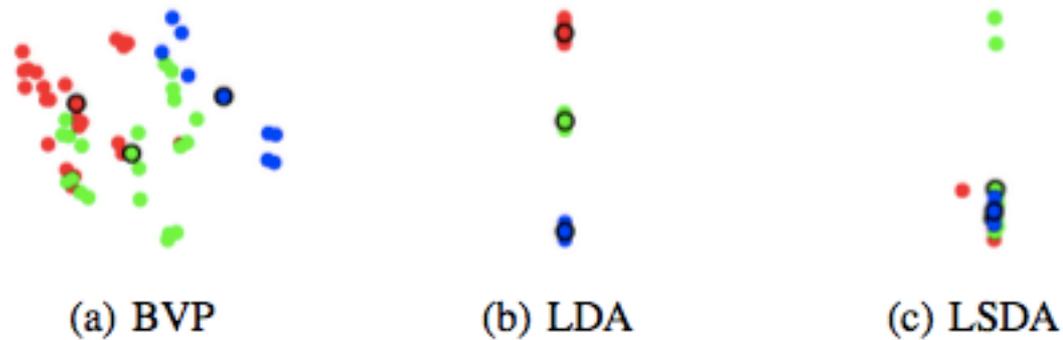
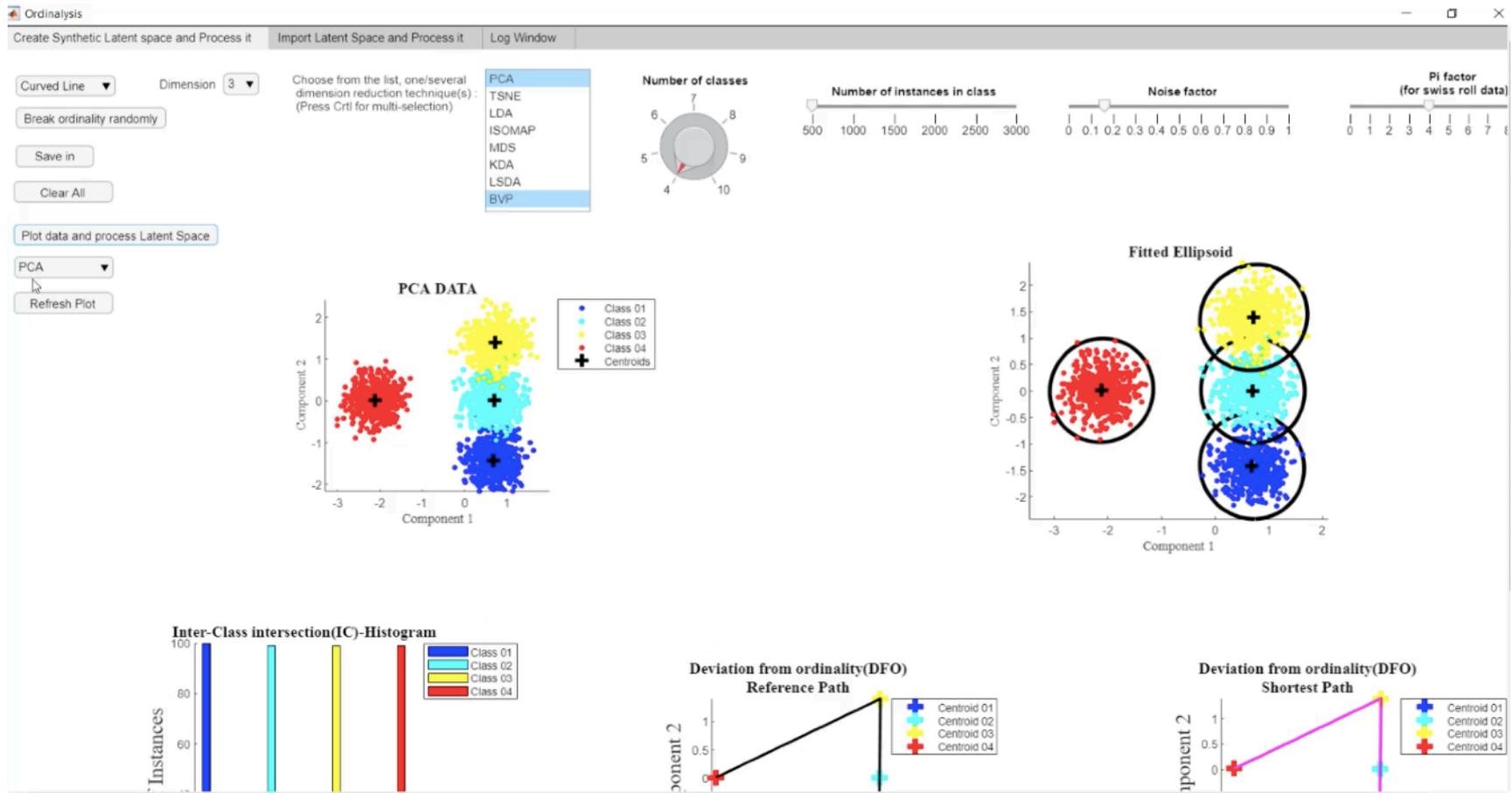


