

# Phenomenal: a software collection for model assisted analysis of high throughput plant phenotyping data

Christian Fournier<sup>1,2</sup>, Simon Artzet<sup>1,2</sup>, Michael Mielewczik<sup>1,2</sup>, Jérôme Chopard<sup>1,2</sup>, Nicolas Brichet<sup>2</sup>, Llorenç Cabrera-Bosquet<sup>2</sup>, Xavier Sirault<sup>3</sup>, Sarah Cohen-Boulakia<sup>1,4</sup>, Christophe Pradal<sup>1,5</sup>

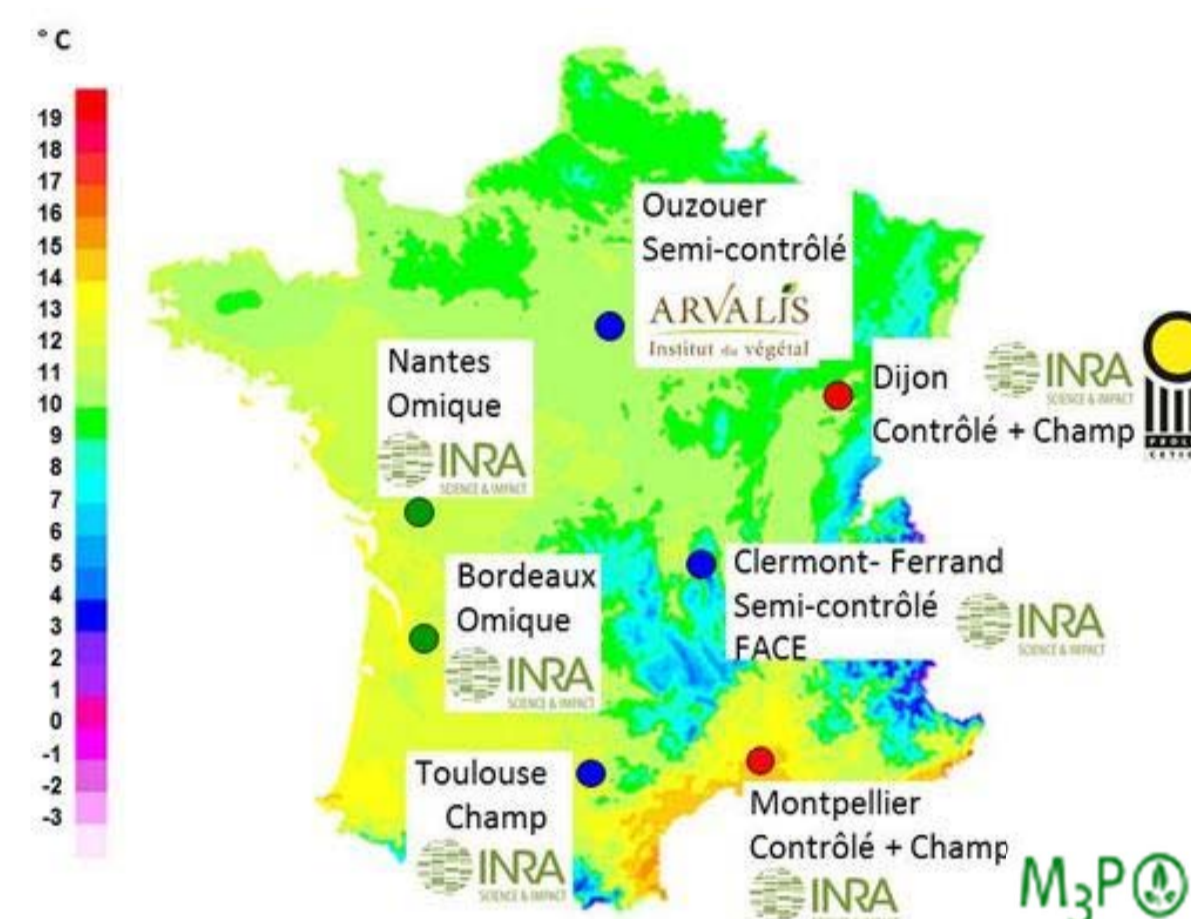
<sup>1</sup> EPI Virtual Plants, INRA-INRIA-CIRAD, Montpellier, France; <sup>2</sup> UMR LEPSE, INRA, Montpellier, France;

