D5.3 Demonstration of indoor (and outdoor), 3D reconstruction of plants

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ROMI
ROBOTICS FOR MICROFARMS

Deliverable			D5.3
Deliverable title: Demonstration of indoor (and outdoor), 3D reconstruction of plants Accompanying report			
Task	**T5.1 Sensors selection and data acquisition rate.** **T5.2 Data management infrastructure.** **T5.3 3D+t plant segmentation**		
Task Leader	**CNRS**	Planned Date	**30.9.2020**
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Executive Summary

Deliverable D5.3 is a demonstrator of 3D reconstruction of plants with the romi plant scanner. The demonstrator is provided as a video at the following addresses:

ROMI website:

https://media.romi-project.eu/documents/ROMI-D5.3-Scanner.mp4

This document accompanies the demonstrator.

1.1 Overview and description of the video's content

The video presents how plant images for phenotyping can be acquired with the **ROMI plant scanner** in a research context.

In order to automatise and speed up the measurements of a specific plant trait (here phyllotaxis) in a model plant (here *Arabidopsis thaliana*), plant scientists use a **phenotyping robot** (**the ROMI Plant Scanner**) that takes pictures all around a still and living plant, with a set-up allowing to collect many details of the plant architecture in 3D along the vertical axis. The video focuses on the mechanics of the robot, showing in action motors that drive xy horizontal movement of the arm (the gantry), the z vertical position of the camera ad the constant reorientation of the camera focus towards the plant as the arm rotates around the plant, with a panoramic movement conferred by a gimbal at the tip of the arm.

The video highlights the compatibility of the hardware system with the other ROMI robots (Rover and Cablebot, see video at time 2min). Also, it presents the current manual set-up for phyllotaxis measurement (at time 55s and 1min53), which is still used to generate ground truth measurements during the evaluation of our robot's performances.

1.2 Partners involved

Leader: **CNRS**
Participants: CNRS, Sony CSL, INRIA, IAAC (video)

1.3 Relation with other work packages and tasks

Relation to WP5 tasks. These first 3D reconstructions required the partial completion of tasks **T5.1**, **T5.2** and **T5.3**, that can be summarized into building the prototype of a plant phenotyping station, creating a database to store, access and visualize all data generated (acquisition and analysis), and developing and testing image analysis pipelines, respectively.

Relation to other ROMI work packages:

The core hardware and OS components of the phenotyping station (CNC arm, gimbal, camera) are shared with the **rover prototype** (**WP2**), implying constant interactions for use and development (mainly with Sony CSL partner).

Our approach makes a strong case for the use of virtual plants, developed in **WP6**: they can either be used as ground truth to evaluate the accuracy of analysis pipelines, or as inexpensive and efficient training dataset, containing a huge amount of plants coming automatically with a relevant labeling.

We closely teamed up with partners **Sony CSL** and **INRIA** to develop and integrate these developments to a functional and user scenario for research plant phenotyping which is presented in the video. This close team interaction and WP synergy around 3D reconstruction of single plant

architecture is also reflected by the very active common code repository and the rapidly growing documentation.

1.4 WebLinks to videos, flyers …

-Examples of 3D-reconstructions can be downloaded at:
https://drive.google.com/drive/folders/1u7FCq0ZtE7G8fgafruMfF16KsD4ZuMp0

1.5 Dissemination / IPR policy (since the beginning of the project)

Articles in peer-reviewed journals:

Chaudhury A., and C. Godin, 2020 Skeletonization of Plant Point Cloud Data Using Stochastic Optimization Framework. Front Plant Sci 11: 773. https://doi.org/10.3389/fpls.2020.00773

Workshops, conferences :

-2018/09/06: Presentation by Timothée Wintz (Sony CSL) of a first image-analysis algorithm at the 'Computer Vision Problems in Plant Phenotyping' (CVPPP) 2018, (September 6, 2018, Newcastle, UK). A version of the submitted work available here.

-2019/09/04-05: Poster presentation at the **Plants, People, Planet Symposium** (Royal Botanic Gardens, Kew, London), by D. Colliaux and A. Lahlou (Sony CSL).

-October 2020: Katia FSPM

Press Release:

-2018/02/07: article in the daily generalist French newspaper "Le Monde". title: "*Comment les plantes excellent en maths*".

Television coverage:

-2020/05: brief featuring in the arte/web video entitled "*Le business des objets connectés | Internet de tout et n'importe quoi | Partie 1*" (written & realised by Brett GAYLOR, produced by Eyesteelfilm & Cbc Television Network, 2019, link). The ROMI coordinator Jonathan Minchin (IAAC) is interviewed in the green Fablab of Valldaura (42-43min); among other things, the video briefly shows the Web Visualiser displaying the reconstruction of an *Arabidopsis* plant.

Outreach:

2019/10/10-12: three days of demonstration at the french festival "La fête de la Science", organized at the ENS Lyon (link). Visits of schools (~20 groups of 10-15 pupils) and general public (~100 persons).