Fig. 6: 2D visualization of the dataset squash-stored

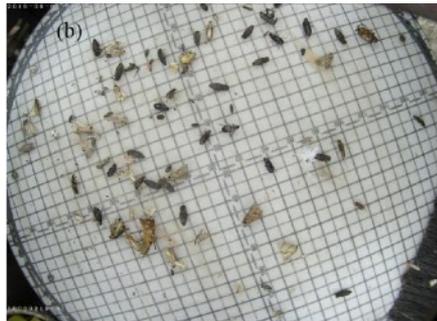


M. Zine El Abidine, H. Dutagaci & Rousseau, D. et al (2022). *SoftwareX*, en préparation

# Caractérisation d'insectes in situ (TI)

Nacir Boutra; Encadrants : Céline Robert, David Rousseau

18 à 20% de la production agricole annuelle dans le monde est détruite par les ravageurs, estimée à une valeur de plus de 470 milliards de dollars [1].



**Inspection visuelle et comptage manuel des ravageurs piégés dans les cuvette.**

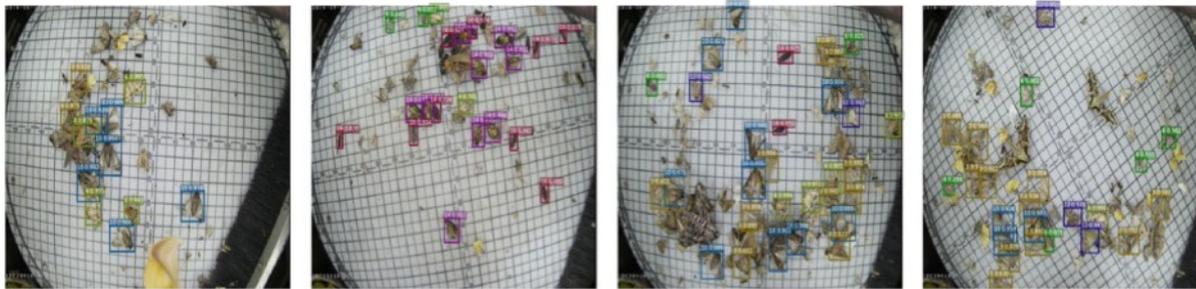
- Demande beaucoup de travail et de temps.
- précisions instables.

**L'automatisation du processus est très utile et La population d'insectes ravageurs sera surveillée plus efficacement par rapport à l'inspection visuelle.**

[1] "AgriPest: A Large-Scale Domain-Specific Benchmark Dataset for Practical Agricultural Pest Detection in the Wild" Sensors 2021, 21, 1601



(a) images from pest recognition datasets



(b) images from non-field environment datasets



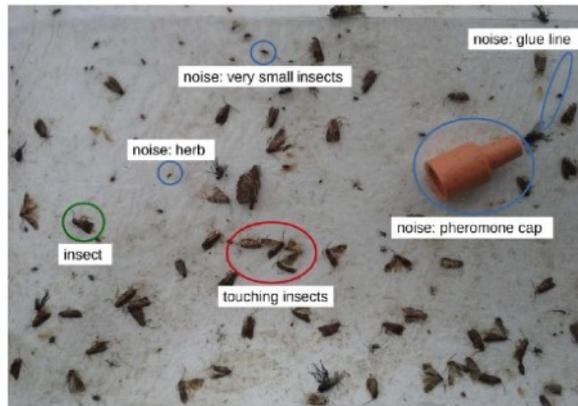
(c) images from AgriPest.