<sup>3</sup> HRPPC, CSIRO Agriculture, Canberra Australia; <sup>4</sup> LRI, CNRS, U.Paris Sud, Orsay, France; <sup>5</sup> UMR AGAP, CIRAD, Montpellier, France

## Background and aims

Plant high-throughput phenotyping aims at capturing the genetic variability of plant responses to environmental factors for thousands of plants, hence identifying heritable traits for genomic selection and predicting genetic values of allelic combinations in different environments. This first implies the automation of the measurement of a large number of traits, to characterize plant growth, plant development and plant functioning. It also requires a fluent and versatile interaction between data and plant response models that are essential in the analysis of the marker x environment interaction and in the integration of processes for predicting crop performance [1]. In the frame of the Phenome high throughput phenotyping infrastructure, we develop Phenomenal, a collection of software tools dedicated to the analysis of high throughput phenotyping data and with models.

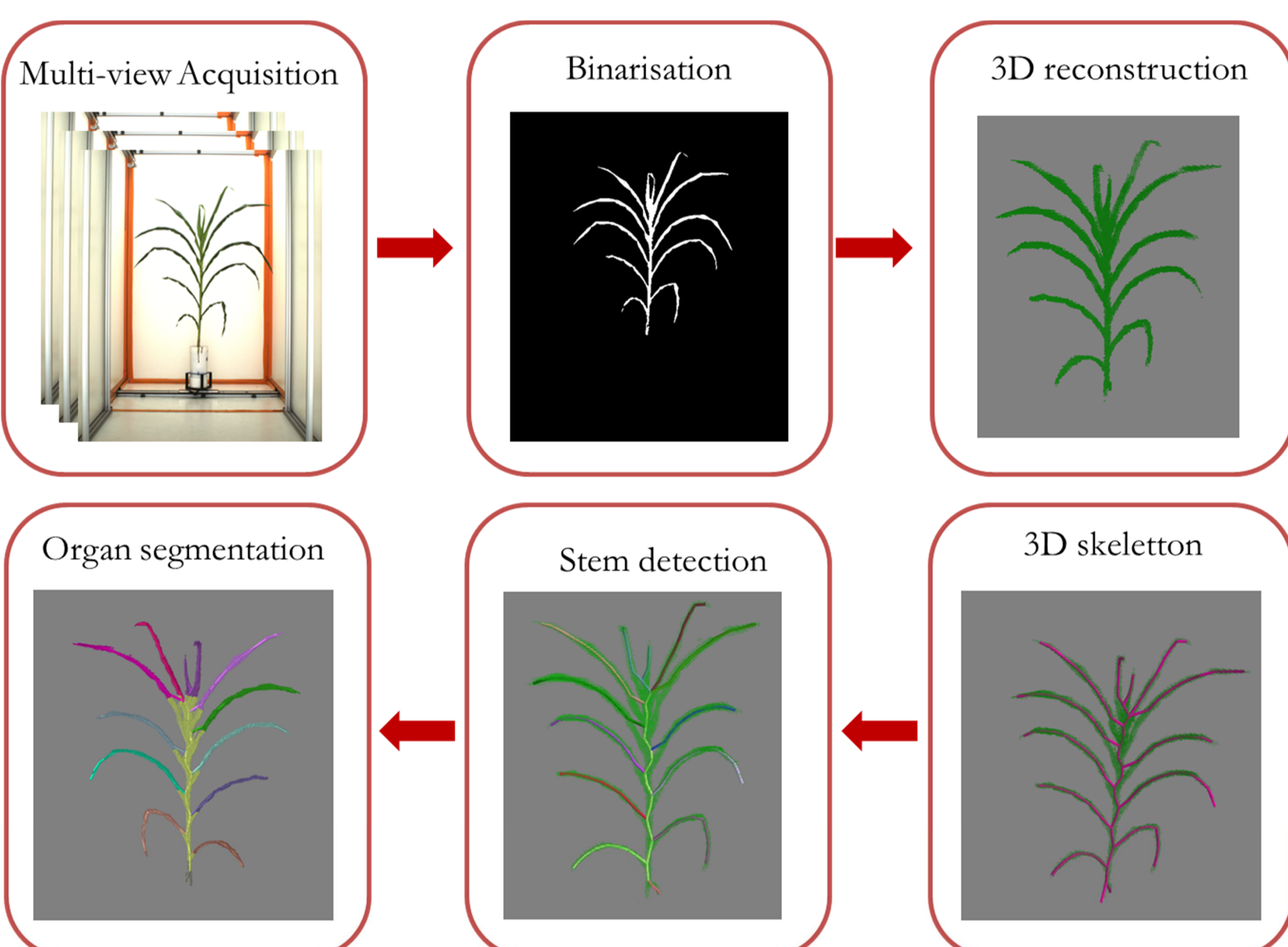
## The Phenome infrastructure and the PhenoArch platform



