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EXECUTIVE SUMMARY (1 page)

Summary of deliverable content and initial objectives:

WP6 is dedicated to designing models of plant development in 3-dimensions and associated machine learning strategies able to make use of these virtual plant models in other WPs of ROMI (mainly WP4 and WP5).

This report describes deliverable D6.2: Model of crop species #1. In the last period (year 1), deliverable D6.1 reported on the design of a simplified model of Arabidopsis thaliana. The model was able to simulate the detailed 3-D architecture of a growing Arabidopsis plant. The first 3-D rendering of this model was of sufficient quality to serve as an input in the learning phase of machine-learning algorithms described in Deliverable 6.3: results of the training models. In this new period of work, building on the work of the first year, we worked along 3 main lines:

i) design a generic methodology to construct realistic 3-D growth models easily for other plant species;
ii) improve the rendering realism of our virtual plant models;
iii) develop a first crop model (tomato plants) and exploit this design phase to demonstrate the use of our new modeling methodology.

We report hereafter about these 3 lines of work through two main sections related to:

1. the design of a generic methodology to construct realistic 3-D growth models
2. the application of this methodology to the construction of a model of a crop species: tomato plants (Solanum lycopersicum L.)

Partners involved:

Leader: Inria
Participants: Inria

Relation with other work packages and tasks:

This work is carried out in close interaction with WP5. WP6 provides support for the model-based 3D-reconstruction algorithms. The plant models are also used to generate synthetic images to train neural networks in WP5.

In the next phase, we will also combine our virtual plant approach with the adaptive learning schemes developed in WP4.

Demonstrator:

- a growing virtual realistic model of Arabidopsis thaliana, whose geometric realism is improved with respect to the original simplified virtual model Arabidopsis of Arabidopsis thaliana:
  - [https://media.romi-project.eu/documents/ROMI-D6.2-Arabidopsis-WT-20fps.avi](https://media.romi-project.eu/documents/ROMI-D6.2-Arabidopsis-WT-20fps.avi)
These simulations are improvement of the corresponding results of Deliverable 6.1 for comparison: https://media.romi-project.eu/documents/ROMI-D6.1-Simplified_Model_Arabidopsis.avi

- a growing virtual realistic model of *tomato plant (crop species)*, with detailed geometric realism;
  - https://media.romi-project.eu/documents/ROMI-D6.2-Tomato-4-seed16-25fps.avi
  - https://media.romi-project.eu/documents/ROMI-D6.2-Tomato-4-seed17-20fps.avi

Dissemination / IPR policy:

Code release:
All the source codes of the plant models are in LPy an python and are available at:
git@github.com:romi/VirtualPlants.git

These source codes are available under the CECIL-C open-software international license.

The work presented in this document will give rise to a scientific publication.
1. Design a generic methodology to naturally control developmental time at different scales in realistic 3-D models of plant development

In the project we want to achieve the development of several plant models with realistic 3-D architectures. Photo-realism is here extremely important as these plants are intended to be used to produce the mass of synthetic data required to train deep-learning networks that will subsequently be used to segment real plant in 3-dimensions. This training must be as unbiased as possible by the potential unrealistic artifacts coming from the virtual models.

Rendering 3-D scenes in a photo-realistic way requires to address a number of features in the construction of synthetic images:

- Precise geometric representation of the object in the scene
- Physical coherence (the object must be physically plausible). This comes in two main aspects:
  - In the interaction between its parts or with other objects (no solid part can for instance penetrate any other solid part)
  - In the interaction with light (object parts must have surface material properties that will make it possible to render realistically their interaction with light).