La classification des images des ravageurs

La détection multi-cibles des ravageurs

## Publications scientifiques sur la reconnaissance automatique des insectes

Studies	Learning	Image Processing	Overlapping	Small Objects	Classes	Mean Precision	DataSet	Image Source
Akintayo et al. (2018)	CNN	preproc.	-	-	2	96%	644	Nematode eggs <sup>a</sup>
Alemayehu et al. (2016)	SVM	segm. <sup>b</sup> + ftr. extr.	-	-	4	93.3%	900	insect on plant
Avila-George et al. (2018)	ANN	preproc., ftr. extr.	-	-	3	97.2%	40	Leaf disease
Bakkay et al. (2018)	Only IP	preproc.	segm. <sup>c</sup>	CLS	3	77%	100	Insect on field trap
Basati et al. (2018)	Decision Tree	preproc., segm.	-	-	2	90.2%	16 <sup>d</sup>	Wheat grains
Bisgin et al. (2018)	SVM	ftr. extr.	-	-	15	85%	6900	Insect
Chen et al. (2018)	CNN	preproc.	-	-	2	95.6%	68 <sup>e</sup>	Insect on leaf
Cheng et al. (2017)	CNN	-	-	-	10	98.6%	550	Insect on leaf
Cruz et al. (2017)	CNN	preproc.	-	-	3	98.6%	224 <sup>f</sup>	Leaf disease
Ding and Taylor (2016)	CNN	preproc.	-	-	2	93.1%	177 <sup>g</sup>	Insect on field trap
Espinoza et al. (2016)	ANN	IP <sup>h</sup>	-	-	2	96%	3185 <sup>i</sup>	Insect on sticky trap
Fuentes et al. (2017)	CNN	n/u	-	-	9	83%	5000 <sup>j</sup>	Leaf disease
Kalamatianos et al. (2018)	CNN	n/u	-	-	2	91.5%	542	Insect on field trap
Li et al. (2019a)	CNN	n/u	-	-	2	88.5%	1228 <sup>k</sup>	Insect on the plant
Li et al. (2019b)	MLE	segm.	LPSA <sup>l</sup>	n/a	6	74.7%	700 <sup>m</sup>	Corn grains
Liu et al. (2016)	CNN	preproc.	-	-	12	95.1%	5000	Insect on the plant
Liu et al. (2019)	CNN	n/u	-	-	16	75.4%	88670 <sup>n</sup>	Insect on field trap
Mousavi et al. (2016)	SVM	ftr. extr.	-	-	5	90%	100	Leaf disease
Nazri et al. (2018)	CNN	Binary filtering	-	-	2	95%	687 <sup>o</sup>	Insect on sticky trap
Partel et al. (2019)	CNN	preproc.	-	-	2	80%	800 + 8000 <sup>p</sup>	Insect on field trap
Picon et al. (2018)	CNN	preproc. + segm. <sup>q</sup>	n/a	Superpixel	3	87%	8178 <sup>r</sup>	Leaf disease
Priyadharshini et al. (2019)	CNN	preproc.	-	-	2	-	-	Plant disease
Ram and Rodríguez (2016)	Only IP	preproc.	FRST	-	2	88.1%	260	Cell nuclei <sup>s</sup>
Ramcharan et al. (2017)	CNN	n/u	-	-	6	93%	2756	Plant disease
Roldán-Serrato et al. (2018)	ANN <sup>u</sup>	ftr. extr.	-	-	2	88%	200	Insect on leaf
Shen et al. (2018)	CNN	preproc.	-	Inception	6	88%	739 <sup>v</sup>	Insect on lab trap
Siva Sangari et al. (2019)	Only IP	preproc.	ACO	-	2	n/a	-	Insect on leaf
Sun et al. (2018)	CNN	preproc.	-	optimization <sup>x</sup>	6	74.6%	2183 <sup>y</sup>	Insect on field trap
Tan et al. (2016)	CNN	preproc.	-	-	4	97.5%	250 <sup>z</sup>	Fruit disease
Wen et al. (2015)	SDAE	ftr. extr.	pose estimate <sup>aa</sup>	-	9	96.9%	728	Insect on sticky trap
Xia et al. (2018)	CNN	preproc.	-	-	24	89.2%	660	Insect on leaf <sup>ab</sup>
Yue et al. (2018)	CNN	preproc.	-	Super resolution	3	n/a	249	Insect
Zhong et al. (2018)	CNN + SVM	ftr. extr.	-	-	6	90.1%	3000/700 <sup>ac</sup>	Insect on field trap