2 Main body

2.1 Context: relations between the current state of plant phenotyping, the objective of this deliverable and the proposed user scenario

Measuring plant architecture is an evident necessity in agriculture and in the all spectrum from applied to basic research in plant science. Despite a wide diversity of plants and culture conditions, **most needs for plant architecture phenotyping would benefit from an automated, precise 3D reconstruction of plant aerial parts** from which different traits could be analysed with downstream software. State-of-the-art techniques of 3D-reconstruction still lack robustness to variations in the conditions of acquisition and are not generic to any type of plants. Moreover current technologies are expensive, resulting in huge, highly specialized and high-throughput phenotyping platforms that only

large companies or institutions can make profitable. **These constraints exclude most small-scale working groups, like micro-farms or single research teams**.

Our goal is to provide both hardware and software solutions tailored for such users. To account for both outdoor and indoor use, we designed an **affordable and minimalist set-up for plant phenotyping** based on a moveable arm holding a sensor, which can be adapted to an indoor static station (laboratory conditions) or to a mobile rover (micro-farm). Beyond price constraints, we also aim at **improving the robustness and genericity of plant 3D reconstruction** by exploring and developing different solutions at the research front of the field. The whole project is **open-source** to ease its dissemination and foster its total or partial reuse and future development.

What does indoor and outdoor mean ?

"Indoor" and "outdoor" conditions can be defined as archetypal "simple" and "complex" situations, respectively. In the **progress report**, we precisely review how such complexity is addressed in the current literature. In brief, critical elements challenge proper plant 3D reconstruction: light intensity, color and texture contrast, background scenography, plant movements (wind, robot-induced), complexity of plant architecture (occluding elements, mixture of plants of different developmental stages or species…). In **outdoor conditions**, all these elements can reach **out-of-range values** and are expected to vary in a largely **unpredictable manner**. By contrast, an indoor acquisition represents a controlled situation where experimenters stably maintain these elements in an appropriate range of values easing the plant acquisition and subsequent 3D reconstruction. Separating the different sources of perturbations is essential to address the specific issues raised by each of them and to assess the improvements brought by our work.

Hence, we start from a **controlled (indoor) environment** with stable and optimal conditions for most of the critical elements identified. This **reference set-up** typically corresponds to plant laboratory conditions. In the future, staying indoor-controlled, we will specifically degrade different elements to **mimic some aspect that could be found outdoors**, ensuring a proper identification of the sources that perturb or not our phenotypic solutions. By the end of the project, we might be able to test our phenotypic pipelines in real uncontrolled outdoor conditions with the rover in the fields of partner **Châtelain**, thanks to the compatibility between the phenotypic station and the rover. However, the hybridization of these tools is not a major objective of the project (see Progress Report).

The user scenario : the proof-of-concept of *Arabidopsis* phyllotaxis

Since the starting point of our research corresponds to laboratory conditions, we choose an objective of plant phenotyping corresponding to a **current laboratory research front in plant science**.

Phyllotaxis is an active research topic that gathers interdisciplinary works to understand how plant shoot stem cells generate geometric patterns of leaves, flowers, fruits, branches,... (called hereafter "lateral organs"). **CNRS** and **INRIA** partners have made significant contributions in the past few years. Phyllotaxis can be characterized by the sequence of divergence angles and internode lengths (distance) between two consecutive lateral organs along a stem. In the last decade, the need for quantitative understanding of the phenomenon has led scientists to perform tedious, labor-intensive and time-consuming manual measurements. In the very widely used model plant *Arabidopsis thaliana*, the finesse of the structures (0.2-1mm for stem diameter and ~0.1 mm for flower or petiole diameter) requires a high precision level for the phenotyping. Moreover, divergence angle is a typical trait requiring 3D data. To our knowledge, no automatic phenotyping solution has been published so far. Most research groups working on this topic are small teams with limited budget and space for their plant culture facilities.

All these reasons make the automatic phenotyping of *Arabidopsis* phyllotaxis **a strategic objective.** It corresponds to the exact need for an **affordable solution** of single plant 3D reconstruction with **high precision**. This active research community could help advert for **this proof-of-concept, disseminate**

to a wider audience and foster re-use and improvements (cf. open-source and modularity of the project).

Although it is not to date a useful agronomic indicator, more knowledge on phyllotaxis could **reveal helpful predictors of plant development**. Indeed, **CNRS** partner published recently that phyllotaxis variability was correlated with differences in meristem size and productivity between two genetic backgrounds (meristems are stem-cell-containing tissues at the origin of new organ production). More research is needed to link such precise plant traits with relevant environmental factors in crop species or control plants used as witness indicators. In a closer future, the progresses in terms of **segmentation precision** could be very useful to improve agronomic tasks like **fruit harvesting**.

2.2 Descriptions and Documentations related to video content

Here, we provide additional data indicating how the images taken by the ROMI plant Scanner can be processed and analysed to provide a 3D reconstruction of the plant architecture and to measure phenotypic traits of plant shape and architecture.