Several works have already successfully addressed photorealistic rendering of plants. Some of these works focus on particular rendering aspects specific to plants, e.g. Fuhrer 2004 for hairy plants or Owens 2016 for modeling dense inflorescences. Other approaches propose a complete methodology to design plants. The seminal approach from Prusinkiewicz and Lindenmayer (1990) introduced a declarative computer language, called L-systems, to model various aspects of plant development and structures. Since then, the language has been augmented to address various aspects of plant growth and has become a major modeling paradigm to model plant development. Other approaches have been proposed to assess the flexibility of other techniques to model plant development, e.g. (de Reffye 1988) who model the development of various plant architectures using stochastic models, (Deussen 1998, 2003) who are using flowchart design for an intuitive design of plant architectures, (Boudon 2007, Wither 2009) for multiscale design of plant architecture or (Longay 2012) for a flexible and fluid design plant tree structures using a space colonization paradigm.

One aspect that is still partially lacking in these approaches is a conceptual strategy to naturally orchestrate the growth of the different plant parts in time and to relate this to developmental descriptions of plant parts development with each other. Our objective during the ROMI project, is to establish a such a methodology to design virtual plants in a natural manner from botanical knowledge and so that different plant species can be constructed with a systematic method. In this work, we addressed this question and designed a new methodology to model plant growth dynamics at different scales, using a multiscale approach. We introduce the notion of **hierarchical developmental timeline warping** (HDTW) to describe the synchronization of events during plant growth in a hierarchical and modular manner.

**Hierarchical developmental timeline warping design of plant models**

From plant architecture point of view, plant growth can be decomposed into two main processes: i) organogenesis that takes place throughout plant development at the level of apical
meristems and ii) organ growth (extension). To model plant architecture development, one thus needs to account for these two processes and for their temporal synchronization.

In plant modeling systems, this usually is done by using the age of each organ (or well identified part of plant) in some given time units (e.g. hours) to control its growth rate and the initiation time of new organs potentially produced by this organ. This makes it possible to precisely tune the initiation time and growth dynamics of each organ in the plant. This is for instance the strategy that we used in our first deliverable on “a simplified model of Arabidopsis thaliana”. However this strategy has a major design drawback hindering flexible model evolution: if one wants to reuse the growth model of an organ like a leaf, a flower or an internode, in a different growth context, or with different growth conditions (lower temperature for instance), one needs to extensively edit the model code to modify all the parts that depend on time thresholds or growth rates. In a realistic models of plant development, which contain many botanical details, this is usually so complex that it prevents the reusability of previously developed models, and lead modelers to redevelop new models for each new species from scratch.

Our approach relies on the conceptual representation of a (hierarchy of) series of events during the plant development. Such a representation is commonly called a timeline. In music it may represent the different isolated instrumental/vocal lines of a music piece. In computer animation, timelines are defined for different scene parameters to control the movement of different objects in the scene. In developmental biology, timeline commonly refers to the sequence of development stages of a particular organ or individual in plants or animals.

Inspired by computer animation, this concept has recently been used in plant modeling to graphically represent the variation of various plant parameters in plant growth simulation to improve “conceptualization, presentation and manipulation”. Each of the numerous parameters used in the simulation can be controlled by a function and corresponds to a distinct “timeline”. A timeline editor makes it possible to control graphically the variation in time of the different parameters. Interestingly, it is also briefly mentioned that the timeline can be defined with respect to the age of their own modules rather than with respect to a global timeline.

Here, to anticipate the development of realistic models of plant architectures for different species (i.e. containing a large number of botanical details) in ROMI, we build up on this previous approach and develop a new methodology, called hierarchical developmental timeline warping (HDTW), to describe plant architecture development with modular and reusable components. For this we assume that the development of plant organs, as well as well identified subparts can be described in a normalized manner using typical stages of the organ development. This normalized development will play the role of a reference development that can subsequently be warped in time and reused in variants of the plant architecture model.