**Table 2** Precision, under- and over-insect segmentation rates – comparison with six existing approaches

Method	Precision rate	Rate of under-segmented insects	Rate of over-segmented insects
Otsu [11]	0.23	0.69	0.08
Otsu [11] + watershed [31]	0.47	0.15	0.38
superpixel [21]	0.23	0.69	0.08
meanshift [5]	0.54	0.15	0.31
K-means [27]	0.31	0.61	0.08
graph cuts [32]	0.38	0.54	0.08
proposed method	<b>0.77</b>	<b>0.15</b>	<b>0.08</b>

[4] Bakkey « Automatic detection of individual and touching moths from trap images by combining contourbased and region-based segmentation.» IET Comput. Vision 12 (2), 138–145.

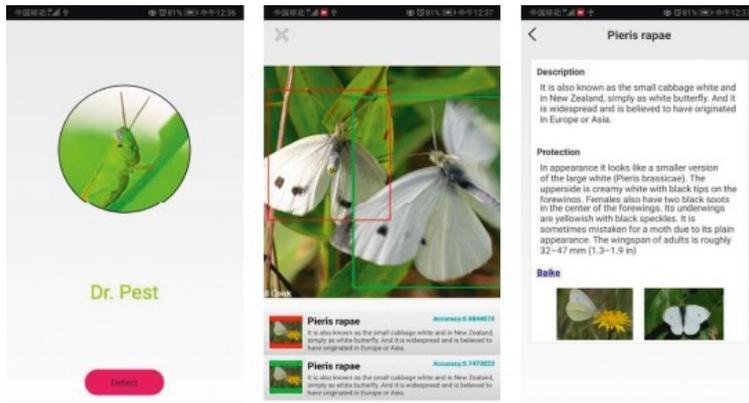


TABLE 1: Details of oilseed rape pest dataset.

Species	Number of images	Number of objects
<i>Athalia rosae japonensis</i>	352	375
<i>Cretonotus transiens</i>	175	182
<i>Entomoscelis adonidis</i>	87	134
<i>Entomoscelis suturalis</i>	30	36
<i>Helicula undalis</i>	320	322
<i>Lipaphis erysimi</i>	150	1474
<i>Mamestra brassicae</i>	334	343
<i>Meligethes aeneus</i>	164	566
<i>Phyllotreta striolata</i>	220	272
<i>Pieris rapae</i>	610	690
<i>Plutella xylostella</i>	475	484
<i>Psylliodes punctifrons</i>	105	138
Total	3022	5016

[5] Yong He , “Application of Deep Learning in Integrated Pest Management: A Real-Time System for Detection and Diagnosis of Oilseed Rape Pests”, Hindawi Mobile Information Systems Volume 2019