In particular, it sheds light on indispensable hidden aspect of the phenotyping workflow, which are yet the more time consuming in terms of development:

- acquisition and analysis pipelines management
- data management system
- 3D reconstruction pipelines and their implementation with the pipeline management system
- result visualisation

As explained in the **progress report**, all these components are developed as **interconnected and independent modules**, to maximise the robustness and evolvability of our phenotyping workflow.

Most of the following descriptions and additional **documentations** (for build and use) can be found online (regularly updated): https://docs.romi-project.eu/Scanner/.

Integral **source code** for this part can be found at https://github.com/romi. Relevant repositories are:

repository name	content
romiscan	this repository gathers most elements used to: -run a real acquisition of images around a real plant with the robot (Task=Scan) -run a virtual acquisition of images around a virtual plants (Task=VirtualScan) -perform different analysis pipeline (different tasks) -store, organize and access generated data in a proper way (romidata submodule) -process data for visualisation with the 3d-plantviewer (Task=Visualisation) All tasks are called by using a simple common command line syntax: `romi run task Task --config config_file.toml other arguments...` (where 'Task' is the task name ; config_file.toml a configuration file) Building of complex task workflows is handled by Luigi[1].
3d-plantviewer	the Node JS web viewer for plant scan, reconstruction and quantification
romicgal	some CGAL bindings used for skeletonization & meshing
bldc_featherwing	the controller for BLDC motor on a feather wing

[1] https://luigi.readthedocs.io/en/stable/index.html#

2.2.1 ACQUISITION

The phenotypic station has a **simple hardware design**: it consists in a rigid aluminium frame holding a CNC gantry[2] controlling XYZ movement of an arm holding an RGB camera. The arm holds the camera through a terminal gimbal that gives one to two (depending one the gimbal version) additional degrees of movement (pan and tilt respectively). The system is directly **controlled from a laptop**, running a Linux OS (Ubuntu 18.04 LTS), via common line interface thanks to a bundle of specific libraries and programs[3]. The total cost of the system, including sensors, is about ~3000 euros.

Contrasting background and controlled lighting can be easily added to the aluminium frame to optimize the quality and contrast of plant pictures.

The set-up could easily be mounted on the rover by simply adapting the arm to the CNC gantry.

A scan is launched with **a simple command line**, providing an input configuration file (`scanner.toml`) to specify the trajectory of the camera and other acquisition specifications:

```
romi_run_task Scan --config scanner.toml /path/to/db/scan_id/ --local-scheduler
```

As all the commands, the acquisition is defined as a "task" of a pipeline which is handled by the Luigi program.

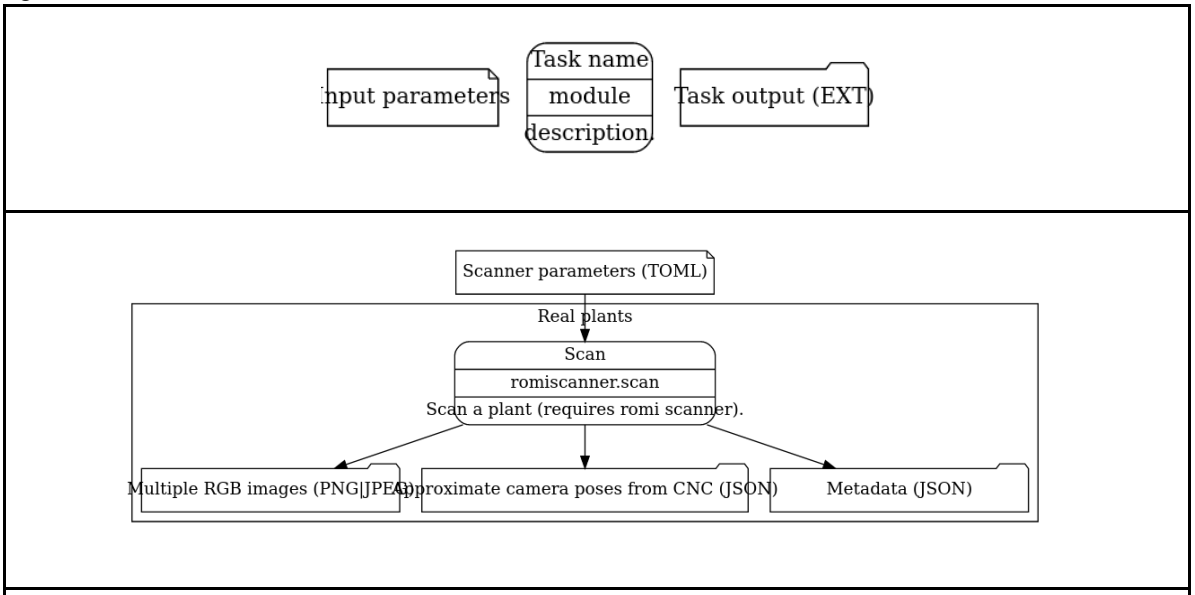

Fig. 1: Image acquisition with the plant scanner is defined as a pipeline task. Upper part: pipeline formalism used with the plant Scanner acquisition and analysis. Lower part: description of the "Scan" Task.

