

Book of Abstracts

Editors

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FSPM2023
March 27-31 2023, Berlin Germany



Book of Abstracts of the 10th International Conference on Functional-Structural Plant Models:
FSPM2023, 27- 31 March 2023. Eds. Tsu-Wei Chen, Andreas Fricke Katrin Kahlen & Hartmut Stützel.

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Welcoming address

Dear colleagues and friends,

It is with great pleasure to welcome you to the 10th International Conference on Functional-Structural Plant Modelling (FSPM2023), to be held at Humboldt Universität zu Berlin, Germany, from March 27-31, 2023. It is especially great to have a physical conference after the last online events FSPM2020. It allows for meaningful in-person interactions and networking opportunities that cannot be replicated online.

FSPM has been at the forefront of plant modelling research and has played a key role in advancing our understanding about the triple-interactions and coordination between plant structure, functions and environments. At this year's conference, we are honored to have Przemyslaw Prusinkiewicz to open the conference with his keynote speech. His pioneering work in the development of L-systems and their applications in plant modeling has paved the way for many significant advancements in the field. Przemyslaw Prusinkiewicz's work has been widely recognized and celebrated, and his contributions have inspired and influenced many researchers, including myself, and students in FSPM. In addition to Prusinkiewicz, other seven keynote speeches will cover a range of topics including using prior knowledge to predict plant phenotype (Christine Beveridge), the power of plant images in the age of deep learning (Andrew French), understanding plant morphogenesis and actuation through engineering methods (Anja Geitmann), phenotyping photosynthesis and stomatal kinetics in leaf and non-foliar tissue (Tracy Lawson), exploring the variation within canopies in controlled environment agriculture (Leo Marcelis), applying robotic vision systems to agriculture (Christopher McCool), and scientific workflows for model-assisted high-throughput phenotyping (Christophe Pradal). The keynote speakers are all renowned experts in their interdisciplinary fields where various disciplines such as plant biology, mathematics, computer science, physics, and engineering are combined.

Besides the keynote speeches, the conference program is packed with 45 exciting oral talks, 48 poster presentations, workshops, and social events that cater to different interests and backgrounds. These presentations will include the use of functional-structural plant models to explore the impacts of climate change on plants, root-shoot interactions, plant-plant competition and the development of new modelling tools, software and techniques for simulating plant growth and development.

We would like to express our gratitude to our sponsors, German Research Foundation (DFG, project number 517091044) and the journal *in silico Plants*, who have generously supported FSPM2023 and made this conference possible. We would also like to take this opportunity to thank our Program Committees to design the program and Scientific Committees to review the abstracts.

Finally, whether you are an advanced researcher or a newcomer to the field, we hope that this year's conference will provide you with a stimulating environment to engage with other researchers, to share ideas and insights and to get a wealth of new research questions and

collaborating from around the world. Thank you for your participation and we hope to make this conference an unforgettable experience for everyone involved.

Sincerely,

Tsu-Wei Chen¹, Andreas Fricke², Katrin Kahlen³, Susann Müller¹ and Hartmut Stützel²
Organizers FSPM2023

¹ Humboldt Universität zu Berlin

² Leibniz Universität Hannover

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Program

Sunday (26. March)

Foyer

17:00-20:00 Welcome reception

Monday (27. March)

Room 1.101

8:00-09:00 Registration

9:00-9:10 Opening session with editors of “in silico Plants”

Session: General theory

Chair: Jochem Evers

9:10-9:50 **Keynote: Przemyslaw Prusinkiewicz** **K01** Experimental data, computational models, and theorems about plants

9:50-10:10 Romain Barillot **O01** Representation and functions of shoot apical meristems in FSPMs

10:10-10:30 Jorad de Vries **O02** Virtual forests under pressure: modelling tree form and function under climate change

10:30-11:00 **Coffee break**

Session: Shoot-root interaction

Chair: Jochem Evers

11:00-11:20 Guillaume Lobet **O03** Quantitative multi-scale analysis of water flow determinants in the soil-root system

11:20-11:40 Mona Giraud **O04** Simulation of the interactions between plant growth and carbon and water fluxes in the soil-plant-atmosphere continuum

11:40-12:00 Adrien Heymans **O05** Modelling root plastic responses to soil water status heterogeneity

12:00-13:30 **Lunch**

Session: Branching

Chair: Katharina Streit

13:30-14:10 **Keynote: Christine Beveridge** **K02** Using prior knowledge to build predictive models for plant success

14:10-14:30 Mik Cieslak **O06** Modeling phenotypic diversity of woodland strawberry inflorescences

14:30-14:50 Nicole Fortuna **O07** Using the emergent properties of network topologies to predict branching phenotypes

14:50-15:20 **Coffee break**

Session: Diverse topics**Chair: Katharina Streit**

15:20-15:40	Frédéric Rees	O08 Quantitative importance of various rhizodeposition processes: lessons from a mechanistic functional-structural root model
15:40-16:00	Ep Heuvelink	O09 Bridging the gap between genotype and phenotype by combining crop models with quantitative genetics
16:00-17:10	Poster flash talks	(2 min per poster)
17:10-19:00	Poster presentation Room 1.103 & 1.401	

Tuesday (28. March)**Room 1.101**

08:00-09:00 Registration

Session: Biophysics and tissue expansion**Chair: Evelyne Costes**

9:00-9:40	Keynote: Anja Geitmann	K03 Plants in motion - using engineering methods to understand plant morphogenesis and actuation
9:40-10:00	Valentin Couvreur	O10 Non-invasive water flow imaging in plant roots at cellular resolution
10:00-10:20	Tom De Swaef	O11 Decomposing grass leaf elongation rate: hydraulics, visco-elasticity and ontogeny
10:20-10:50 Coffee break		

Session: Plant-plant interaction**Chair: Evelyne Costes**

10:50-11:10	Rik Rutjens	O12 Simulating common bean in a three sisters polyculture using GroIMP
11:10-11:30	Jorad de Vries	O13 Unravelling drivers of local adaptation through evolutionary functional-structural plant modelling
11:30-11:50	Gaëtan Louarn	O14 Modelling the impact of intraspecific genetic diversity on the botanical composition of forage mixtures
12:00-13:30 Lunch		

Session: Robotics and point cloud**Chair: Mikolaj Cieslak**

13:30-14:10	Keynote: Christopher McCool	K04 Exploiting spatial-temporal information in robotic vision systems: with applications to agriculture
14:10-14:30	Brian Bailey	O15 Enabling high-throughput field phenotyping of whole-plant physiology via FSPM
14:30-14:50	Alvaro Lau Sarmiento	O16 Use of LiDAR data for the design of functional-structural plant models of tropical trees
14:50-15:20 Coffee break		

Session: FSPM and tree**Chair: Mikolaj Cieslak**

15:20-15:40	Inigo Auzmendi	O17 Using FSPM to understand the physiological mechanisms that reduce fruit yield in high planting density orchards
15:40-16:00	Frédéric Boudon	O18 Integrating the effect of light quantity and quality in the V-Mango model to optimize cultural practices
16:00-16:20	Raphaël Perez	O19 Testing the capacity of an oil palm FSPM to simulate changes in water and carbon dioxide fluxes under a climate change context
16:20-16:40	Jochem Evers	O20 Simulating pruning responses in a FSP model of cocoa
16:40-17:00	Peige Zhong	O21 An evaluation of light distribution and light interception efficiency within Chinese bayberry tree canopy
17:00-19:00	Poster presentation Room 1.103 & 1.401	

Wednesday (29. March)**Room 1.101**

08:00-09:00 Registration

Session: Digital twin I**Chair: Tom de Swaef**

9:00-9:40	Keynote: Leo Marcelis	K05 Crop models in controlled environment agriculture: exploring the variation within canopies
9:40-10:00	Christopher Bahr	O22 Towards berry sunburn simulations with the functional-structural plant model <i>Virtual Riesling</i>
10:00-10:20	Arnaud Bouvry	O23 Digital twin of an indoor plant phenotyping facility: use of high frequency aerial biomass monitoring for improved data assimilation between measured and simulated point cloud data in the CPlantBox FSPM

10:20-10:50 Coffee break

Session: Digital twin II**Chair: Tom de Swaef**

10:50-11:10	Katarina Streit	O24 From functional-structural tomato model to tomato digital twin
11:10-11:30	Abderrahman Sghaier	O25 A turgor-driven functional-structural model of spring wheat development for vertical farming and extra-terrestrial life support systems
11:30-11:50	Christophe Godin	O26 Hierarchical developmental timeline warping: a generic method to design realistic plant architecture models
12:00-17:30	Excursion with lunch box	

18:30-22:30 Conference dinner

Thursday (30. March)**Room 1.101****08:00-09:00** Registration**Session: Software I****Chair: Guillaume Lobet**