Phenome initiative provides France with high throughput phenotyping platforms in the field and in controlled conditions. Current phenomenal application mostly deals with data acquired on the PhenoArch facility hosted at the M3P, Montpellier Plant Phenotyping Platforms (<https://www6.montpellier.inra.fr/lepse/M3P/plateforme-PHENOARCH>)

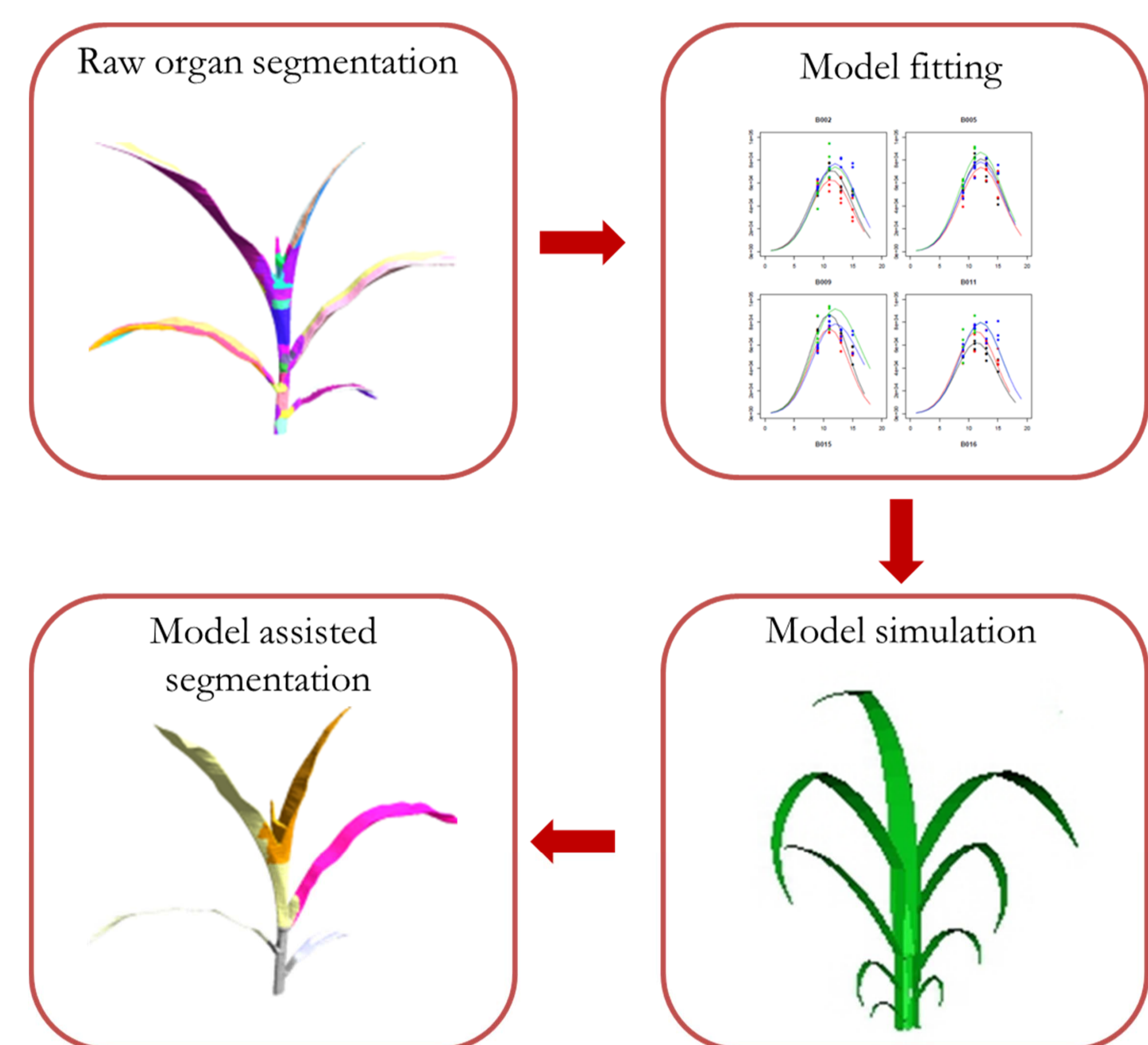
PhenoArch is an automated phenotyping platform based on a Phenoware 3D imaging system. This platform allows the capture of multi-view RGB images for 1680 plants on a daily basis as well as precise control of soil humidity during growth.