Sensors

A few sensors have been tested (see progress report). The video shows the camera which is currently used at the time of the review.

Table 1: sensor used in the video

[2] We use X-carve (link), a popular and open source machine available as a DIY build kit. NEMA stepper motors of the X-carve control x,y,z movement of the arm. We replaced its spindle by an arm holding the vision sensor.
[3] https://github.com/romi/romiscan; submodule "romiscanner"

Sensor	type	Specifications	Price	Results
RX-0	2D RGB	Sensor resolution: 15 Mp Focal length : 7,9 mm opening (fixed): 4 Wifi available	~ 600 €	3D-reconstruction possible. Under thorough testing. Problem with wifi connection

2.2.2 DATA MANAGEMENT

To start the project, we first created a simple data architecture based on a file system to store all data generated along the workflow from acquisition to analysis. We developed romidata, a dedicated ROMI package to create, organize and access data. Note that we are now developing a more advanced data management system based on a relational database, allowing the use of a data model compliant with plant phenotyping guidelines and FAIR science practices (see progress report and corresponding ROMI package romidata2).

A database is a parent folder containing several “datasets” and it is represented by a FSDB database object in Python. Basically, a dataset contains the raw images of one plant, the corresponding metadata and all the data generated by the analysis.

Here is an overview of the database structure using the ROMI database terminology:

```
romidb_root/
├── dataset_001/
│   ├── fileset_A/
│   │   ├── file_A_001.ext
│   │   ├── [...]
│   │   └── file_A_009.ext
│   ├── fileset_B/
│   │   ├── file_B_001.ext
│   │   ├── [...]
│   │   └── file_B_009.ext
│   ├── metadata
│   │   ├── fileset_A.json
│   │   ├── fileset_B.json
│   │   └── metadata.json
│   └── files.json
├── dataset_002/
│   └── [...]
├── [...]
├── (lock)
└── romidb
```

Note the presence of the **`romidb`** marker so it may be used by FSDB class. We may also find the **`lock`** file used to limit the access to the database to only one user.

Before running an analysis, here is the content of a dataset resulting from an simple acquisition (**`myscan_001`**):

```
mydb/
├── myscan_001/
│   ├── files.json
│   ├── images/
│   │   ├── scan_img_01.jpg
│   │   ├── scan_img_02.jpg
│   │   ├── [...]
│   │   └── scan_img_99.jpg
│   ├── metadata/
│   │   ├── images
│   │   │   ├── scan_img_01.json
│   │   │   ├── scan_img_02.json
│   │   ├── [...]
│   │   │   └── scan_img_99.json
│   │   └── metadata.json
└── romidb
```

2.2.3 3D RECONSTRUCTION PIPELINES

Given a dataset containing raw images and appropriate metadata (stored below in the bash variable `$DATASET`), a 3D-reconstruction is launched with a this simple generic command line:

```
romi_run_task AnglesAndInternodes ~/db/$DATASET --config configs/original_pipe_0.toml
```

In our proof-of-concept scenario, measuring angles and internodes is the last step of the phenotyping workflow. The pipeline can be started by calling the last corresponding last Task of the pipeline, while the input configuration file (`.toml`) indicates the precise chaining of Tasks and the required parameters to be used at each step.

Fig. 2 and Fig. 3 illustrate the two main pipelines (geometric and machine-learning) used to analyse the images of plants acquired with the plant Scanner, relying on two different algorithmic strategies.

Fig. 4 indicates how this workflow is implemented with Luigi Tasks.