**IDENTIFICATIONS DISPONIBLES :**

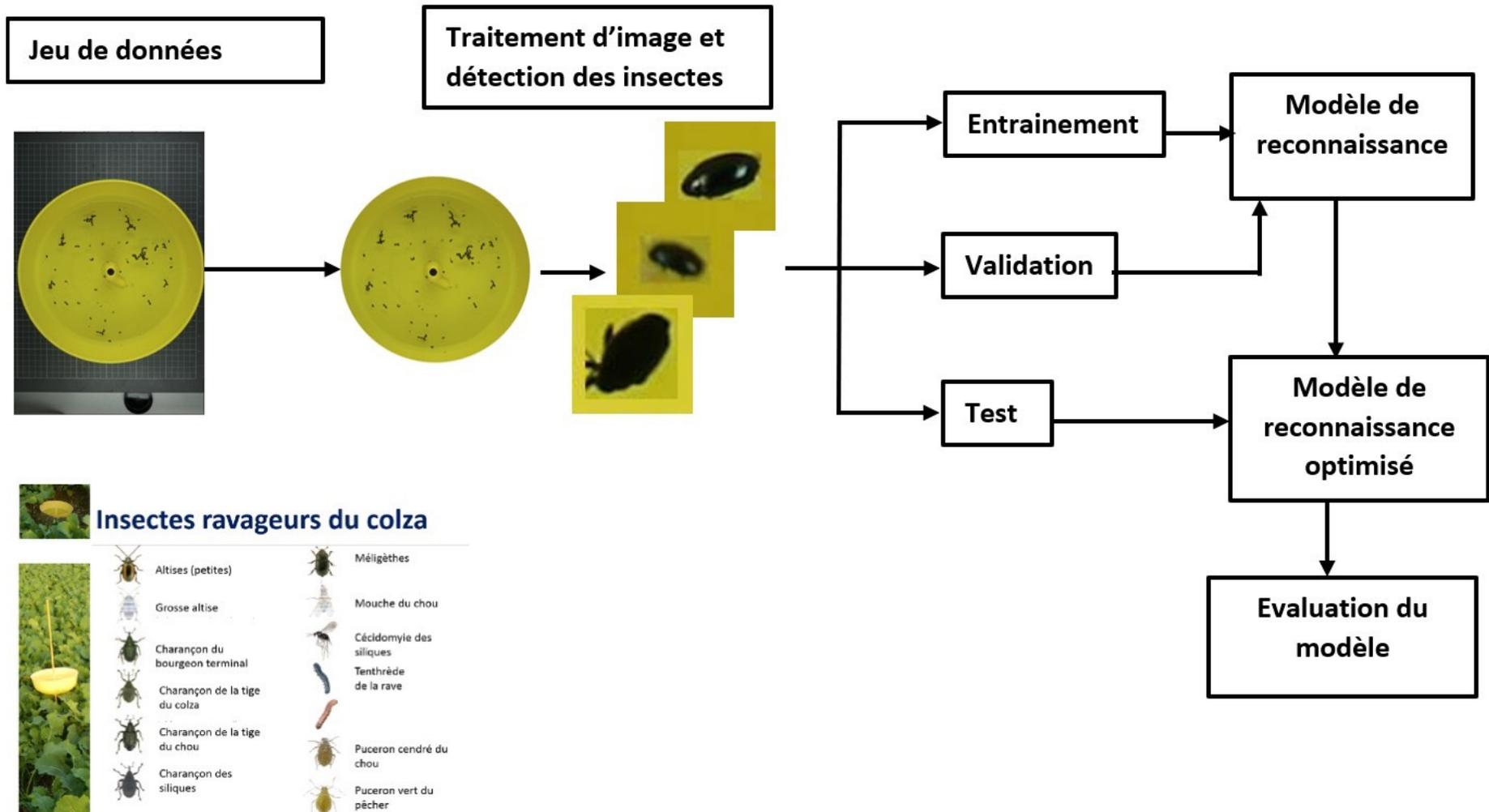
- Pucerons
- Cicadelle
- Carpocapse
- Meligèthe
- Charançon
- Tordeuse(s)
- Thrips

**Contrôle des insectes ravageurs**

Au lieu de contrôler manuellement les cultures jaunes dans une parcelle de colza, SCOFI INC contrôle et classe automatiquement les insectes pour vous.

**Comment ça marche ?**

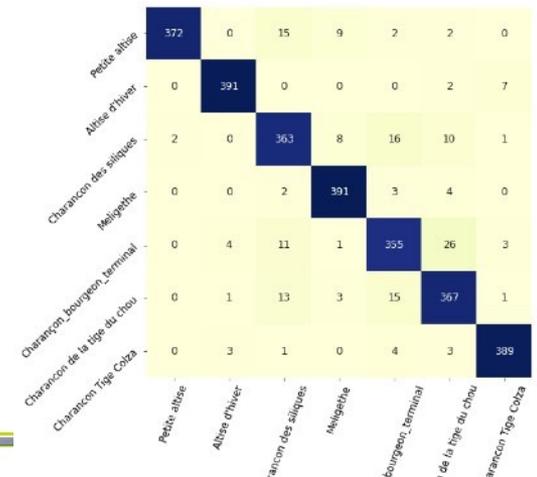
Les insectes posent sur le colza sont complétement identifiés par espèces. L'algorithme différencie les insectes suivants : méligèthe, charançon de la tige du colza, charançon de la tige du colza, charançon des épis, cicadelle.