For instance, consider the development of a flower as described by biologists (Fig 1). This is often made on a reference typical individual, and consists of well characterized stages of development, with possibly an indication of a reference time (see the olive flower in Fig. 1). Usually, these stages are very stable from individual to individual of a given genotype, ecotype or even species. However, the actual timing that each stage will take depends on various parameters, genetic or environmental (e.g. see Fig 1, third row).
Figure 1. Biological descriptions of plant organ development: First row: development of an Olive flower according to (Alagna et al. 2016). The description by biologists often shows a sequence of stages of development, with approximate dates for each stage. Second row, development of the flower of Arabidopsis thaliana (WT) (Chen et al. 2019) and last row, inflorescence of Arabidopsis thaliana in WT (A) and mutants showing different flower development precocity (Hou et al. 2018).

To account for this, botanical studies usually assume that the development of a plant organ can be described along an axis that depends on the physiological stages of development rather than on the actual time, and that is usually referred to as physiological age in botanical studies (Barthelemy et al 2007). As the physiological age augments, the organ passes through its successive physiological stages.

Reference developmental timeline of an organ. To formalize this, we assume here that this physiological age can be described by a normalized variable $\tau$ in $[0,1]$. The organ is initiated at age $\tau=0$ and goes successively through all the stages of development as $\tau$ varies from 0 to 1, value at which the organ dies out (Fig. 2, red solid lines). A discrete set of successive stages of organ development are arbitrarily associated with successive values of $\tau$ (Fig. 2, red dashed lines). It is assumed that for intermediate values of $\tau$, the corresponding organ shape is also intermediate between the two known neighbouring shapes (we will see below how this is computationally achieved). For each organ $i$, this defines a function $\bar{D}_i(\tau)$ from $[0,1]$ to the set of organ geometries called the reference developmental timeline of organ $i$.

Importantly, this definition does not make reference to any real time units. The variable $\tau$ represents a time proper to the description of the organ growth.
Figure 2. Definition of a reference developmental timeline for the growth of a structure (here a flower) and of a warping function. A reference developmental timeline maps an index variable $\tau$ (in red) varying from 0 (birth of the structure) to 1 (death of the structure) to stages of developments. Here we use the stages of development of a WT flower of Arabidopsis thaliana (photo from Shin et al. 2018). Note that no actual time information is involved in this definition. In blue, a warping function $W_i$ makes it possible to map real time $t$ to the developmental timeline of the organ $i$. This function is increasing (cannot reverse the order of developmental stages), but non-linear in general.

**Developmental timeline of an organ in a simulation.** Given a reference developmental timeline $\bar{D}_i$ for organ $i$, it is then possible to describe its actual development in real time by mapping the real time to the physiological age. For this, we define a warping function $W_i$ that maps the real time $t$ to organ $i$’s physiological age, $W_i: \mathbb{R} \rightarrow [0,1]$, such that $W_i$ is an increasing function of time (but not necessary linearly increasing), Fig. 2 blue lines. Then the growth of organ $i$ in real time can be described by the composition of the warping function and of the reference developmental timeline, $D_i(t) = \bar{D}_i \circ W_i(t) = \bar{D}_i(W_i(t))$. $D_i$ corresponds to a developmental timeline of organ $i$ indexed by a time variable $t$ expressed in real time units, e.g. hours or days.