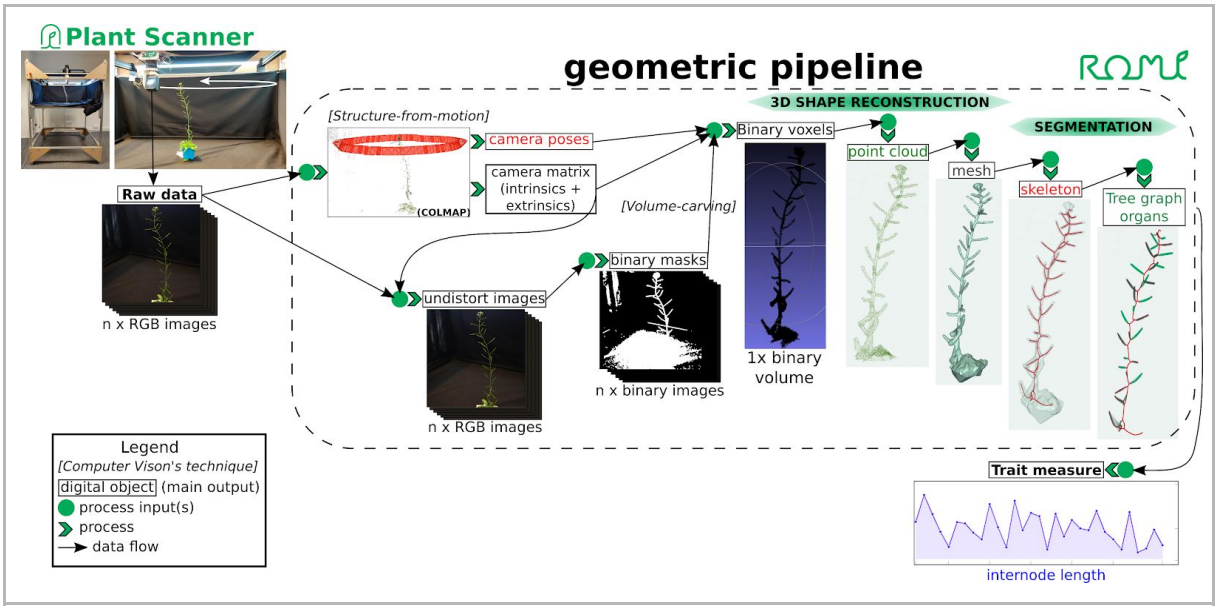

Figure 2: **Overview of the process of measuring phyllotaxis in an *A. thaliana* inflorescence using the geometric pipeline**. Key steps from plant imaging to automated trait measurement are depicted with snapshots featuring the main outputs. The dashed rectangle groups all steps related to the 3D reconstruction of plant architecture using only geometric and algebraic methods (the so-called **geometric pipeline**). The segmentation is generated on the 3D object based on geometric priors. The final output of the

geometric pipeline is a tree graph representing the initial inflorescence, on which precise measures can be computed (e.g. here: internode length). Precise description of the geometric pipeline has been presented in CVPPP conference[4].

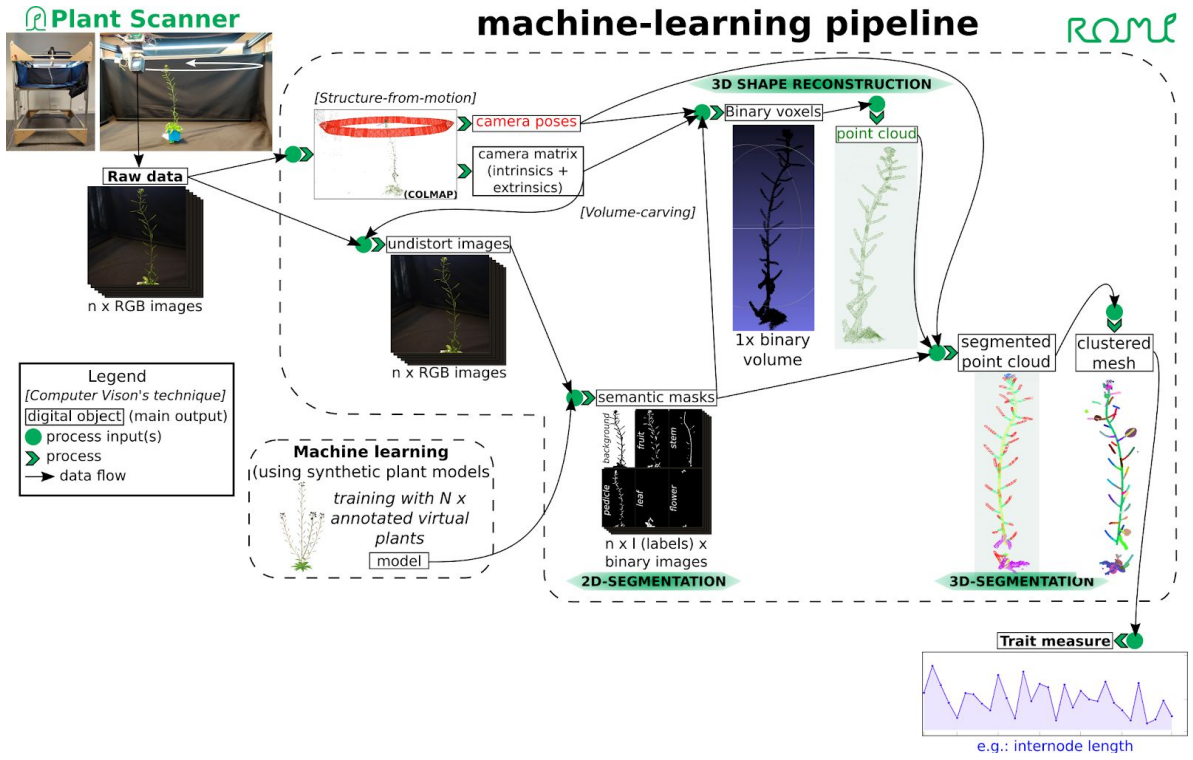

Figure 3: **Overview of the process of measuring phyllotaxis in an *A. thaliana* inflorescence using the machine-learning pipeline**. Key steps from plant imaging to automated trait measurement are depicted with snapshots featuring the main outputs. The larger dashed rectangle groups all steps related to the 3D reconstruction of plant architecture using geometric and algebraic methods as well as the input from machine-learning (the so-called **machine-learning pipeline**). The smaller dashed rectangle represents the training phase where convolutional neural networks have learned from 2D images of synthetic virtual plants to classify plant sub-parts as different semantic classes (fruits, pedicles, etc.). The resulting deep-learning model can be used to classify pixels in new images. Compared to the geometric pipeline, the segmentation is computed on 2D data. The final output is a segmented point cloud on which precise measures can be computed (e.g. here: internode length). Precise description of the machine-learning pipeline is the subject of Deliverable **D6.3**.