## 3D plant reconstruction and segmentation



Multi-view plant images from PhenoArch are binarised and used to reconstruct plants in 3D. The 3D skeleton is extracted and separated into stem (central vertical skeleton elements) and leaves. 3D voxels are segmented by propagating skeleton segmentation.

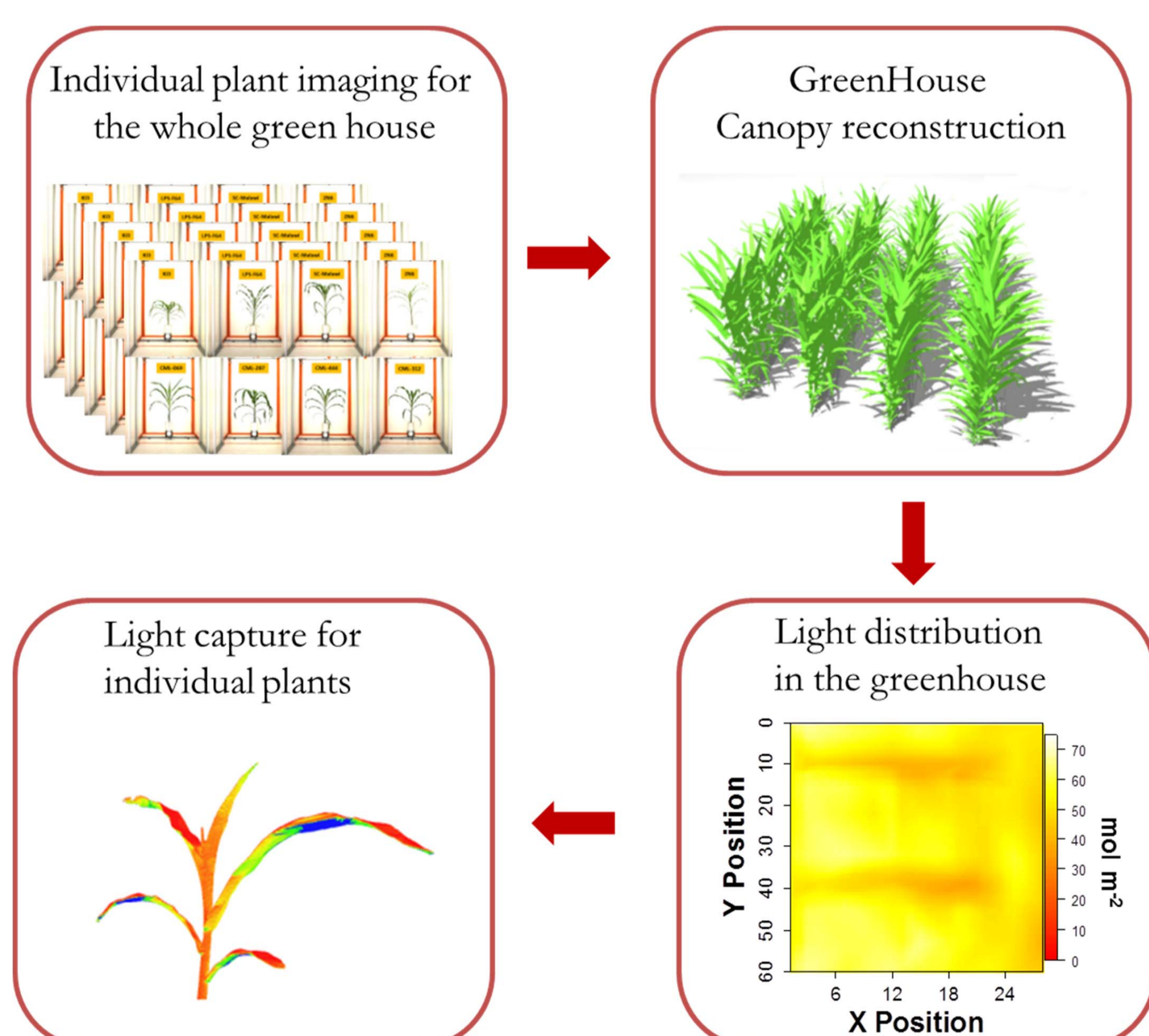
## Model assisted segmentation



Organ segmentation is used to fit a 3D model of architectural development [4]. The model is run and the output is compared to the raw segmentation to get a identification and measure of the entities defined in the model.