9:00-9:40	Keynote: Christophe Pradal	K06 Data-intensive scientific workflows for model-assisted high-throughput phenotyping
9:40-10:00	Andrea Schnepf	O27 Benchmarking of functional-structural root architecture models
10:00-10:20	Winfried Kurth	O28 The FSPM platform GroIMP, its ongoing upgrading and some new extensions and plugins

10:20-10:50 **Coffee break****Session: Software II****Chair: Guillaume Lobet**

10:50-11:10	Thomas Arsouze	O29 MacS4Plants: A mathematic & computer science network for FSPM
11:10-11:30	Rémi Vezy	O30 PlantBiophysics.jl: a Julia package for fast and easy calibration, prototyping and simulation of biophysical models
11:30-11:50	Olivier Pieters	O31 Comparing FSPMs using unconventional computing methods
12:00-12:20	Christophe Godin	O32 Exploring symmetries in plant architectures

12:20-13:30 **Lunch****Session: Phenotyping I****Chair: Brian Bailey**

13:30-14:10	Keynote: Andrew French	K07 Data is everything: the power of plant images in the age of deep learning
14:10-14:30	Bolai Xin	O33 Realtime input of sensor-based phenotypic traits for functional-structural plant modelling of tomato
14:30-14:50	Romain Fernandez	O34 High-throughput 2D+t root system architecture reconstruction and modelling from time-lapse phenotyping data

14:50-15:20 **Coffee break****Session: Phenotyping II****Chair: Brian Bailey**

15:20-15:40	Celine Mercier	O35 From tree growth modelling to synthetic point clouds: applications to data science
15:40-16:00	Katarina Streit	O36 Towards automated functional-structural plant model parameterisation
16:00-16:20	Lim Chi Wan	O37 Species model parameterisation
16:20-16:40	Francesca Grisafi	O38 Analysing the architecture of <i>Corylus avellana</i> and parametrizing L-HAZELNUT FSPM
16:40-17:00	Jie Lu	O39 Optimizing plant traits for efficient nitrogen use in maize using functional-structural plant modelling

17:00-18:00 **FSPM-Forum**

18:00-20:00 Parallel software presentation

Alejandro Morales Room 1.402	S01 The Virtual Plant Laboratory: developing, simulating, and visualizing functional-structural plant models in the Julia programming language
Tim Oberländer Room 1.403	S02 Making the FSPM platform GroIMP better accessible for non-modelers
Benjamin Spehle Room 1.404	S03 Conveying the effects of climate change - interfacing Virtual Riesling with an interactive R shiny application
Andrea Schnepf Room 1.405	S04 Hands on FSPM with CPlantBox

Friday (31. March)**Room 1.101**

08:00-09:00 Registration

Session: Photosynthesis**Chair: Katrin Kahlen**

9:00-9:40	Keynote: Tracy Lawson	K08 Phenotyping photosynthesis and stomatal kinetics in leaf and non foliar tissue
9:40-10:00	Jan Graefe	O40 Identification of various supplementary parameters of a recent extended model of C ₃ leaf photosynthesis from many CO ₂ response curves
10:00-10:20	Mathilde Millan	O41 Impact of leaf angle orientation on gas exchange and leaf temperature on a grapevine population using HydroShoot, a functional structural model

Coffee break**Session: Coupling carbon and water****Chair: Katrin Kahlen**

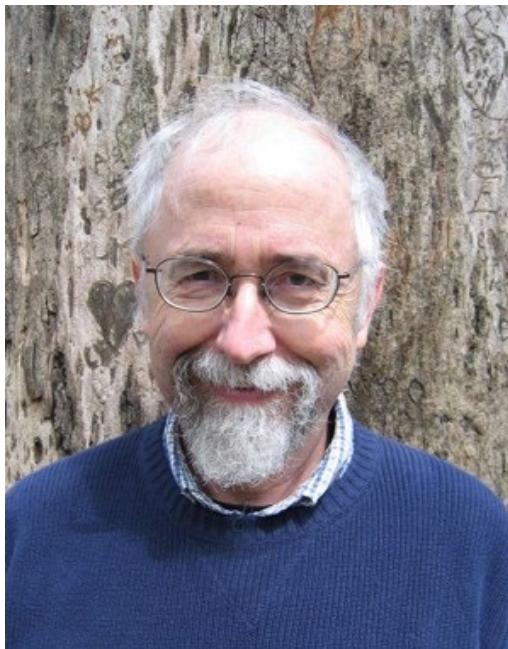
10:50-11:10	Sarah Verbeke	O42 Turgor-driven water flow and carbohydrate storage in wheat stems increase hydraulic capacitance during drought
11:10-11:30	Victoria Acker	O43 Simulation of leaf growth response to elevated [CO ₂] using CN-Wheat, a model of morphogenesis driven by trophic dynamics
11:30-11:50	Annette Manntschke	O44 Architectural plasticity in response to plant density increases canopy light interception
11:50-13:00	Lunch	
13:00-13:30	Closing session & Poster award ceremony	With Editors of <i>in-silico Plants</i> about publishing Special Issue

Keynote speakers

Mon, 27. March, 9:00-9:40

K01 Przemyslaw Prusinkiewicz: Experimental data, computational models, and theorems about plants

University of Calgary



Short Bio: Przemyslaw Prusinkiewicz is a Professor Emeritus of Computer Science at the University of Calgary, Canada. He is a pioneer of computational modeling, simulation and visualization of plant development. His current research is focused on computational models of development that link molecular-level processes to macroscopic plant forms. Professor Prusinkiewicz is a Fellow of the Royal Society of Canada, a honorary member of Polish Botanical Society, and a recipient of the Association for Computing Machinery SIGGRAPH Achievement Award and the Canadian Human Computer Communications Society Achievement Award for his work on plant modeling.

Abstract: I will present a perspective on the role of models and mathematical reasoning in studies of plant development, focusing on the multiple connections between biology and geometry. The emphasis will be on the 20th and 21st century mathematics that significantly extends concepts already recognized as relevant to biology, such as fractals and L-systems. In this context, I will show how the theories of quasicrystals, aperiodic patterns and point distribution (the three gap theorem) are contributing to our understanding of the phyllotaxis and structure of flower heads. Interestingly, some precursors of these theories appeared in biological literature before they became the subject of mathematical studies that are now used to further advance biology.

Twitter account: <https://twitter.com/pprusinkiewicz>

List of three indicative publication:

T. Zhang, M. Cieslak, A. Owens, F. Wang, S. K. Broholm, T. H. Teeri, P. Elomaa, **P. Prusinkiewicz**. Phyllotactic patterning of gerbera flower heads. *Proceedings of the National Academy of Sciences USA* 118(13), e2016304118, 2021.

P. Prusinkiewicz, T. Zhang, A. Owens, M. Cieslak, P. Elomaa. Phyllotaxis without symmetry: what can we learn from flower heads? *Journal of Experimental Botany*, erac101, 2022.

J. Battjes, **P. Prusinkiewicz**. Modeling meristic characters of Asteracean flowerheads. In R. V. Jean and D. Barabé (Eds.): *Symmetry in Plants*, World Scientific, Singapore, 1998, pp. 281-312.

Mon, 27. March, 13:30-14:10

K02 Christine Beveridge: Using prior knowledge to build predictive models for plant success

ARC Centre for Plant Success in Nature and Agriculture, University of Queensland



Short Bio: Prof Christine Beveridge graduated with a BSc (Hons) and PhD in Plant Science at the University of Tasmania in 1994. After a two-year Postdoctoral Fellowship at the National Institute of Agricultural Research (Versailles, France) Christine took up a competitive University of Queensland (UQ) Fellowship, then an Australian Research Council (ARC) Postdoctoral Fellowship, teaching and research positions, an ARC Future Fellowship and Deputy Dean and Associate Dean Research (Science) position at UQ. Christine is now the Director of the ARC Centre of Excellence for Plant Success in Nature and Agriculture (CoE), a Fellow of the Australian Academy of Science, an

ARC Georgina Sweet Laureate Fellow and a highly cited researcher. Christine was both the first female and first Australasian president of the International Plant Growth Substances Association and is a Life Member of the Australian Society of Plant Scientists. Christine discovered strigolactone as a plant hormone and that sugar signalling is a driver of shoot branching. Christine founded the CoE of 175 members including 17 Chief Investigators across five Universities to enhance the use of prior knowledge in breeding, enhance food diversity, and to promote an inclusive interdisciplinary research culture to future proof Australian agriculture, biodiversity and sustainability.

Abstract: The plant phenotype is the emergent property of a huge number of interactions among environment, life history, internal signals (e.g., hormones) and genome. For this reason it is challenging to predict the phenotype of plants. We seek a step-wise manner in which to use diverse prior knowledge to build models that can enhance our ability to predict plant phenotype for benefit in fundamental science, crop improvement and the understanding of evolution. This presentation will focus on our related work in modelling shoot branching.