On a remote server with adapted computing resources, analysis of a scan with 72 images takes about 3 min with the geometric pipeline and 5 min for the machine learning pipeline.

[4] 'Computer Vision Problems in Plant Phenotyping' (CVPPP) 2018, (September 6, 2018, Newcastle, UK): pdf of the submitted article.

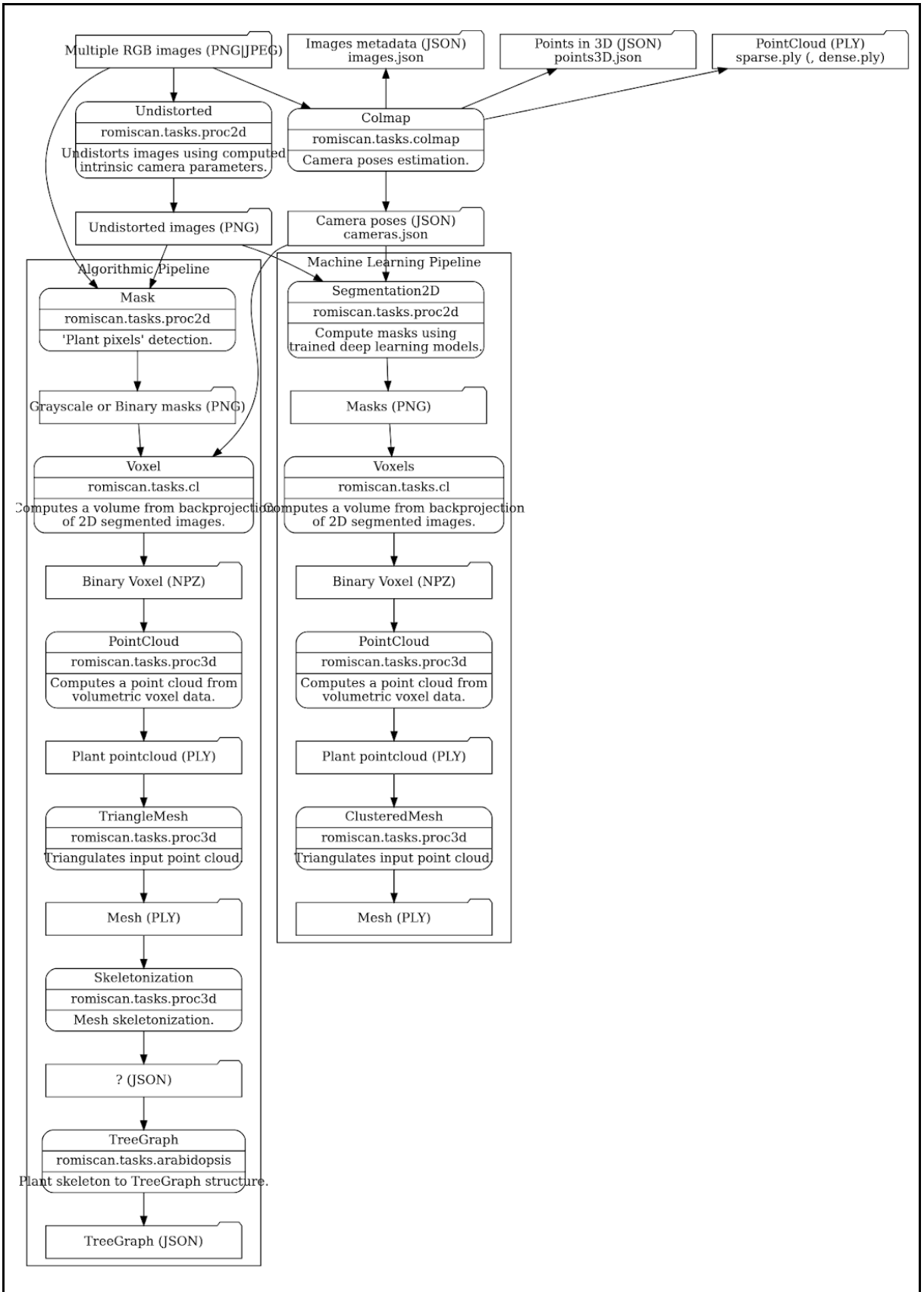

Figure 4: **Luigi pipelines** used to implement the geometric analysis (left) and the machine-learning analysis (right).