**Composed versus simple organs.** To define computationally organ developmental timelines, one needs to make a difference between simple organs, that cannot be decomposed into smaller components, and composed organs either made of other composed organs or of simple organs. Simple organs are associated with a parametric geometric model able to represent the variations of its shape in time. For this, we follow a procedure previously described in (Boudon et al. 2012). For example, a petal is a simple organ that is represented in our model by the surface of a generalized cylinder $G$ using 5 parameters: a nerve curve, a width curve, a width function, a length scale and a width scale (see Fig 3. B). The nerve curve is scaled by the length factor and the organ surface is constructed by positioning the width curve at regular intervals along the scaled nerve curve and by scaling it as well according to the width function depending on the curvilinear abscissa along the nerve. This generates a surface that represents the organ shape (Fig 3.B).
Figure 3. Construction of the developmental timeline of a simple organ (petal). A. Curves characterizing the petal nerve (yellow), section (green) and function defining the width (purple) of the petal along the nerve. Several curves (4 leftmost curves) corresponding to nerve at different stages of development of the petal have been defined. B. Generalized cylinder model (lateral and front views in 3D) resulting from a nerve defined by the curve petal_nerve2 (yellow) together with the section curve (green) and width function (purple) scaled by length and width factors. C. General shape of the warping function \( W(t) \) as a Hill function of parameters \( y_{\text{min}}, y_{\text{max}}, t_0, T, n \). The higher \( n \) the steeper the slope of the curve. D. Continuous development of a petal using interpolations between stages of development defined by the nerve curves in A combined with a warping function. This models the developmental timeline of the petal \( D_{\text{petal}}(t) \).

As a series of curves were defined for the nerve, these are taken to correspond to the petal nerve at consecutive stages of development (here four stages, Fig3. A). It is therefore possible to define a geometric model of the petal surface for any \( \tau \) by simply linearly interpolating curves between two the two consecutive stages. We thus obtain a reference developmental timeline \( \bar{D}_{\text{petal}}(\tau) \) of the petal that is a continuous function of a developmental time \( \tau \in [0,1] \) and that defines a reference developmental timeline of the petal.

By using a warping function it is then possible to adapt the dynamics of this reference development to that of an application with a specific progression of time. As most plant organs develop following a sigmoidal curve in their size, we assume for sake of simplicity here that this warping function is a sigmoidal function of time defined by a general parametric Hill function (Fig. 3.C) and defined by the equation:
\[ \text{Hill}(t) = y_{\text{min}} + \frac{(y_{\text{max}} - y_{\text{min}})(t - t_0)^n}{T^n + (t - t_0)^n}, \]

where parameters \( y_{\text{min}}, y_{\text{max}} \) that are respectively the minimum and maximum values of the function, \( t_0 \) represents a delay before the function starts to increase, \( T \) corresponds to the half-time period (amount of time after \( t_0 \) before the function gets halfways between \( y_{\text{min}} \) and \( y_{\text{max}} \)), and \( n \) is a real exponent. The development of the petal can thus be represented by the function \( D_{\text{petal}}(t) \) for specific values of \( y_{\text{min}}, y_{\text{max}}, t_0, T, n \), for \( t \) varying over the simulated interval of time \([t_b, t_e]\). This assumption is made for convenience to use a homogeneous form of function in our plant design. Should it be necessary, it could be replaced by any growing function warping thus one time scale onto the other one.

**Figure 4. Hierarchical developmental timeline warping.**

A. Decomposition tree of a flower. The nodes represent the different categories of organs. The numbers labelling the edges indicate the number of instances of this category. Geometric models have been constructed for each organ (upper right grey box). B. Corresponding developmental timeline decomposition of the flower developmental timeline: it aggregates the different developmental timelines of its constituents warped on its own developmental time \( t_{\text{flower}} \) by the warping functions represented above each developmental timeline of each constituent (pedicel, sepal whorl, petal whorl, stamen, carpel). C. The nodes that can be further decomposed have their own developmental timeline decomposition, here we see the decomposition of the petal whorl developmental timeline as 4 instances of the petal developmental timeline warped onto its developmental time \( t_{\text{petal whorl}} \). D. Resulting developmental model of a flower showing the dynamics of the different flower organs. The green bar at the bottom represents
Contrary to simple organs, composed organs can be further decomposed into finer constituents or sub-parts. This decomposition into finer plant constituents can be represented as a tree graph, Fig. 4.A. Some constituents like organ whorls can be further decomposed into more detailed organs such as petals, sepals or stamens, which are simple organs. To define the developmental timeline (DT) of a composed organs, we associate a warping function with each constituent DT that maps the reference development of the constituent to that of the flower in the particular application, Fig 4.B. In turn, if one of the constituent is a composed organ, this operation is repeated (Fig 4.C), until one reach simple constituents that cannot be further decomposed (here pedicel, sepal, petal, stamen and carpel). For these simple constituents, the warping function described above how the time of the composed organ containing this simple organ is mapped onto the reference time of the simple organ reference developmental timeline (see above). Fig 4.D illustrates the result of such a recursive decomposition, where all the organs growth are synchronized by the induced hierarchy of warping functions. Note that for a particular organ, two notions of time are used and mapped onto eachother: i) the reference time ii) the time of the composed organ in which this organ appears (this later time is itself the reference time of the composed organ).