Twitter account: <https://twitter.com/cabeveridge29>

List of three indicative publications:

Powell, O. M., F. Barbier, K. P. Voss-Fels, C. **Beveridge** and M. Cooper (2022). Investigations into the emergent properties of gene-to-phenotype networks across cycles of selection: A case study of shoot branching in plants. *in silico Plants* 4(1): diac006. Bertheloot J, Barbier F, Boudon F, Perez-Garcis MD, Péron T, Citerne S, Dun E, **Beveridge** C, Godin C, and Sakr S (2020). Sugar availability suppresses the auxin-induced strigolactone pathway to promote bud out-growth. *New Phytologist* 225:866-879.

Dun EA, Hanan J, **Beveridge CA** (2009) Computational modeling and molecular physiology experiments reveal new insights into shoot branching in pea. *Plant Cell* 21: 3459-3472.

Tue, 28. March, 9:00-9:40

K03 Anja Geitmann: Plants in motion - using engineering methods to understand plant morphogenesis and actuation

McGill University



Short Bio: Dr. Geitmann's research focuses on the cellular processes driving plant reproduction and morphogenesis. She holds the Canada Research Chair in Biomechanics of Plant Development and leads an interdisciplinary team of biologists and engineers. Her research combines cell biology with high-end imaging, micromanipulation, and computational modeling to study the mechano-structural underpinnings of plant functioning. Dr. Geitmann has served as the President of the International Association of Plant Reproduction Research, the Microscopical Society of Canada and the Canadian Society of Plant Biologists. She serves on the editorial boards of multiple scientific journals including *Cell* and *Plant Physiology*.

Abstract: During the plant's life cycle, organs and tissues change shape and deform both elastically and plastically. Permanent shape change is characteristic of plant growth processes whereas reversible (elastic) behavior is typically associated with responses to environmental triggers. Both behaviors rely on mechanical processes involving the cell wall and turgor pressure. Through computational modeling and micromechanical testing we interrogate the mechanical underpinnings of these processes.

Twitter account: <https://twitter.com/GeitmannLab>

List of three indicative publication:

- Sleboda DA, **Geitmann A**. Sharif-Naeini R. 2022. Multiscale structural control of hydraulic bending in the sensitive plant *Mimosa pudica*. bioRxiv doi.org/10.1101/2022.02.28.482281
Bidhendi AJ, Altartouri B, Gosselin FP, **Geitmann A**. 2019. Mechanical stress initiates and sustains the morphogenesis of wavy leaf epidermal cells. *Cell Reports* 28: 1237-1250
Bidhendi AJ, **Geitmann A**. 2018. Finite element modeling of shape changes in plant cells. *Plant Physiology* 176: 41-56

Tue, 28. March, 13:30-14:10

K04 Christopher McCool: Exploiting spatial-temporal information in robotic vision systems: with applications to agriculture

University of Bonn



Short Bio: Chris is a Professor at the University of Bonn and leads a group which develops robotic vision algorithms that enables robots and autonomous systems to work in challenging environments (especially agriculture). Prof. McCool received his PhD in 2007 from the Queensland University of Technology (QUT), Australia. He has previously worked at the Idiap Research Institute (Switzerland), National ICT Australia and the Queensland University of Technology (Australia).

Abstract: Robotic platforms are designed to traverse an environment in order to automate tasks such as crop or plant monitoring. Current approaches to crop monitoring are dominated by deep learning approaches that generally use snapshots, or still images, of the scenes. Despite the success of these approaches there are also major limitations. In this presentation, I will discuss recent developments in the robotic vision systems at the University of Bonn which exploit the fact that we have a robot moving in the field. This enables us to exploit a rich set of both spatial and temporal information, available from robots, which can be used to enhance vision systems to provide greater and more accurate information.

List of three indicative publication:

- C. Smitt, M. Halstead, A. Ahmadi, and **C. McCool**, “Explicitly incorporating spatial information to recurrent networks for agriculture”, accepted to Robotics and Automation Letters, 2022.
- M. Halstead, A. Ahmadi, C. Smitt, O. Schmittmann, and **C. McCool**, “Crop Agnostic Monitoring Driven by Deep Learning”, Frontiers in Plant Science, 2021.
- A. Ahmadi, M. Halstead, and **C. McCool**, “Virtual Temporal Samples for Recurrent Neural Networks: applied to semantic segmentation in agriculture”, GCPR/DAGM, 2021.

Wed, 29. March, 9:00-9:40

K05 Leo Marcelis: Crop models in controlled environment agriculture: exploring the variation within canopies

Wageningen University, The Netherlands



Short Bio: Prof dr Leo Marcelis is head of the chair group Horticulture and Product Physiology at Wageningen University. Leo has a strong background in plant physiology, crop monitoring, computational modelling and experimentation. He has extensively studied the physiology, growth and development of plants in order to improve sustainability and quality of crop production in greenhouses and vertical farms. In particular fluxes of assimilates,

water and nutrients in the plant, sink/source interactions and partitioning among plant organs in response to abiotic conditions (including LED lighting) are subject of study.

Abstract: This presentation will describe some approaches for mechanistically simulating growth, development and plant architecture of greenhouse-grown crops in response to abiotic constraints. Some examples of exploring the variability of light distribution and photosynthesis within canopies will be shown; this will include examples of different row orientation or different types of LED lighting. It will be discussed how these models may be used for prediction and planning of production, decision support systems, control of the greenhouse climate, supply of water and nutrients, and phenotyping. It will be discussed how models help us in exploring new avenues, and how the combination of models and sensors is powerful in both monitoring and phenotyping.

Twitter account: <https://twitter.com/leomarcelis>

List of three indicative publication:

Schipper, R., van der Meer, M., de Visser, P.H.B., Heuvelink, E., and **Marcelis L.F.M. 2023.** Consequences of intra-canopy and top LED lighting for uniformity of light distribution in a tomato crop. *Frontiers in Plant Science* 14:1012529

Van Der Meer, M., De Visser, P. H. B., Heuvelink, E. & **Marcelis, L. F. M.** 2021. Row orientation affects the uniformity of light absorption, but hardly affects crop photosynthesis in hedgerow tomato crops. *in silico Plants*. 3, 2, diab025.

Zhang, N., Van Westreenen, A., Evers, J. B., Anten, N. P. R. & **Marcelis, L. F. M.** 2020. Quantifying the contribution of bent shoots to plant photosynthesis and biomass production of flower shoots in rose (*Rosa hybrida*) using a functional-structural plant model. *Annals of Botany*. 126, 4, p. 587-599

Thu, 30. March, 9:00-9:40

K06 Christophe Pradal: Data-intensive scientific workflows for model-assisted high-throughput phenotyping

CIRAD & inria, Montpellier



Short Bio: Christophe is a Senior Researcher at CIRAD, Montpellier and an associate researcher at inria. He co-leads the interdisciplinary group PhenoMen at the crossroads of Data science (modeling & phenotyping), ecophysiology and agro-ecology in the AGAP Institute with Christine Granier. In the last 20 years, he has worked in the FSPM community, leading the OpenAlea platform, and designing models, algorithms and data structures in plant phenotyping and modelling at different scales. He served during 5 years as an associate editor of *Plant Methods*.

Abstract: High-throughput phenotyping platforms allow the study of the form and function of a large number of genotypes subjected to different growing conditions (GxE). Automatic computational pipelines for phenotyping are able to characterize the structure and the development of plants at an unprecedented resolution. Scientific workflows are a way to schedule these complex pipelines on distributed cloud infrastructure, to manage the huge amount of data and to enhance the reproducibility of such experiments. In this presentation, I will discuss the recent developments in root and shoot phenotyping methods, how it challenges FSPM formalisms and platforms, and how scientific workflows management system can help to improve the connection between phenotyping and modelling communities while reducing the processing and environmental cost of the computation.

Twitter account: <https://twitter.com/agapinstitut> #PhenomenTeam

List of three indicative publications:

- G. Heidsieck, D. De Oliveira, E. Pacitti, **C. Pradal**, F. Tardieu, P. Valduriez (2021). Cache-aware scheduling of scientific workflows in a multisite cloud. Future Generation Computer Systems, 122, 172-186.
- B. Daviet, R. Fernandez, L. Cabrera-Bosquet, **C. Pradal***, C. Fournier* (2022). PhenoTrack3D: an automatic high-throughput phenotyping pipeline to track maize organs over time. bioRxiv.
- H. Takahashi, **C. Pradal** (2021). Root phenotyping: important and minimum information required for root modeling in crop plants. Breeding Science, 71(1), 109-116.