Espèces	Nombre d'images	Nombre d'images utilisées	Jeu d'entraînement (%)	Jeu de validation (%)	Jeu de test (%)
Charançon bourgeon terminal	26	400*5 = 2000	72%	8%	20%
Charançon siliques	18	400*5 = 2000	72%	8%	20%
Charançon Tige Chou	29	400*5 = 2000	72%	8%	20%
Grosses altises	24	400*5 = 2000	72%	8%	20%
Meligèthes	19	400*5 = 2000	72%	8%	20%
Petites Altises	33	400*5 = 2000	72%	8%	20%
Charançon tige de colza	71	400*5 = 2000	72%	8%	20%

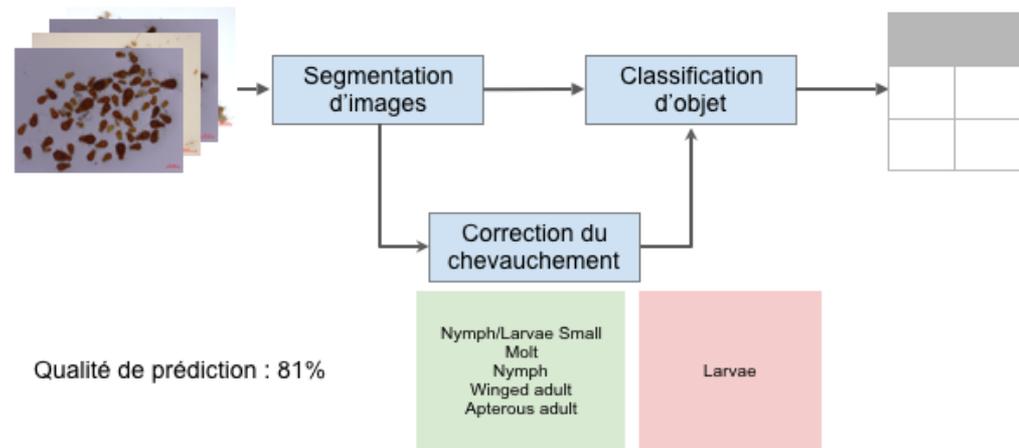
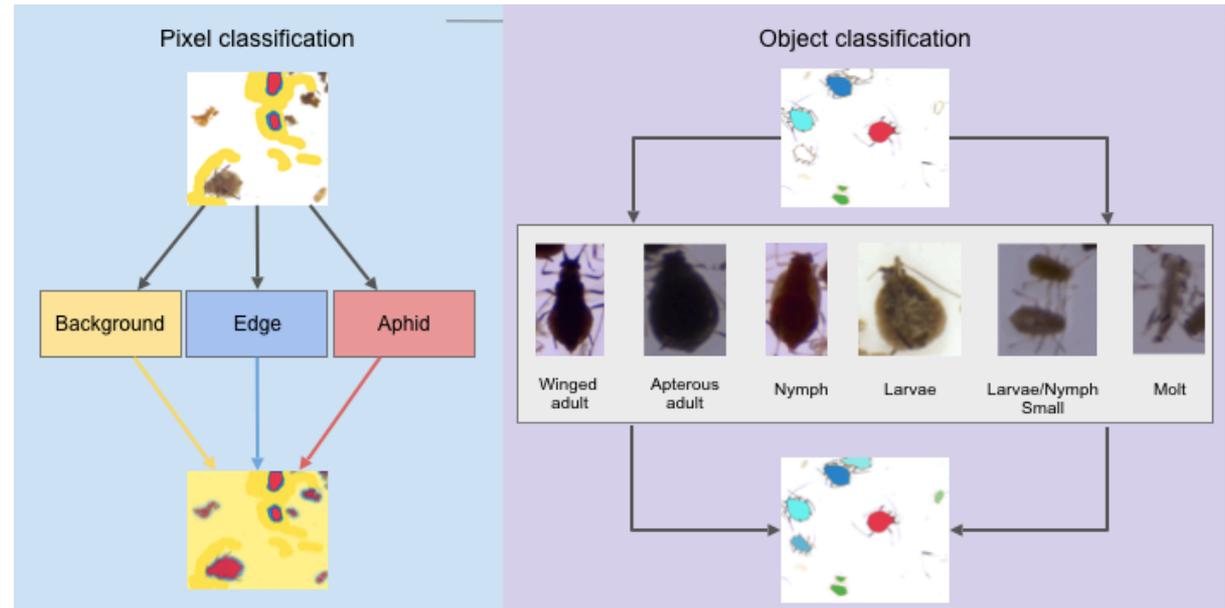
$$Justesse = \frac{\text{Nombre de prédictions correctes}}{\text{Nombre de total prédictions}} = 93.86\%$$