Every organ, be it composed or simple, is in addition associated with a length, a diameter, a width, an opening angle (insertion angle on its parent organ) and a lifespan. These quantities make it possible to control their size (scaling in different directions), their orientation with respect to their parent entity and the span of their existence. Except for the last one, these parameters may be controlled using their own timeline expressed in reference to their organ’s developmental time and contribute to the definition of the organ’s developmental timeline.

**Modeling the developmental timeline of plants with L-systems**

To model the plant growth dynamics, we extended our developmental timeline model to the whole plant and generalized the approach that we developed to model the growth of *Arabidopsis thaliana* in the first phase of the project. For this we defined a generic model to control the development of the stem apices (meristems). We assume that each plant apex passes during its life through a number of physiological stages. What each apex produces at a certain time depends on its current physiological state. For instance, for *Arabidopsis thaliana*, we considered four main stages of plant apices: i) vegetative, where the apex produces lateral leaves, internodes are not elongating and lateral apices are not developing, ii) mixed, where the apex still produces (smaller) leaves, but internodes are growing and lateral apices develop iii) inflorescence, where the apex produces lateral flower apices, and iv) flowers, were the apices are only able to produce a pedicel and a flower.

Altogether, this produces a developmental timeline for the plant associated with the development of its main apex. However, now, the composed model that correspond to the plant development is made of a multitudes of components, internodes, leaves, flowers whose temporal and spatial organization is now defined procedurally, using L-systems formalism (Prusinkiewicz et al., 1990, Godin et al. 2005).

In this formalism, a plant stem is represented by a string of elementary modules. Consecutive modules in the string correspond to consecutive organs (internode, leaf, flower, meristem) in the stem. Strings can be nested using parentheses to represent plant branching networks of stems. Starting from a string, called the “axiom”, and representing the initial plant apex, the
modeler defines a number of development rules (called *production rules*) that express how apices and other types of organ change throughout time and within its context in the plant. Rewriting rules related to apex productions correspond to plant organogenesis. Rewriting rules related to change of other organs (leaf, internode, flowers, flower organs) express how the shape, volume and orientation of these organs changes according to time and context.

The following pseudo L-system code gives the sketch of the main procedural way to construct the plant developmental timeline using production rules:

```plaintext
1 Axiom : Apex(age=0,stage=0,duration=0,active)
2
3 Apex(age,stage,duration,activity):
4   if duration > max_stage_duration:
5     stage = stage+1
6     duration = 0
7   if stage == 'vegetative' :
8     produce div [ Leaf(age,0) Apex(0,stage,0,dormant) ]
9     produce I(age,0) Apex(age+dt,stage,duration+dt,growing)
10    elif stage == 'mixed' :
11     produce div [ Leaf(age,0) Apex(0,stage,0,growing) ]
12     produce I(age,0) Apex(age+dt,stage,duration+dt,growing)
13    elif stage == 'inflorescence' :
14     produce div [ Apex(0,'flower',0,growing) ]
15     produce I(age,0) Apex(age+dt,stage,duration+dt,growing)
16    elif stage == 'flower' :
17     produce div Flower(0,stage)
18
19 I(age,stage):
20   produce I(age+dt,stage)
21
22 Leaf(age,stage):
23   produce Leaf(age+dt,stage)
24
25 Flower(age,stage):
26   produce Flower(age+dt,stage)
```

The axiom defines the initial state of the plant, here composed of a single apex. Modules (indicated in bold) have parameters that characterize their state in time. Apices are characterized by their age, physiological stage, the duration that they have spent in the current physiological age, and their activity status (here active or dormant). Physiological stage can take the integer values 0 (vegetative), 1 (mixed), 2 (inflorescence), 3 (flower). The initial apex starts to grow at vegetative stage (0).