Thu, 30. March, 13:30-14:10

K07 Andrew French: Data is everything: the power of plant images in the age of deep learning

Computer Vision Lab, University of Nottingham



Short Bio: Andrew is a Professor of Computer Science at the University of Nottingham, where he co-leads the Computer Vision Laboratory. For 15 years he has worked closely with the plant science community, developing software tools and new data analysis approaches, looking at plants from the cell to the field scale. Deep machine learning drives much of the image analysis in the lab today. Andrew currently leads a project developing data science training for plant phenotyping (DataCAMPP – Training in Data Capture, Analysis and Management for Plant Phenotyping).

Abstract: Deep learning has unquestionably changed the way we use predictive modelling in plant science. For ten years, deep models in the form of convolutional neural networks have been conceived, developed and refined, to the point where we now have a suite of powerful models for most common phenotyping tasks. But the problem is not solved. The more powerful the model, the greater the demands on the datasets on which they must be trained. This has never been more true than with the latest advances in transformer models, which are largely pretrained on enormous datasets. This talk will concentrate on the data side of the deep learning coin, and will look at some novel ways of boosting data set sizes we have developed at Nottingham.

List of three indicative publication:

Ganana: unsupervised domain adaptation for volumetric regression of fruit. ZKJ Hartley, AS Jackson, M Pound, **AP French**. Plant Phenomics (2021)

Domain adaptation of synthetic images for wheat head detection. ZKJ Hartley, **AP French**. Plants 10 (12), 2633 (2021)

Learning to Localise and Count with Incomplete Dot-annotations. F Chen, MP Pound, **AP French**. Proceedings of the IEEE/CVF International Conference on Computer Vision (2021)

Fri, 31. March, 9:00-9:40

K08 Tracy Lawson: Phenotyping photosynthesis and stomatal kinetics in leaf and non foliar tissue

University of Essex



Short Bio: Tracy is Group Convener, Director of Plant Phenotyping and Director of Impact at Essex, with over 25 years' experience in photosynthesis research. Her research focuses on the stomatal control of atmospheric gas entry into the leaf, associated water loss and the mechanisms that regulate this process. Recent research has paid particular attention to stomatal kinetics and the impact of dynamic environments on both photosynthesis and stomatal behaviour. Tracy's work also

concentrates on phenotyping including chlorophyll fluorescence techniques (for quantifying light use and photosynthetic efficiency) and thermal imaging (for measuring stomatal responses and kinetics). Lawson's lab developed the first imaging system for screening plant water-use-efficiency (McAusland et al., 2013).

Abstract: In order for leaf photosynthesis to take place CO₂ must enter the leaf through adjustable pores, called stomata, and at the same time water is lost through these pores which also aids in cooling of the leaf. As stomatal behaviour controls photosynthesis, water loss and leaf temperature these pores are an unexploited but important targets for manipulation to improve crop productivity. Stomata are found on both leaf and non-leaf material in significant and differential numbers. Here we use chlorophyll fluorescence imaging and thermograph to explore the role of stomata in gaseous exchange and evaporative cooling for improved photosynthesis under different climatic conditions.

Twitter account: <https://twitter.com/drtracylawson>

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Representation and functions of shoot apical meristems in FSPMs

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Functional Structural Plant Models (FSPMs) are individual-based models that explicitly account for the interactions between plant architecture and its abiotic and biotic environment. Plant morphogenesis, growth and grain or fruit production are among the most represented processes in FSPMs. These biological processes are largely determined at the Shoot Apical Meristem (SAM) level as it drives the rate of leaf initiation, phyllotaxy, leaf geometry, floral induction and the production of reproductive organs. Nevertheless, not all FSPMs are based on an explicit representation of SAMs, their functioning is then ignored in the case of non-dynamic models or embedded in parametric or statistical functions of plant morphogenesis in dynamic models. For FSPMs that include an explicit representation of SAMs, they are mainly constructed on the L-systems formalism, which is well suited to describe plant development (Boudon et al., 2012). First, one of the main functions of SAMs in these FSPMs is the production of new leaves or growth units, usually at a constant rate expressed in thermal unit. In some cases, the rate of leaf production by SAMs is coordinated with the rate of leaf emergence, leading to the concept of self-regulated architecture. However, the effect of substrate or water availability on the functioning of the SAM in terms of the size or properties of the emitted primordia is not accounting for. Secondly, the representation of apices in models is also used to simulate axillary bud break and the production of tillers, branches or new growth units. In these cases, the transition from a latent to an active SAM is controlled by light intensity and its spectrum (Verdenal et al., 2008; Faverjon et al., 2019), or temperature or hormones (Prusinkiewicz et al., 2009) or is based on stochastic approaches. Finally, some FSPMs also account for the production of reproductive organs like grains and fruits by SAMs (Boudon et al., 2020; Rouet et al., 2022). Nevertheless, this aspect of SAM functioning remains poorly described in FSPMs despite its importance in plant production, yield and ecology. We believe that a better integration of SAMs functioning and control in FSPMs is a promising way to assess functional hypotheses and predict plant plasticity to the environment.

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Virtual forests under pressure: modelling tree form and function under climate change

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Keywords: drought, forest management, carbon allocation, water balance

Introduction

In recent years, we have seen an increase in the strength and frequency of droughts as a result of climate change. These droughts shape the composition, structure and functioning of forest ecosystems by reducing tree growth and increasing tree mortality (McDowell *et al.*, 2020). In turn, the composition, structure and functioning of forest also mediate drought impacts, which are more pronounced in dense stands where competition for resources is strong, and are alleviated in open stands where limiting resources are spread over fewer individuals. However, these interactive effects between the abiotic environment and forest structure are poorly understood, which is a major knowledge gap that limits predicting the future of forests under climate change (Trugman *et al.*, 2021).

Methods and Results

Most current forest models either do not explicitly consider mechanisms that act on the individual tree level and its local environment or do not consider vegetation level processes, thereby neglecting potential interaction effects that cross spatial scales. This calls for the development of novel modelling approaches that scale from individual tree form and function to community-level dynamics (Keane *et al.*, 2015). We developed such a novel functional-structural tree (FSTree) model that simulates interactions between individual tree form and function and the local environment on a daily time scale, and scales from individuals to forests and from days to years. The model incorporates detailed submodels of light interception, photosynthesis, water dynamics, and carbon allocation to calculate individual tree growth and survival, and used allometric relations to translate these functional model components into tree structure.

To calibrate and validate this modelling approach, we use empirical data collected during the establishment of a large-scale forest experiment in the Netherlands in 2019. This experiment consists of fifteen 1-ha forest plots that are situated on poor sandy soils, with 5 replicate plots dominated by beech (*Fagus sylvatica*), 5 by Douglas fir (*Pseudotsuga menziesii*) and 5 by Scots pine (*Pinus sylvestris*). For model parameterisation, we used tree-level data on allometric relations and tree physiology, as well as plot-level data on tree density and stem diameter distributions. To validate model output, we used sapwood growth from tree-ring cores, which showed significant effects of species, rainfall and temperature on sapwood growth. Taking daily weather data over the past 28 years (1990-2018) as input, the model was able to match both the species and environment effects found in the tree ring data. In particular, the model was able to reproduce the growth in exceptionally dry years (i.e. 1996 and 2018), showing its potential to simulate the effects of climate change on tree growth.

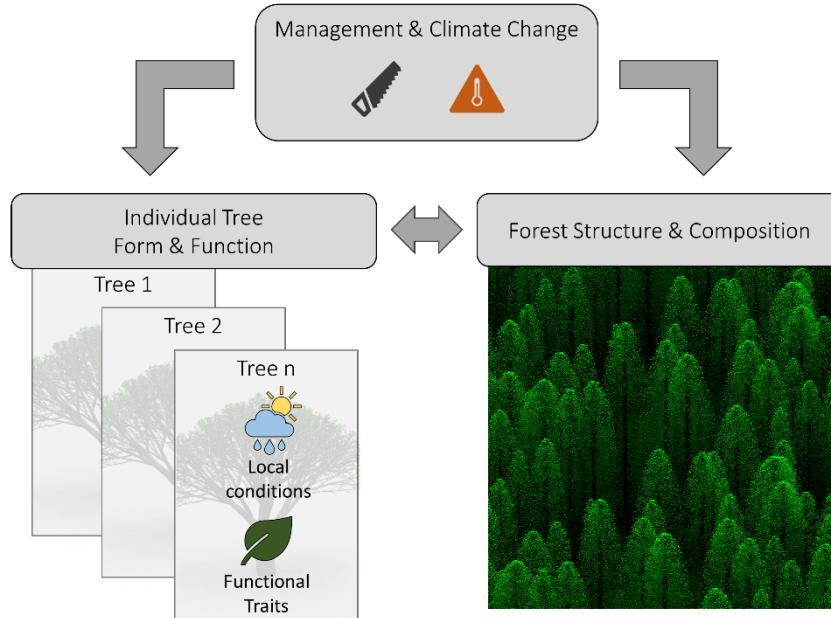


Figure 1. To predict the management and climate change impacts requires an individual based forest model that scales from individual tree form and function to forest structure and composition.