After a run of analysis, the content of a dataset is modified by the addition of data. Each Task generates at least one folder containing related files and additional metadata describes this new content (using json files). For example, after running the geometric pipeline, the previous dataset “myscan_001” will look like (figure 5):

```
mydb/
├── myscan_001/
│   ├── AnglesAndInternodes_1_0_2_0_0_1_dd8d67653a
│   │   └── AnglesAndInternodes.json
│   ├── Colmap_True____feature_extrac_3bbfcb1413
│   │   ├── cameras.json
│   │   ├── images.json
│   │   ├── points3d.json
│   │   └── sparse.ply
│   ├── CurveSkeleton_out__TriangleMesh_6a92751c20
│   │   └── CurveSkeleton.json
│   ├── files.json
│   ├── images
│   │   ├── pict20190201_110110_0.jpg
│   │   ├── [...]
│   │   └── pict20190201_111209_0.jpg
│   ├── Masks_True_5_out_9adb9db801
│   │   ├── pict20190201_110110_0.jpg
│   │   ├── [...]
│   │   └── pict20190201_111209_0.jpg
│   ├── measures.csv
│   ├── metadata
│   │   ├── AnglesAndInternodes_1_0_2_0_0_1_dd8d67653a.json
│   │   ├── Colmap_True____feature_extrac_3bbfcb1413.json
│   │   ├── CurveSkeleton_out__TriangleMesh_6a92751c20.json
│   │   ├── images
│   │   │   ├── pict20190201_110110_0.json
│   │   │   ├── [...]
│   │   │   └── pict20190201_111209_0.json
│   │   ├── images.json
│   │   ├── Masks_True_5_out_9adb9db801
│   │   │   ├── pict20190201_110110_0.json
│   │   │   ├── [...]
│   │   │   └── pict20190201_111209_0.json
│   │   ├── Masks_True_5_out_e90d1804eb.json
│   │   ├── metadata.json
│   │   ├── PointCloud_1_0_1_0_False_9ab5a15d9b
│   │   │   └── PointCloud.json
│   │   ├── PointCloud_1_0_1_0_False_9ab5a15d9b.json
│   │   ├── PointCloud__200_0_1_0_False_4ce2e46446.json
│   │   ├── TreeGraph_out__CurveSkeleton_5dca9a2821.json
│   │   ├── TriangleMesh_out__PointCloud_80dc94ac81.json
│   │   ├── Undistorted_out_____fb3e3fa0ff
│   │   │   ├── pict20190201_110110_0.json
│   │   │   ├── [...]
│   │   │   └── pict20190201_111209_0.json
│   │   ├── Undistorted_out_____fb3e3fa0ff.json
│   │   ├── Voxels_False____False_567dc7f48b
│   │   │   └── Voxels.json
│   │   ├── Voxels_False____False_567dc7f48b.json
│   │   ├── Voxels_False____True_af037e876e.json
│   │   └── Voxels_False____True_cd9a5ff06b.json
│   ├── pipeline.toml
│   ├── PointCloud_1_0_1_0_False_9ab5a15d9b
│   │   └── PointCloud.ply
│   ├── TreeGraph_out__CurveSkeleton_5dca9a2821
│   │   └── TreeGraph.p
│   ├── TriangleMesh_out__PointCloud_80dc94ac81
│   │   └── TriangleMesh.ply
│   └── Voxels_False____False_567dc7f48b
│       └── Voxels.npz
├── colmap_log.txt
├── lock
└── romidb
```

Figure 5: structure of a folder after an analysis through a romi pipeline (initial folder contained only raw images and metadata), see above.

2.2.3 RESULT ASSESSMENT

The results of the acquisition, all the 3D objects and the computed measures can be visualized in a unique environment provided by the Plant Visualizer.