Then the system proceeds by applying the rewriting rules defined above at while advancing time by dt increments between two steps. At each time step, the system goes through the string of all modules (this characterizes the current system’s state) and applies if possible to each found module the first rewriting rule that matches that module. Hence at time 0, the system finds an Apex in the string of modules (only module in the current string) and applies the rule Apex (starting at line 3) as its left-hand side matches the module’s name Apex of the current string. This will add new modules in the string that will define the system’s state at time t+dt, and that will be processed likewise at subsequent time steps by the system.

Altogether, this procedure constructs a developmental timeline of the entire plant.

**Connection of the plant and organ developmental timelines.** The plant developmental timeline is connected with the timeline of its organs through the age variable. This variable is expressed in the same unit of time as the time defined for the reference developmental timeline.
of the entire plant (the value of this variable is computed within the plant model by adding \( dt \) units at each time step of the organ growth (lines 20, 23 and 26).

Contrary to the plant developmental model that changes of structure in time and must be computed with ‘production rules’ (rules that describe how plant components are produced or change in time), the organ models are much simpler as their basic organization into subcomponents does not change much in time (e.g. a flower always contains a rather invariant organization in terms of sepals, petals, etc) and can be easily re-evaluated at each time step. The geometric shape of the different organs is thus recomputed at each time step simply based on their age, through a mapping between their age as defined by the plant model and their reference developmental timeline. This is done in so called ‘interpretation rules’ (as opposed to production rules) that interpret the L-string symbols in terms of geometric models at each time step.

Let us consider the example of the flower. Several levels of interpretation rules are used to account for the multilevel decomposition of the flower (Fig. 4.A).

The flower module makes a mapping between the plant reference time and the flower reference timeline (corresponding to the module FlowerRef), through a first warping function, using parameters \( \text{flower}_t0, \text{flower}_ymin, \text{flower}_ymax, \text{flower}_T, \text{flower}_n \) that are defined at the application level. These parameters make it possible to control the rapidity of the expansion of the whole flower in time, relative to the date of birth of the flower expressed in plant time units. Then, the module FlowerRef implementing the flower reference developmental timeline in turn combines the different whorl timelines without time warping (assessed as unnecessary in this model). The PetalWhorlRef module itself wraps the developmental time of the petal whorl onto that of its petal components (we have chosen here to wrap all components with the same function).

Finally the PetalRef module implements the petal developmental timeline and maps the petal reference time to that of the geometric model chosen to represent a petal (here a generalized cylinder primitive called sweep). The wrapping is made through parameters \( \text{petal}_t0, \text{petal}_ymin, \text{petal}_ymax, \text{petal}_T, \text{petal}_n \), that are defined at the level of the whole application model and define a reference petal developmental timeline.
Simple organ models
Simple organs (organs that are not further decomposed) such as simple leaves, internodes, petals, stamens, etc. are modeled by a parametric geometric model (here e.g. a sweep model is used for petals). The parameters of the can be a function of time that defines a timeline for each of them (Prusinkiewicz 2018). These functions can be sigmoidal, for instance in the case of internode diameter and length, or not, for instance if a petal first opens and then closes during the day (the petal’s opening angle function would then be increasing first and then decreasing).