Future Perspectives

The forest experiment that was established in 2019 is unique in its setup and spatial scale; in each of the 15 plots, stand density treatments have been applied to four ¼-ha subplots: clear-cut (all trees removed), shelterwood-system (~2/3 removed), high-thinning (~1/3 removed), and control (no removal). The forest experiment is currently used to monitor forest structure, tree-level functional traits, growth and water fluxes, and the water status, carbon content and nutrient stocks of the soil. This offers a unique dataset that links tree growth to forest structure and the subsequent heterogeneity in resource distribution, allowing us to further develop, calibrate and validate the FSTree model to accurately simulate the interactions between tree growth, the abiotic environment and forest structure. We then aim to use this model to improve predictions of long-term climate change impacts on temperate forests, and offer a tool to assess the effectiveness of management interventions aimed at mitigating these climate change impacts (Sterck *et al.*, 2021).

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Quantitative multi-scale analysis of water flow determinants in the soil-root system

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Keywords: root, sensitivity analysis, architecture, anatomy, hydraulics

Finding plants that are well adapted hydraulically to specific pedo-climatic environments is aimed for present and future yield improvement and increasing the sustainability of our crop systems. Cultivated plants that have been selected through traditional farming systems in a region are most likely to express very different root anatomies and root hydraulic properties from place to place. These germplasms may have developed a root system hydraulic architecture particularly adapted in their location. A better understanding of the underlying properties could be put at use to target strategies, if needed, which could increase their water uptake in these specific environments.

Here, we associated different models into a structured network (figure 1) to virtually simulate water flow in the soil-root system over 30 days of crop development. This pipeline was built so we could pinpoint specific root anatomical traits, sub-cellular hydraulic properties and maturation rate which could improve the root water uptake in a chosen pedo-climatic environment. We tested this hypothesis on maize plants (*Zea mays* variety B73) and in three pedological conditions under a high evaporative demand and water limiting conditions. We generated 7168 maize plants from a single set of architecture traits but varying sets of anatomical traits, sub-cellular hydraulic properties and maturation rates and analysed their root water uptake dynamics in all three environments.

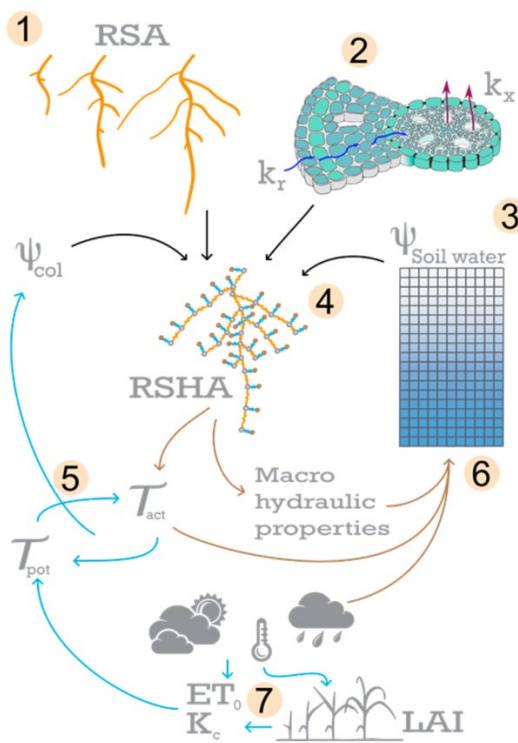


Figure 1 : Overview of the virtual phenotyping pipeline for root water uptake (Hydraulic Viper). (1) Generation of the root system architecture (RSA) (Schnepf et al. 2018); (2) association of the k_r and K_x , on the root types axis (Heymans et al. 2021, 2020); (3) simulation of an initial soil water profile ($\Psi_{soil,water}$); (4) Solving the root system hydraulic architecture (RSHA); (5) comparison between the root water uptake rate (T_{act}) with the potential water demand (T_{pot}). If needed, update of the collar water potential (Ψ_{col}); (6) updated the soil water profile based on the implicit root water uptake model, and the atmospheric data. From this point, there is a loop on the soil water profile and the RSHA. (7) The atmospheric data were used to estimate the evapotranspiration rate of reference (ET_0) and the Leaf Area Index (LAI). From the LAI, the crop coefficient (K_c) was estimated which was used to estimate the T_{pot} .

We identified that the root radius of zero-order roots were the most influencing variables over the root water uptake of these *in silico* phenotypes. The phenotypes with a high contribution of aquaporins to the cell membrane permeability and short delay between the suberin deposition and the maturation of the meta-xylem vessels increased their root water uptake when water was available. In each of the three environments, we observed significant differences in terms of root radii optimum when aiming for phenotypes which expressed high cumulative water uptake and high cumulative water uptake per unit of root volume. Next, we generated three batches of 56 new plants designed for each one of the three tested environments. They were able to take up high amount of water in total, at a low carbon cost.

Therefore, using our new modelling pipeline, it was possible to estimate potential optimum traits depending on pedo-climatic constraints. These early *in silico* results suggest that root radii, the contribution of aquaporins to the cell membrane permeability, and maturation rates are important traits to target when looking for adapted traits in specific environments.

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Simulation of the interactions between plant growth and carbon and water fluxes in the soil-plant-atmosphere continuum

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Keywords: CPlantBox, PiafMunch, FSPM, carbon partitioning, phenotypic plasticity

Introduction

Plant modelling is a useful tool to test hypotheses regarding the influence of plant traits on plant fitness and yield for various weather and climate scenarios. 3-dimensional functional structural plant models (3D-FSPMs) are especially adapted for this task: by simulating cell-scale processes, they yield emerging properties at the plant and field scale for specific environments. One objective for FSPM developers is therefore to go from empirical to mechanistic models, which are more generally applicable in terms of locations and forcings, and provide a fundamental understanding of plant reactions to environmental changes. This work shows the latest developments of CPlantBox, an open-source 3D-FSPM. This new version simulates the feedback loops between plant development and the water and carbon fluxes within one single framework. Model outputs can thus be used to understand the relations driving observed results.

Materials and method

CPlantBox (Zhou et al., 2020) represents plants as 1D graph (nodes linked by segments) in a 3D space. In this work, the following modules were added or adapted compared with the original model: **(a)** water- and carbon-limited growth was implemented, **(b)** the pre-existing xylem water flux analytical solver (Meunier et al., 2017), using Poiseuille's law (axial flow) and Ohm analogy (radial flow), was expanded from the root to the whole plant **(c)** the implicit numerical solver PiafMunch (Lacointe and Minchin, 2019) for phloem flows driven by hydrostatic pressure gradients was adapted for tight coupling to CPlantBox **(d)** the DuMu^x PDE solver (Koch et al., 2021) simulating soil water fluxes with a cell-centered finite volume method, and **(e)** a coupled photosynthesis (FcVB)-stomatal opening (Tuzet et al., 2003) were implemented. At each (user-defined) time step, CPlantBox does a fixed-point iteration between the xylem flux and FcVB-stomatal modules. The other modules are run sequentially (Fig 1A) and yield a value for each plant node or soil voxel. The model was calibrated from experimental and literature data for a generic C3 monocot. It was used with weather scenarios selected to give insights into the effects of expected climatic shifts: the German June weather of 2010 (*wetter&colder*) and of 2100 (*drier&warmer*). *drier&warmer* was characterized by lower soil and air water potentials, and higher temperatures. Plant growth was simulated empirically up to day 7 (resp. 21). The mechanistic growth and flows were then simulated up to day 14 (resp. 28), thereafter called simulation 7-14d (resp. 21-28d). The current implementation of the model is available on GitHub at *Plant-Root-Soil-Interactions-Modelling/CPlantBox*.

Preliminary results

For *drier&warmer*, the overall lower plant water potential limited the growth but was above the stomatal closure threshold, allowing for higher cumulative transpiration (Fig 1B). The resulting lower leaf area (Fig 1C) caused lower assimilation for 7-14d *drier&warmer* compared with *wetter&colder*, in spite of higher temperatures. For 21-28d *drier&warmer*, we observed however increased cumulative assimilation thanks to the larger initial leaf area. For

drier&warmer, 7-14d, the potential gradient also influenced the carbon partitioning: lower growth in the higher organs leading to a lower leaf-to-plant structural carbon ratio, deeper basal roots and fewer lateral roots (Fig. 1C). This strong variation of the plant's structure affects in turn its water uptake capacity and suggests that the dry spell will have a long-lasting effect on the development of 7-14d.