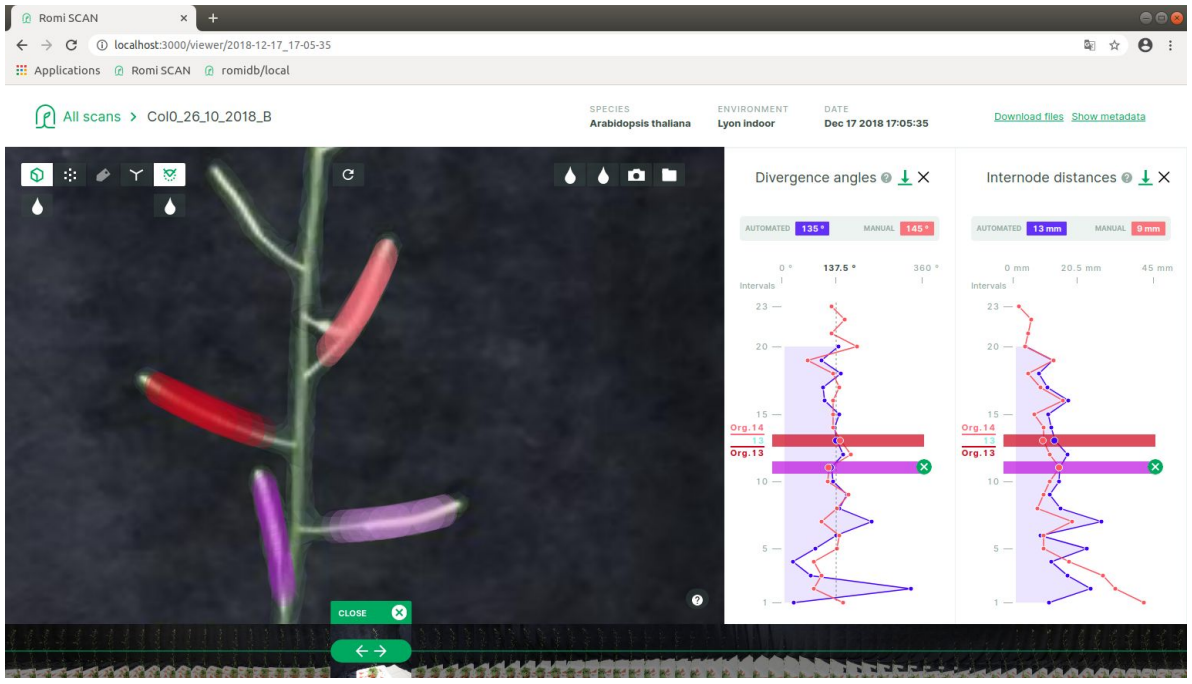

Figure 6: **snapshot of the 3D plant Viewer**. The main panel on the top left shows the overlay of (raw or processed) pictures with the 3D reconstructed objects (point cloud, meshes, skeleton, ...) that can be selected and customized separately. Graphs on the right display the automated (blue) and ground truth (i.e. manual, red) measures of phyllotaxis (angles and internodes). Graphs are interactively (by mouse over) connected with the 3D view (red and purple shading in the screen shot example). Bottom carousel displays thumbnails images of the entire scan, active view is boxed.

A test version of this web server can be accessed here: https://db.romi-project.eu/viz/ (user: sony / password: plantes). Note that a more recent version is now used by developers, although it is not accessible online outside project members.

The quality of the 3D reconstruction can be scrutinized and the automated measurements compared with manual ground truth measurements(if provided).

2.3 Deviations in respect to the plans

Contrary to the title of the deliverable, **no data on outdoors trials are presented here**. From our first efforts indoors, results of fine analysis of 3D plant architecture (using *Arabidopsis* inflorescence phyllotaxis as an experimental proof-of-concept) are encouraging but of insufficient precision to reliably measure fine traits like divergence angles or internode lengths. Indeed, a few segmentation errors or skeleton aberrations can have important impacts on the final analysis.

As mentioned above, outdoors phenotyping is challenging because of unpredictable variations of different parameters (light conditions, plant movements). Tracking the origin of problems outdoors can then be very challenging and barely efficient. To reach a mature advancement allowing fruitful outdoor testing, we decided to **focus our current efforts indoors** with the following working plan:

1. implement automatic methods to quickly but systematically assess outputs of pipeline analysis at different steps so as to track the source of problems and identify the
2. using these methods, improve the current analysis results obtained indoors so as to reach high-quality performances (e.g. 5% precision in measures and >95% segmentation accuracy).
3. Still indoors, add controlled variations separately on different parameters of interest, to assess the sensitivity of our phenotyping and predict results outdoors
4. Finally, test outdoors the phenotyping pipeline(s) that showed the greatest robustness to variation of relevant parameters.

This revised working plan should not impact other tasks significantly.

2.4 Conclusion and next steps

In this demonstrator, we showcase an integrated indoor phenotyping procedure dedicated to a typical user scenario: measuring the phyllotaxis of *Arabidopsis thaliana*. This requires high precision 3D measurements in the shoot system of a plant of intermediate size and can be of interest for a large community of plant phenotyping.

We built every module of this approach: the plant Scanner for automated acquisition, the data management system for organizing and accessing data, the analysis pipelines to automate the analysis of collected images. This ensures that every piece is Open Source, evolvable and reusable. We dedicate a special care to the user experience, by implementing a high level of integration, especially with the pipeline management and with a unique visualisation environment for all results. Automation is also really advanced for both acquisition and analysis. Such automation is required at the end of the project to perform real phenotyping experiments but it is also crucial in the development phase, because it enables extensive testing and benchmarking.

In the next period, we will use this solid foundation to improve both the acquisition set-up and parameters and the analysis software. As mentioned above, this will be done using automatic and quantitative assessment, with increasing challenging variations for image acquisition and 3D reconstruction as long as our solutions prove to be robust.

3 Bibliography and technical annexes

Chaudhury, A., and Godin, C. (2020). Skeletonization of Plant Point Cloud Data Using Stochastic Optimization Framework. Front. Plant Sci. *11*, 773.