Figure 5. Virtual plant constructed with the new HDTW methodology. The model is intended to be geometrically as accurate as required by the application. On the left: Arabidopsis thaliana individual after 30 days of development. On the right: close-up showing the organ details. One can observe the developmental timeline of a flower along each branch from young flowers at the tip to older ones further down the stem.

2. Application: design of a HDTW model for tomato plants

We developed a model of tomato plant growth based on our new HDTW modeling strategy. For this, we had basically to adapt the description of the different developmental timeline constructions to our tomato model. This adaptation comes in two aspects: i) definition of the hierarchy of plant organs specific to the tomato plant, ii) definition of the growth rules (production rules) specific to the growth strategy of tomato plants.

Observation of tomato growth
To construct a HDTW model for the tomato plant, the method consists of describing precisely the different timelines of the tomato plant organs and to wrap them onto each other using the Hill function as described above. Several organs were considered: leaves, internodes, flowers and flower organs (sepals, petals, stamens/carpels, fruits). For each one, a developmental timeline was defined starting at the birth of each organ (age 0) and going up to its death (age 1).
Based on literature data (Chitwood 2019, Barczi 2008, Dong 2008), internet movies (Videos 2020), and our own measurements of developing plants, we first constructed a table gathering the necessary quantitative parameter describing every organ growth used by our model (Table 1).

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<th>Internode</th>
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<th>Sepal</th>
<th>Petal</th>
<th>Stamen/carpel</th>
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*Table 1. Geometric and dynamic parameters necessary to construct a HDTW model of the Tomato plant development.*

Then, we designed developmental rules to describe apical meristem development in tomato plants. Contrary to *Arabidopsis thaliana* whose growth is monopodial (the main apical meristem keeps on functioning and producing all the lateral organs of the main stem), the development of tomato meristems is sympodial. This means that meristems produce rather short shoots made of a few leaves and then differentiate to form a terminal inflorescence, Fig. 6.
Figure 6. (reproduction of part of Fig. 1 in Park et al. 2012). Sympodial growth of a tomato plant stem. (A) the main meristem (Red tissues) becomes an inflorescence (red arrow) meristem. A lateral meristem just below (green tissues) takes over the growth of the main stem and produces a new stem with lateral leaves. (B) schematization of this sympodial growth: the main stem (vertical) is actually the aggregation of several pieces of sympodial shoots (alternating nuances of green). SYM denotes the apical sympodial meristem.

To model sympodial growth, we assumed that shoot apical meristems undergo a series of 3 developmental stages: stage 1 corresponds to a vegetative phase in which meristems are producing lateral leaves, stage 2 corresponds to an inflorescence stage where lateral meristems produce lateral flowers and stage 3, corresponds to production of terminal flowers. Each meristem stays a predetermined amount of plastochrons (average time separating the production of two lateral organs by the apex) in each stage that depends on growth conditions and time, and that contains a part of randomness to allow plants to vary between individuals. Lateral meristems start their own growth after a delay of a few plastochrons (parameter of the model, here fixed to 10 days in the simulations). When an apical meristem differentiates into an inflorescence, the last lateral meristem production acquires the traits of the apical meristem, in particular it is created with developmental stage 1. This makes it possible for lateral production to take over the growth of the previous apical meristem and continue the edification of the main stem.

Growth and plot simulations
Altogether, the model simulates the growth of tomato plants over a period of a few shoots (~40 to 80 days). Fig. 7 illustrates the growth of a typical individual. Starting from the cotyledons (upper row first image), the main apical meristem produces between 7 and 9 leaves (Park et al, 2013 upper row) and then differentiates to inflorescence where it produces a varying number of flowers (upper row last image and bottom row, first image). From a mechanical point of view, we assume that this differentiation induces a loss of tissue rigidity, resulting in an apical part of the stem that becomes more sensitive to gravity. This stronger gravitropism induces the bending of inflorescences (bottom row, first two images). Lateral flowers produced by the
inflorescence then start to grow, open and their carpels transform into fruits (bottom row, first three images). Then, a new shoot starting from the last lateral meristem before the inflorescence start to grow out (bottom row, third image), produces a few leaves and finally terminal inflorescence (bottom row last two images). This sympodial growth could continue likewise for a few additional shoots.