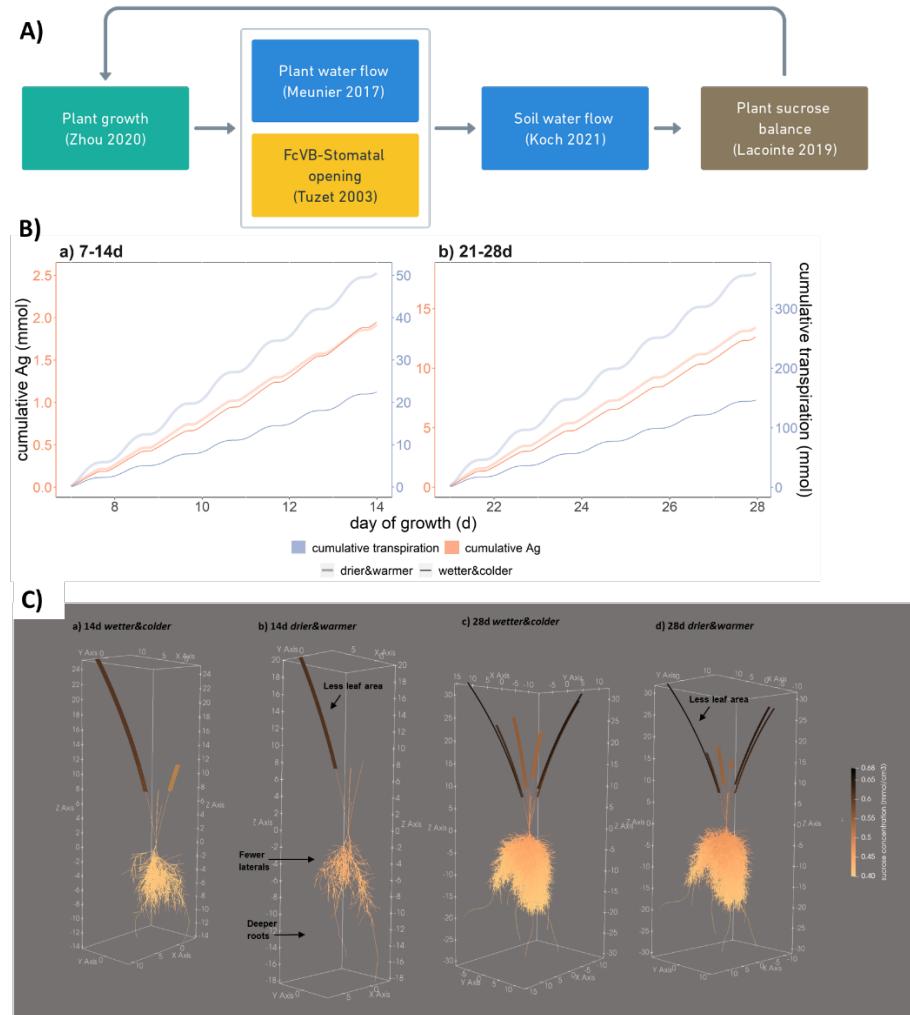


Figure 1: (A) Computation loop, (B) cumulative transpiration (blue) and assimilation (orange) during the simulations from (a) 7-14 against (b) 21-28 days after sowing, under wetter and colder (thin line) against drier and warmer (thick line) conditions (C) plant topology and phloem sucrose concentration at the end of the simulations.

Conclusion

Via its mechanistic representation of plant processes, CPlantBox simulates how water and carbon fluxes (e.g., transpiration and carbon partitioning) and plant growth depend on weather and soil conditions and on the initial structure of the plant. Next steps in the development of CPlantBox will include the setup of calibration pipelines to make simulation outputs closer to experimental results.

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Modelling root plastic responses to soil water status heterogeneity

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Keywords: Hydropatterning, Xerobranching, soil compaction, macro-pores.

Although root system development is known to be highly influenced by the soil water status, only a few models explicitly include root responses to the soil heterogeneity in their growth module. Experimentally, a couple of structural mechanisms of root plasticity to soil water have been observed, such as the orientation of root lateral root emergence in the direction of the higher water potential (Bao et al., 2014), or the lack of lateral roots in air filled macro-pores (Orman-Ligeza et al., 2018). The Hydropatterning mechanism orient lateral root emergence toward water and is supposed to increase water availability for the plant. While the Xerobranching phenomena might allow carbon saving by avoiding lateral root growth where those roots face no water availability. In addition, soil strength, which also depends on soil water, affects root development and thereby generates an additional indirect response of plant development to soil water status (Landl et al., 2019).

To investigate the consequences of these processes, and their combinations, on root system hydraulic architecture, we added response functions to the root growth model (Somma et al., 1997) implemented in the 3D root and transient soil water flow model R-SWMS (Javaux et al., 2008). These response functions consisted in changing the azimuthal angle of lateral root emergence in the direction of the higher water potential, influencing the root growth rate and the heading component as a function of the soil strength and water potential, and suppressing the initial lateral root growth if the water potential around the root was below a threshold value. The objective of the study is to investigate how combinations of direct or indirect short-term response functions to soil water affect root system water uptake efficiency.

We developed scenarios where we could evaluate the impact of each response function on root system architecture and on water uptake under water-limiting situations. In each scenario, the different response functions were combined or silenced. To assess that root architecture plasticity does increase root water uptake, we compared the whole root system conductance, the cumulative root water uptake, and the Carbon cost of each root system.

These simulations allowed us to qualify the impact of root architectural plasticity on maize water uptake performance.

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Modeling phenotypic diversity of woodland strawberry inflorescences

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Keywords: *Fragaria*, branching, L-system, phenotypic diversity, vegetativeness

In many plants, small variations in the genotype can produce significant differences in the resulting phenotypes. Understanding the underlying mechanisms contributes to the fundamental biology of plant development and has potential applications to agri- and horticulture, where plants with distinct phenotypes may have unequal commercial value. With this motivation, we have studied inflorescences in the woodland strawberry, *Fragaria vesca*, known for its extensive morphological diversity (Darrow 1929). The experimental component of our study consisted of macroscopic observations of the inflorescence architecture in wild type and genetically manipulated plants, recordings of developmental sequences of sample plants, and microscopic (SEM) imaging of meristems at different developmental stages. Contrary to previous descriptions of strawberry architecture as cymes (i.e., structures with a consistently sympodial branching), we observed that strawberry inflorescences are closed thyrses (Prenner et al. 2009), with a monopodial primary axis supporting sympodial higher-order branches.

Based on experimental data, we then constructed an L-system model of the strawberry inflorescences capable of reproducing a wide range of phenotypes for different parameter values, and calibrated it to real plants using the image-driven method described by Cieslak et al. (2022). Consistent with the theoretical model of inflorescence development and evolution proposed by Prusinkiewicz et al. (2007), the simulated development of strawberry inflorescences is controlled by a synthetic variable called vegetativeness (veg), assumed to decrease over time. Production of new meristems and their transitions from the vegetative state (initiating new lateral branches) to the flowering state occur as the veg values cross specific thresholds, which depend on the meristem type (monopodial or sympodial) and position within the developing plant. Investigation of the model parameter space revealed that the key differences in the observed inflorescence architectures can be attributed to changes in the decline rate of veg. A comparison of our models with genetic data suggests that the observed diversity can be plausibly explained in terms of the antagonistic action of two genes: *FvTFL1* (woodland strawberry homologs of *TERMINAL FLOWER 1*), which decrease this rate and thus delays transition to flowering, and *FvFT1* (a homolog of *FLOWERING LOCUS T*), which has the opposite effect (Fig. 1).

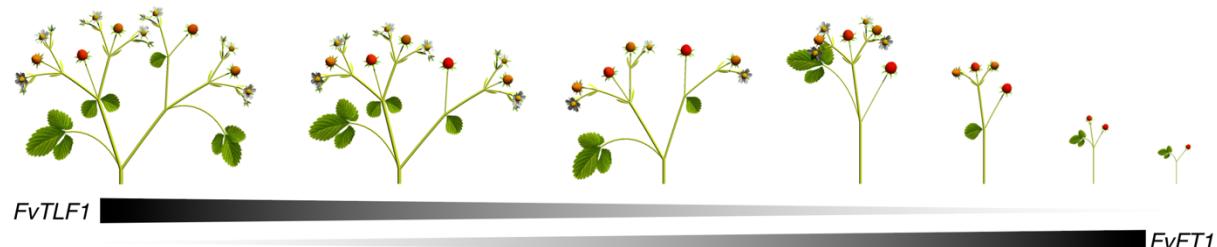


Figure 1: Diversity of wild strawberry architectures, captured by the models, reflects antagonistic action of genes *FvTFL1* and *FvFT1*.