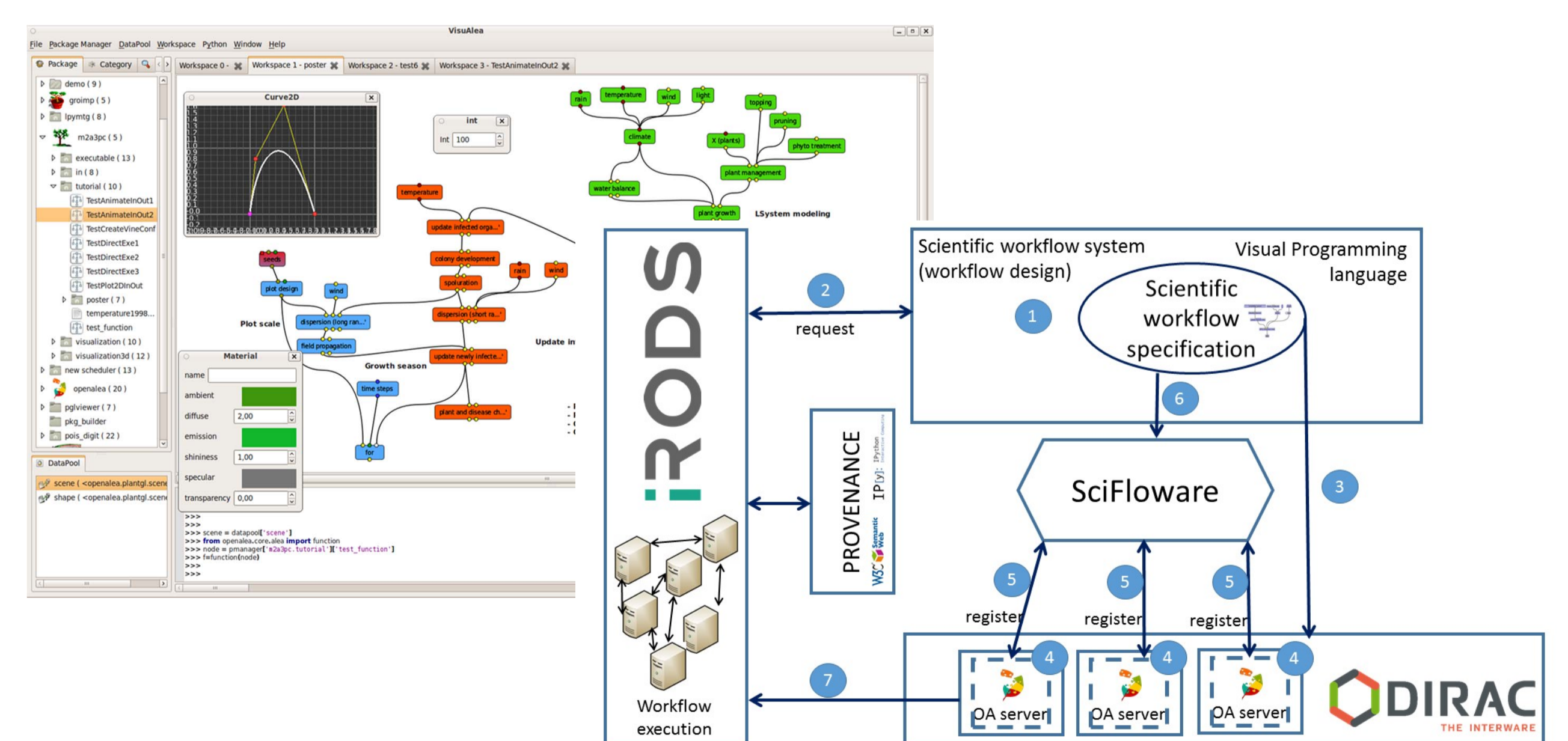
## Light capture by plants

Computing of light interception by individual plants is needed for estimating the radiation use efficiency of individual plants. An in-silico representation of all plants in the greenhouse is generated by combining the 1600 individual 3D plants into a single canopy. A 3D light interception model [5] computes light intercepted by each plant, using the reconstructed 3D canopy and a precise map of incident light distribution [6].



## OpenAlea and Grid computing

OpenAlea [2] provides methods and software for the modelling of plants, together with a user-friendly visual interface for the design and execution of scientific workflows. InfraPhenoGrid infrastructure allows high throughput computation and recording of provenance during the execution [3].



## Future directions

We plan to scale the approach to allow analysis of more complex plants (wheat) and images acquired in the field. We also aim to automatize the connection between plant response models and the data extracted from images, to get directly an estimation of the crop performance in a large range of context.