**Figure 7.** Simulation of the growth of a tomato plant. The simulation starts from the cotyledons (upper left) and proceeds by adding leaves along the main stem. After a period of xx days, the apical meristems switches to an inflorescence state and starts to produce flowers that then turn into fruits. Then, a lateral buds takes over and prolongate the main stem growth (bottom line, middle). This apical meristem in turn produces a stem with a few leaves, followed by an inflorescence and a terminal flower.

Fig. 8 shows the final architecture of a couple of individuals after a growth period of 40 days. Different parameters (such as the length of the period spent by meristems in each phase, the possibility for vegetative lateral meristems to grow out themselves even if they are not taking the follow of the leader, the size and orientation of the different organs, their rate of growth, etc.) have been randomized to allow for variations between individuals. The individual in Fig 8.A only displays the geometry of the organs with a uniform color. To create first more realistic rendering, it is possible to add textures on the different organ geometry. Fig 8.B illustrates such a rendering with a texture coming from real tomato leaves projected onto the leaves. A close-up on flower and fruit details (Fig. 9) illustrates the ability of our new methodology to describe fine grain aspects of plant architecture and critical synchronization of their development. Finally, we used out model and a stochastic variation of the growth parameters to generated a plot composed of 35 virtual plants grown over 65 days (Fig. 10). This type of scene will be used in the future scenarios to help the machine learning algorithms to learn how to detect plants and organs in the context of other plants.
**Figure 8.** Results of the HDTW model. A. Simulated tomato plant after 40 days of growth. B. a different simulated tomato plant with leaf textures added.

**Figure 9.** Fruit development simulation. A. Photos of the development of real tomato fruits at different stages of development. B. Simulation of similar stages of development using the virtual plant model.
Deviations in respect to the plans:

No deviations were made with respect to the plan.

Conclusion and next steps:

The HDTW modelling methodology developed during this period, provides us a powerful tool to simulate the development of various plant architectures with realistic geometries. The main advantage of the new method is that it provides us with an hierarchical strategy to construct plants from elementary botanical observations, and a conceptual way to map these botanical descriptions at different levels of organization in the plant and to synchronize them easily. We demonstrated it on monopodial and sympodial growth, two main growth strategies in the plant kingdom. We also showed how this strategy can be used for non-cultivated plants type plants as Arabidopsis thaliana as well as for crop plants.

Now, our next step concerning the development of these virtual models will be twofold. First we will use our strategy to create models of development of other plant species, including both crop and non-crop plants. This will make it possible to produce a first library of plant development models available for and from the ROMI project. This will make it possible to train our machine learning algorithm over a reasonably wide range of plant species (WP6), to test the robustness of both our reconstruction algorithms (WP5) and our adaptive learning algorithms to optimize the discovery of efficient learning viewpoints in plant canopies (WP4). Second we will work and integrate other aspects of photo-realistic rendering of plants. In particular, we will integrate the promising automatic detection and correction algorithms of physical intersection of organs (see for example the flowers and fruit in Fig. 8A). We will also work on the material rendering of the plant organs and of the scene by operating a coupling between our simulation tools and powerful rendering tools such as Blender (https://www.blender.org) to achieve high quality photo-realistic rendering from virtual plants.
BIBLIOGRAPHY and TECHNICAL ANNEXES


HSP70


Videos 2020: Films (available on internet) on tomato growth used for calibrating our tomato plant development simulations:

- https://www.youtube.com/watch?v=31us20fy6sw
- https://www.youtube.com/watch?v=dTo19IRiZyE
- https://www.youtube.com/watch?v=LICDb8nM5rs
- https://www.youtube.com/watch?v=3z0pZbskMM