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Using the emergent properties of network topologies to predict phenotypic change

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Keywords: *in silico*, SBGN, peaSoup, parameter free

The task of crop improvement requires significant financial input to achieve a small amount of genetic gain each year. The task of crop improvement is predicted to become increasingly difficult in the years to come due to climate change. As a result of these conditions, it will become necessary to improve the efficiency at which candidate genes are chosen for crop improvement.

Part of the difficulty involved with improving agricultural crops is due to the difficulty involved with translating laboratory findings in an agricultural setting, due to the artificial conditions within a lab. Much fundamental research requires that complex systems be simplified before knowledge can be produced. While this is a necessary first step for discovery, the entirety of the system must be considered if changes are to be implemented outside of a laboratory environment. Plants are complex biological systems that respond not only to internal signalling, but also to external stimuli. Therefore, when selecting candidate genes for achieving phenotypic gain in breeding programs, the effects of those mutations in relation to the whole system must be considered.

To address these issues, a new workflow is being proposed to provide breeders with a method of predicting which genes, or gene combinations, will be useful for acquiring favourable phenotypic traits in crops. This method is designed to both capture the various interactions within a network, while moving away from a high level of parameterisation. The proposed workflow will consist of the following: collating established knowledge, translation of knowledge into a diagrammatic representation of the network, translation of the diagram into a series of equations in order to model the system, and testing model predictions in the biological system.

Prior knowledge will be expressed in a diagrammatic form to capture the interactions between nodes in a simple manner using the systems biology graphical notation (SBGN) activity flow language. SBGN is a standardised form of communicating biological systems. It can describe a variety of different modulations between nodes: stimulation, inhibition, and necessary stimulation. It can also allow for the compartmentalisation of different nodes, as well as the use of a variety of different operators that can communicate if nodes need to interact in combination to affect downstream nodes. Such a representation reduces the system to the topology of the network, and whether there is a positive or negative effect between nodes. Algebraic rules can then be used to convert the diagram into a series of difference equations. 'Genotypes' are applied to nodes that allow the user to modify the output of the node relative to the baseline. The outcomes of simulations that have been run with modified genotypes can then be compared to the wildtype baseline condition. This method does not provide predictions relating to the amount of change in a system, but rather the direction of change and whether change can be expected.

Biological networks have often been shown to be highly robust, and that much of the action of the network is a result of the topology of the network itself. Here we provide a method of testing if our understanding of the network is enough to recover biological outcomes under different experimental conditions. If it is the case that the network can recreate the outcomes of experiments, then the model can be used as a means of predicting which genes may have a beneficial agricultural outcome. To date, this method has been used to successfully describe the branching outputs of pea plants under a variety of grafting conditions.

The functionality needed to execute this workflow will be made available in an R package called peaSoup which will be made available on GitHub. This package comes with functions that translate SBGN diagrams into a series of equations and simulate the outcomes of networks given different sets of genotypes. The package is being designed with the goal of allowing users to easily modify and create nodes in the network, to facilitate novel findings being incorporated into the model.

peaSoup is currently being extended to communicate with an L-system model via an environment program. In this context, peaSoup will function to establish hormonal levels in different compartments of the plant, while the L-system model passes information between compartments. This will allow users to combine the model generating properties of peaSoup with the capacity to produce 3D structural representations of plants.

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Quantitative importance of various rhizodeposition processes: lessons from a mechanistic functional-structural root model

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Keywords: FSPM, root exudation, mucilage, border cells, root hairs, wheat

Introduction

Rhizodeposits, defined here as any organic materials released by living roots, can represent up to 15% of net amount of carbon (C) photosynthesized by a plant (Pausch and Kuzyakov, 2018). Rhizodeposits have been shown to play an important role in plant growth through various mechanisms (e.g. by favoring water uptake through mucilage secretion, or nutrient uptake through the exudation of soluble compounds), and to represent a major contributor to the formation of stable soil organic matter - and thus to the mitigation of climate change through soil C sequestration. Decomposing rhizodeposition into its elementary processes (e.g. exudation, mucilage secretion, cells sloughing) is required for a better understanding of the response of rhizodeposition to various environmental constraints and of its associated-benefits. While many works have attempted to quantify the exudation of soluble organic compounds at the scale of a plant or the net rhizodeposition of C in soils, very few studies have been able to estimate the amount of mucilage or sloughed cells released by a whole root system over time. Consequently, while it has been claimed that the amount of soluble organic C is much higher than the amount of C released as mucilage or sloughed cells by roots (Nguyen, 2003; Rees et al. 2005), the relative importance of distinct rhizodeposition processes in plant's and soil's C balance remains largely unknown. While the comparison of mucilage secretion and citrate exudation within a FSPM has been recently attempted (Landl et al. 2021), no model has been developed so far for simulating such rhizodeposition processes as part of plant's C management. The present work aimed to give a better assessment of the contribution of distinct rhizodeposition processes to the total amount of organic C released by roots, for different plant species, growth stages and environments.

Modelling approach

We used the recently developed root model *RhizoDep*, which aims to simulate rhizodeposition over time and space as a function of plant's environment. Its originality lies in the calculation of a full C balance in each part of the root system, which enables to simulate physiological processes (e.g. growth, maintenance and rhizodeposition) in a plastic way, depending on the variations of root sugar concentrations (Figure 1). Three distinct rhizodeposition processes have been implemented: the exudation of soluble organic compounds, the secretion of mucilage and the sloughing of root cells. The present version also explicitly considers the dynamics of root hairs, as it may significantly influence rhizodeposition processes, e.g. by changing root external surface. Model's parameters were taken from literature or recalculated from published data. The amount of C allocated to the root system over time, which is the major input variable of the model, was either estimated from literature data or simulated by the wheat FSPM *CN-Wheat* (Barillot et al. 2016; Gauthier et al. 2020).

Simulations & first results

We simulated the amount of C released by roots from species that contrast in terms of root architecture and rhizodeposition (e.g. wheat, oilseed rape, faba bean). Simulations were done for different growth stages and environmental conditions (e.g. nitrogen availability, light availability and soil mechanical impedance). Our results show that the exudation of soluble compounds is predominant compared to other rhizodeposition processes, but the secretion of mucilage and the release of cells are substantially increased in certain situations. Mucilage secretion or cells sloughing had until now been investigated only at the scale of a single root and over periods of a few hours. Our work shows that FSPM-modelling offers a unique opportunity to integrate these processes at plant's scale over the whole growth period, while considering various environmental influences on root growth and rhizosphere processes.

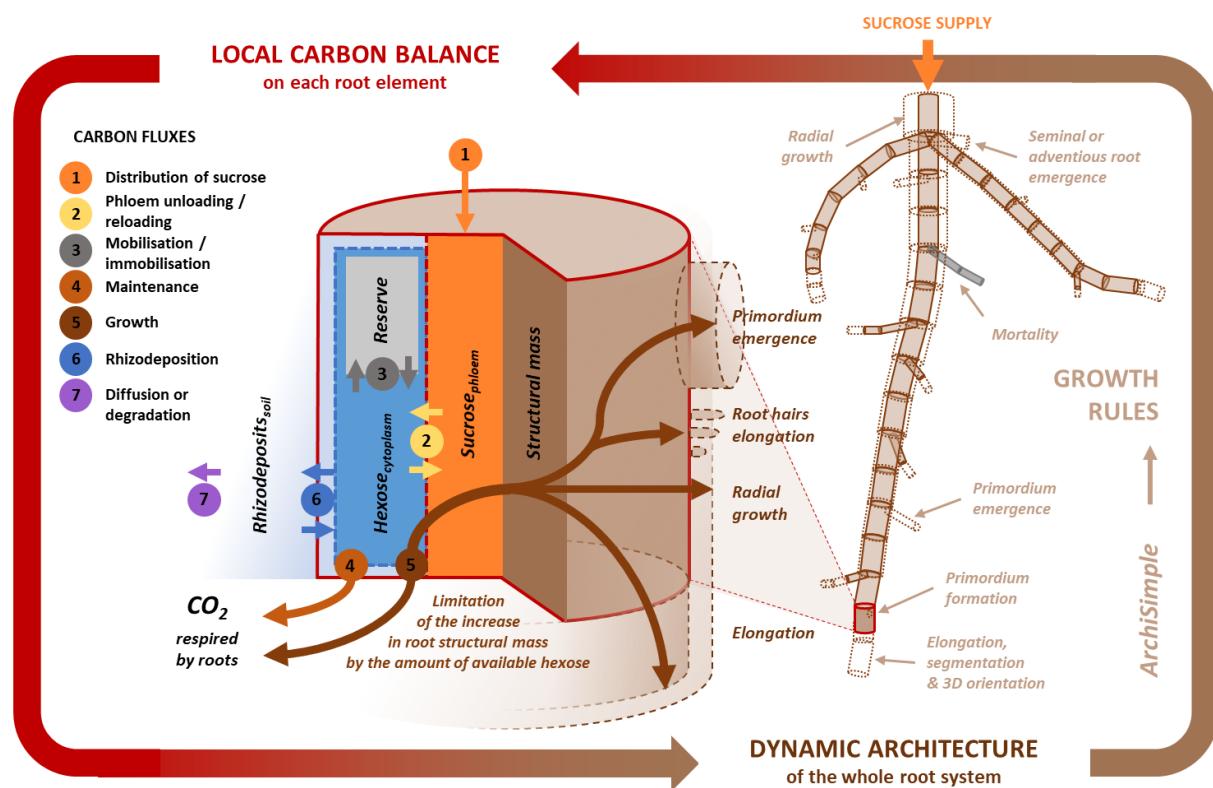


Figure 1: Principles of *RhizoDep* for simulating various rhizodeposition processes within a 3D root system

