GrapeInSilico: a modelling framework for building grapevine FSPMs

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Introduction

Winegrowing must innovate to adapt to the climatic, biotic or socio-economic constraints of today and tomorrow. Integrative functional-structural plant models are particularly relevant tools for supporting this innovation, as they make it possible to explain the influence of the genotype as well as cultivation practices on the phenotype (structure) and to link them to the consequences on yield and its quality (function). They therefore make it possible to jointly reason about selection targets and new practices in order to adapt vineyards to the evolution of constraints, technological innovations or new expectations. The design of such tools requires the aggregation of research models, focused on different aspects of vine functioning or development. These elementary models are numerous, and can address targeted questions, but they do not individually account for all possible impacts on the plant and its environment. The objective of the GrapeInSilico is to create a modular, integrative and high quality software modelling and simulation environment that can easily bring together and mobilise these research findings. GrapeInSilico is developed within the OpenAlea platform, which is internationally recognised and adopted by a large community in the field of plant modelling, in order to benefit from existing generic modules (biophysical calculations, epidemic dynamics, etc.) and proven integration technologies.

Materials and Methods

GrapeInSilico consists of a set of interoperable models dedicated to vine modelling. Elementary models are hosted as regular software packages on the Openalea platform. A dedicated website is implemented, designed to include the GrapeInSilico model catalog, a specific presentation of models in the context of their use in GrapeInSilico, and a set of tutorials demonstrating how these models can be coupled for particular applications. GrapeInSilico currently includes TopVine (Louarn et al., 2008), HydroShoot (Albasha et al., 2019) and MuSca (Reyes et al., 2020) models. It also includes several grapevine canopy digitising datasets. TopVine simulates the canopy architecture as affected by the genotypic variability of the grapevine, using statistical distribution of shoot position, length and axis orientation. HydroShoot simulates gas-exchange, energy budget and shoot hydraulic architecture. Finally, MuSca simulates carbohydrate allocation among organs with a multi-scale approach. Two other models will join the framework in the near future : Virtual Berry (Dai et al., 2009), which simulates development and sugar accumulation at the berry scale, and Vignoid (Calonnec et al., 2008), simulating the intensity of damages on the foliage caused by fungal (powdery mildew) diseases (Figure 1). Beyond these first examples, GrapeInsilico has the ambition to host other FSPM models developed on vine. The Multiscale Tree Graph (MTG) is the data structure used for coupling the models and structuring the datasets in GrapeInSilico. Developing GrapeInSilico involved ensuring that all models were consistent with this view, engineering GrapeInSilico catalog (doc, test) and revisiting their interface to ensure their interoperability. To do so, our strategy was to design realistic use-cases that require operating different combinations of models, and publish them as tutorials publicly available on the GrapInSilico web portal.

Use Cases

A first application was dedicated to simulate the impact of the genotypic variability on canopy architecture and, consequently, on canopy photosynthesis, transpiration and temperature distribution.
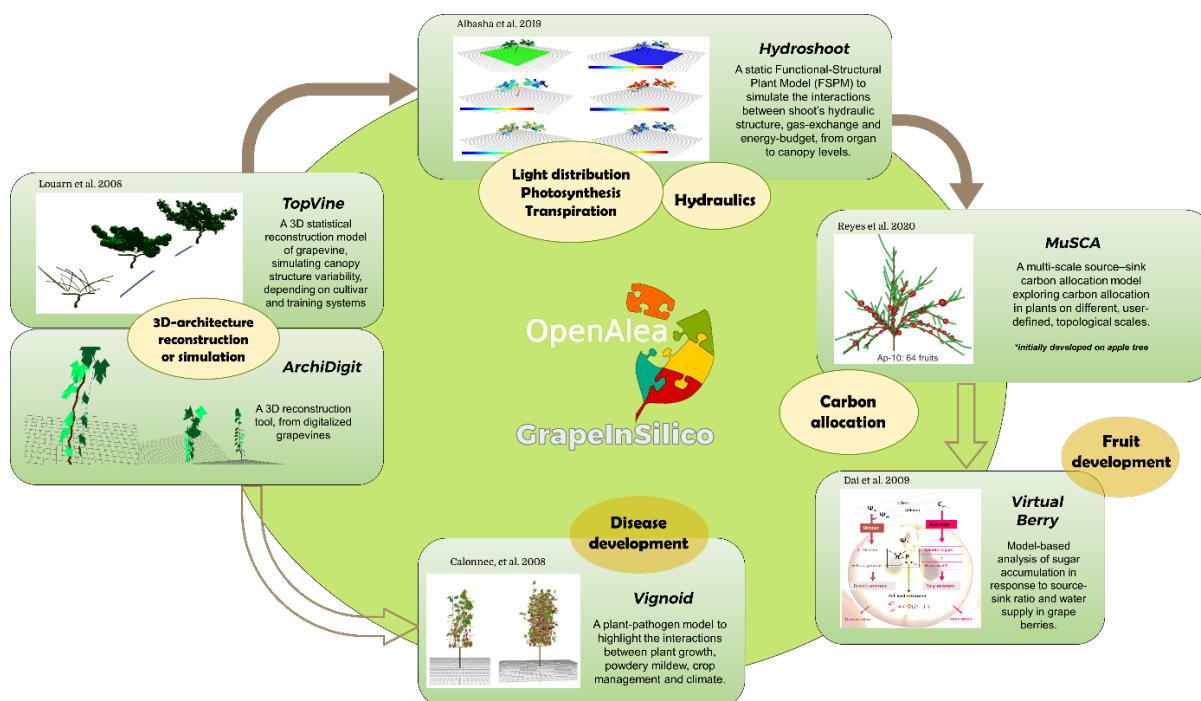
Figure 1: The GrapeInSilico framework allows to integrate a variety of processes coming from various models from the OpenAlea platform. The above figure illustrates the main coupling pipelines of its models, aimed at gaining a better understanding of the interactions among the simulated ecophysiological processes.

TopVine and HydroShoot were coupled to this aim. Model parameters that account for the genotypic variability are those controlling leaf orientation, secondary axis growth, shoot length and individual leaf area.

A second application was to run a complete pipeline, including 3D digitising mock-ups, simulations of light interception and photosynthesis and the Musca model, calculating carbon allocation towards the fruits and vegetative axes. This pipeline allows us to quantify the relative importance of each process in the elaboration of yield in grapevine. Ultimately, the virtual berry module will be coupled with this pipeline, such that we can eventually simulate the effects of canopy architecture in grape development.

Conclusion

We created GrapeInSilico, a modular framework that allows constructing integrative FSPM by coupling existing models. The framework already allows to simulate plant architecture, plant functioning (photosynthesis, transpiration) and plant carbon economy. The framework will incorporate in forthcoming works other models that have been developed, such as simulations of sugar accumulation at the berry scale or of the evolution of a fungal disease on the plant. From a socio-economic point of view, the challenge is to guide and accelerate varietal improvement (graft or rootstock) as well as to design innovative management methods adapting to the new constraints of the sector. The applications envisaged are (i) the identification, via model-assisted high-throughput phenotyping, of the genetic bases of responses to the environment and to practices (ii) the in-silico evaluation of new varieties and practices in current and future scenarios, (iii) the design of sensors or model-assisted data processing chains for vineyard monitoring and management and (iv) assistance in the design of new practices in the field of agronomy and crop protection, via their in-silico testing.

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