

What structural plant modelling and image-based phenotyping can learn from each other?

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Introduction

High throughput phenotyping technologies have spread rapidly in the recent years to meet the demand for phenotyping of large panels of plants, covering a large genetic diversity and a large range of environmental conditions. Image-based technology, which allows following the architectural development of plant over time, is among the most popular, due to its simplicity, to a high degree of automation of the acquisition process, and to the richness of the information acquired. The automation of the analysis process is also actively developing (Ubbens et al., 2020), which offers unprecedentedly large and detailed dataset for plant modelling and for the development of new applications. Linking phenomics and crop modelling allows for example already to integrate the genetic variability of responses of plants to the environment, and to reason which combination of alleles is desirable for different pedo-climatic conditions, for present and future climate (Tardieu et al, 2017). By design, crop models however do not capture in details the architectural development of plants, that is the core data produced by image based phenomics. Using and adapting structural (functional) plant models for the analysis of such data will potentially minimise the loss of information, improve the modelling at fine scale and provide simulation tools that can be used as new source of information for crop modelling. Our objective is to experiment such a coupling for maize architectural development, and discuss how it may affect modelling and phenotyping.

Materials and Methods

Multi-view images from a large phenotyping experiment (1600 plants, 40 days) performed on the PhenoArch platform (<https://www6.montpellier.inra.fr/lepse/M3P/PHENOARCH>) are analysed with the Phenomenal image analysis pipeline (Artzet et al., 2019), which generates, for each plant, a sequence of 3D reconstructions at different stages of development (Figure 1A). Phenomenal also allow to segment the plant into smaller components (stem and individual leaves), and extract phenotypic feature such as leaf length, leaf width and leaf angles. We first use these data to parameterise, one-time point at a time, a static structural model of maize (Fournier et al., 2012) (Figure 1B). The different time points are then used together to estimate a dynamic model of plant development as a function of temperature (ADEL-maize, Fournier et al., 1998) (Figure 1C). To evaluate the quality of the representation of these two nested levels of simplification, virtual plants are illuminated with a light model and compared for their interception efficiency in several conditions (isolated plants and self-similar canopies, under clear sky and overcast conditions). We also assess how the raw phenotypic features extracted by Phenomenal compare to those simulated by the dynamic model.

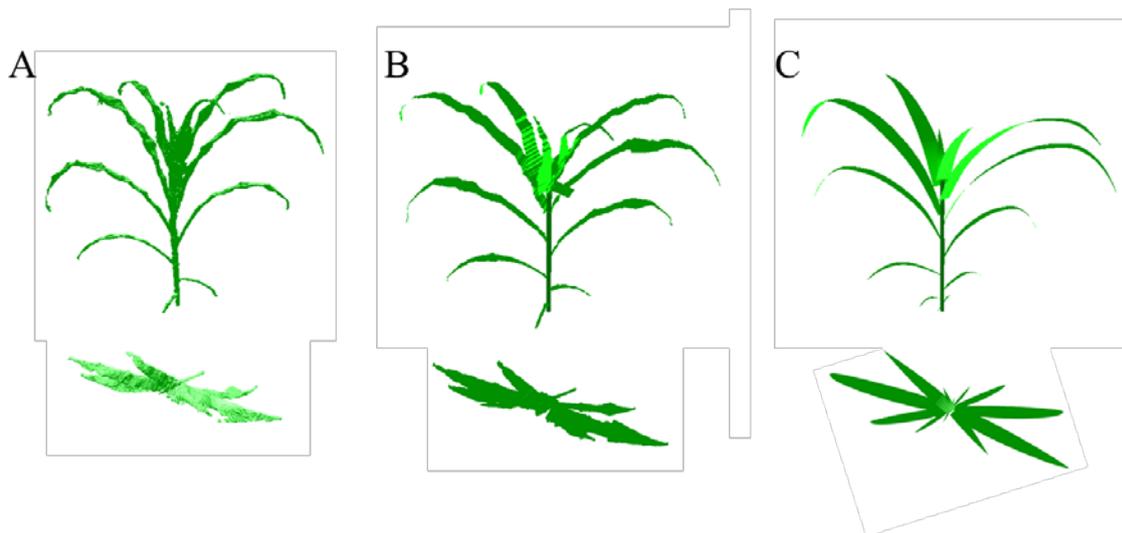


Figure 1: 3 Perspective and top view of maize plants, at different stages of the analysis pipeline. A : Raw 3D plant reconstructed as a set of voxels, with the Phenomenal pipeline. B: 3D virtual plant simulated by a static plant model fitted to the data. C: 3D virtual plant simulated by a dynamic plant model fitted to the entire developmental sequence.

Result and discussion

Each modeling step results in a high level of compression of the data, the highest level being between the raw plant and the static model (from 1A to 1B). The first compression is essentially linked to the simplification of the specification of the geometry (from voxels to meshes) and to the use of construction rules. The second compression is linked to the use of parametric models that capture the evolution of the objects with time, but with simplifications. In terms of light interception, all models yield similar value for self-similar canopy simulation. For isolated plants, the static model produces interception values similar to raw data, but the dynamic model can have up to 50% difference on interception in zenithal direction. This is explained by an over simplification of the leaf reorientation patterns. Fitting the dynamic model allows to improve the different measurements of plant organs (lengths, width, ..). This is explained by the compilation of the repetition of the measurements over time. The dynamic model allows to get temporal leaf tracking and to identify artifacts in the segmentations. Combining raw data and leaf tracking finally allows to extract dynamics patterns of development, including the sequence of leaf reorientation, that could be used for modelling.

Conclusions

Fitting a structural plant model to elaborated phenotyping data acquired in a platform was beneficial both for model improvement and data analysis. The improved model more closely matches the interception efficiency of observations and has more robust parameterisations. Data analysis was enriched with dynamical features and benefits from averaging of repeated measurements. As a result, we obtain a fully parameterised structural model for hundreds of genotypes. Foreseen application of such a model range from multi-genotype analysis of plant development, use in interpretation of phenotyping data in the field and ideotyping.

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