Méthode	Espèces						
	PA CTC H	AH CTC	CS	ME	CBT		
Resnet50	93%	97.75%	90.75%	97.75%	88.75%	91.75%	97.25%



# Extension vers les pucerons

## Aphids



## • Objectives

- Characterize, detect, recognize, quantify, track, monitor biotic interactions (pathogenic and mutualistic) at all scales/ stages of plants from seed to adult including shoot and root.
- Based on state of the art imaging : RGB, LIDAR, Multispectral, NIR-SWIR, Fluorescence.
- Working under controlled or field conditions

## • Methods & Methodology

- Generic methodological image processing tools (preprocessing, deep learning, ML-based data mining on processed images)
- Applied first on a representative set of biological use-cases already funded on phenotypic hubs (pragmatism+link with ontology in MCP2)
- Create a community of knowledge via training

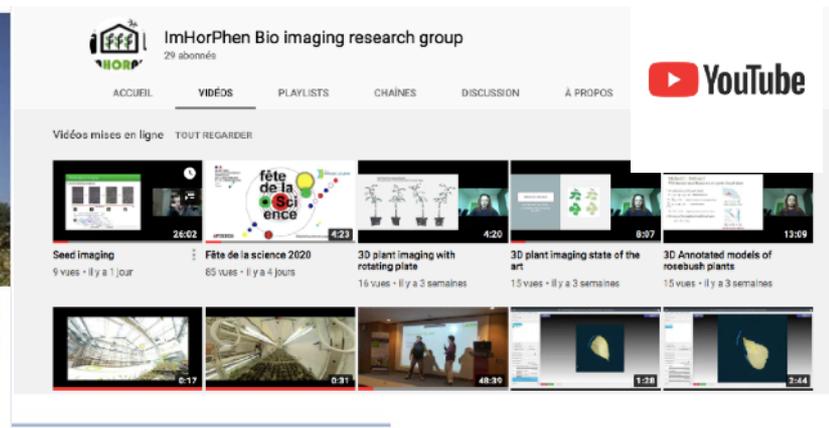
## • Objectives

- Characterize, detect, recognize, quantify, track, monitor biotic interactions (pathogenic and mutualistic) at all scales/ stages of plants from seed to adult including shoot and root.
- Based on state of the art imaging : RGB, LIDAR, Multispectral, NIR-SWIR, Fluorescence.
- Working under controlled or field conditions

## • Methods & Methodology

- Generic methodological image processing tools (preprocessing, deep learning, ML-based data mining on processed images)
- Applied first on a representative set of biological use-cases already funded on phenotypic hubs (pragmatism+link with ontology in MCP2)
- **Create a community of knowledge via training**

- Cours, TP sur chaîne youtube
- GT deep learning (tous les 2 mois)
- 1 training (tous les 6 mois)
  
- Utilisateurs autonomes (Montpellier, Toulouse, Dijon, ...)
- Collaboration à travers le réseau (Thèse Toulouse, Angers, Colmar)



# Merci pour votre attention

5 avril, Paris

David Rousseau



ANR11-INBS-0012

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