[1] Parent, B. and Tardieu, F., 2014. Can current crop models be used in the phenotyping era for predicting the genetic variability of yield of plants subjected to drought or high temperature? Journal of Experimental Botany, 65(21): 6179-6189.

[2] Pradal, C., Dufour-Kowalski, S., Boudon, F., Fournier, C. and Godin, C., 2008. OpenAlea: a visual programming and component-based software platform for plant modelling. Functional Plant Biology, 35(9/10): 751-760.

[3] Pradal, C. et al., 2015. InfraPhenoGrid: A scientific workflow infrastructure for Plant Phenomics on the Grid. Future Generation Computer Systems (submitted).

[4] Fournier, C. and Andrieu, B., 1998. A 3D architectural and process-based model of maize development. Annals of Botany, 81(2): 233-250.

[5] Sinoquet, H., Le Roux, X., Adam, B., Ameglio, T. and Daudet, F.A., 2001. RATP: a model for simulating the spatial distribution of radiation absorption, transpiration and photosynthesis within canopies: application to an isolated tree crown. Plant, Cell and Environment, 24: 395-406.

[6] Cabrera-Bosquet L., Fournier C., Welcker C., Suard B. and Tardieu. High throughput estimation of incident light, light interception and radiation-use efficiency of thousands of plants in a phenotyping platform (submitted)