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Bridging the gap between genotype and phenotype by combining crop models with quantitative genetics

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Keywords: crop model, Quantitative Trait Loci (QTL), yield components, yield dissection

Introduction

Crop models are powerful tools in research and decision support. Often these models are calibrated and validated for one or only a few genotypes. To improve the representation of genetic diversity in crops and advance selection strategies for breeding we used crop yield dissection models that link QTLs to yield components rather than to yield itself. We hypothesize that this allows us to draw the yield response (surface) as a function of yield components and corresponding QTLs, making use of the crop model. To investigate our hypothesis we applied the following five steps on data from greenhouse experiments for pepper (*Capsicum annuum*) and tomato (*Solanum lycopersicum*): (1) Dissect yield into yield components, (2) Identify the genetic basis (QTL) for these components, (3) Build a prediction model for these yield components, (4) Insert the predicted yield component values in a crop model to predict yield. (5) Use the resulting yield response (surface) to determine breeding paths from a known starting position (the best current genotype) to an ideotype (the desired future phenotype).

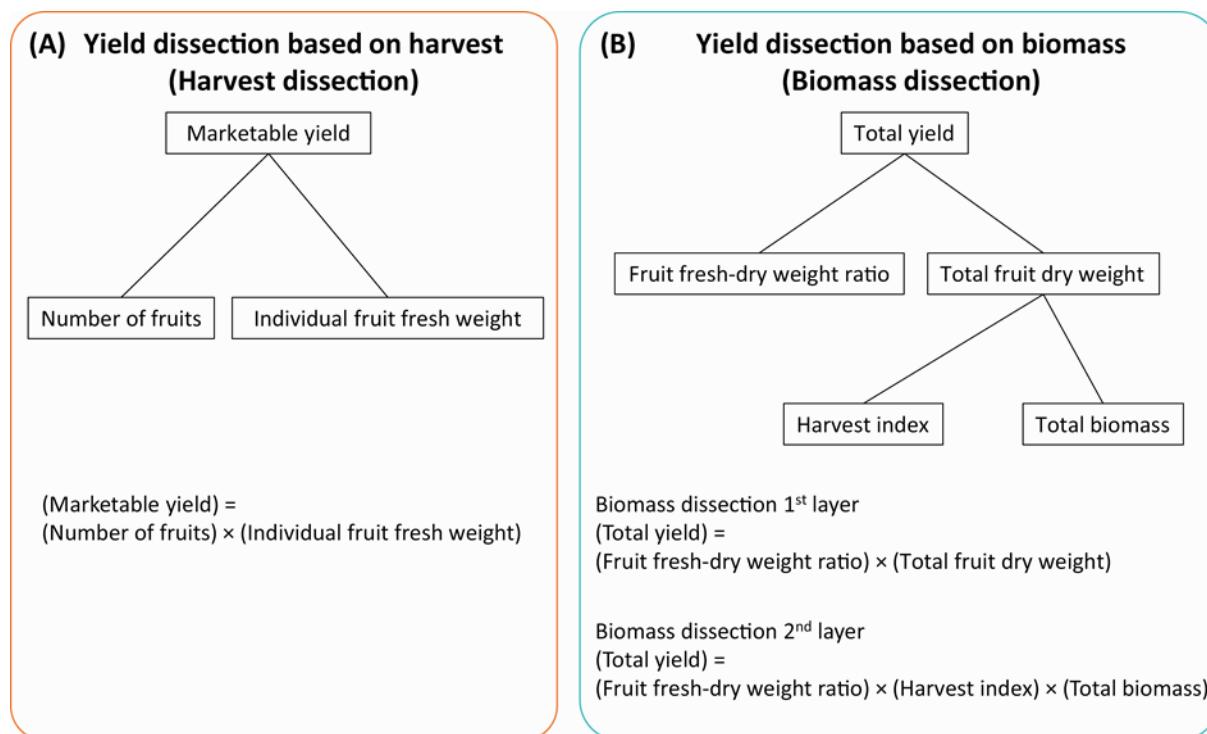


Figure 1. Dissection models for yield: (A) Harvest dissection, (B) Biomass dissection (Tsutsumi-Morita et al., 2021).

Material and Methods

For indeterminate tomato and for sweet pepper, the utility of two yield dissection models (Fig. 1) was investigated for identifying promising yield components and corresponding QTLs. In a harvest dissection, marketable yield was the product of number of fruits and individual fruit fresh weight. In a biomass dissection, total yield was the product of fruit fresh-dry weight ratio and total fruit dry weight. Data for tomato were collected in a greenhouse experiment in the Netherlands with a population of hybrids produced from two tester parents and 342 four-way recombinant inbred lines (RILs). For details on molecular markers and marker map used see Tsutsumi-Morita et al. (2021). For pepper, a RIL population (parents: Yolo Wonder and Criollo de Morelos CM 334) of 149 genotypes was phenotyped in greenhouses at two locations (the Netherlands and Spain) and two seasons (spring and autumn).

Results and Discussion

The heritability for several component traits (e.g. the number of fruits and the individual fruit fresh weight) was higher than for yield. Trade-offs were observed between the component traits in both dissections. Genetic improvements were possible by increasing the number of fruits and the total fruit dry weight to offset losses in fruit fresh weight and fruit fresh-dry weight ratio. Many yield QTLs colocalized with component QTLs, offering options for the construction of high-yielding genotypes. An analysis of QTL allelic effects in relation to parental origin emphasized the complementary role of the parents in the construction of desired genotypes. Multi-QTL models were used for the comparison of yield predictions from yield QTLs and predictions from the products of components following multi-QTL models for those components. Component QTLs underlying dissection models were able to predict yield with the same accuracy as yield QTLs in direct predictions. Yield improvements could be more attributed to the number of fruits than individual fruit fresh weight, more attributed to total fruit dry weight than fruit fresh-dry weight ratio, and more attributed to total biomass than harvest index.

Our approach allows us to draw the yield response (surface) as a function of yield components and corresponding QTLs, making use of the crop yield dissection model. This surface is used to investigate in which direction we will move across the yield response surface when we change the values of component traits and underlying QTLs. Yield dissection models allow us to calculate the length and cost of different breeding paths for improved yield from a known starting position (the best current genotype) to an ideotype (the desired future phenotype).

Conclusion

Combining crop models with quantitative genetics can help bridging the gap between genotype and phenotype as shown here for yield. Yield dissection or more in general crop models, combined with QTL models for component traits underlying yield provide insights into yield response surfaces as functions of these component traits. The high accuracies of yield prediction from yield dissection models, where each component trait was predicted by its own QTLs, suggests that breeding for high yields can be done by selecting for component traits. Some component traits do not need a complete harvest season to be determined, possibly shortening the breeding cycle. This may become more relevant as the measurement of several component traits is becoming easier and cheaper, and feasible for larger numbers of genotypes by new phenotyping technologies (e.g. by using drones, or high throughput phenotyping platforms).

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Non-invasive water flow imaging in plant roots at cellular resolution

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Keywords: Hydraulics, modelling, advection-diffusion, anatomy, xylem

A key impediment to studying water-related mechanisms in plants is the inability to non-invasively image water fluxes in cells at high temporal and spatial resolution. Here, we report

that Raman microspectroscopy, complemented by hydrodynamic modelling using MECHA (Couvreur et al., 2018; Pascut et al., 2021), can achieve this goal - monitoring hydrodynamics within living root tissues at cell- and sub-second-scale resolutions. Raman imaging of water-transporting xylem vessels in *Arabidopsis thaliana* mutant roots reveals faster xylem water transport in endodermal diffusion barrier mutants. Furthermore, transverse line scans across the root suggest water transported via the root xylem does not re-enter outer root tissues nor the surrounding soil when en-route to shoot tissues if endodermal diffusion barriers are intact, thereby separating 'two water worlds' (Fig. 1).

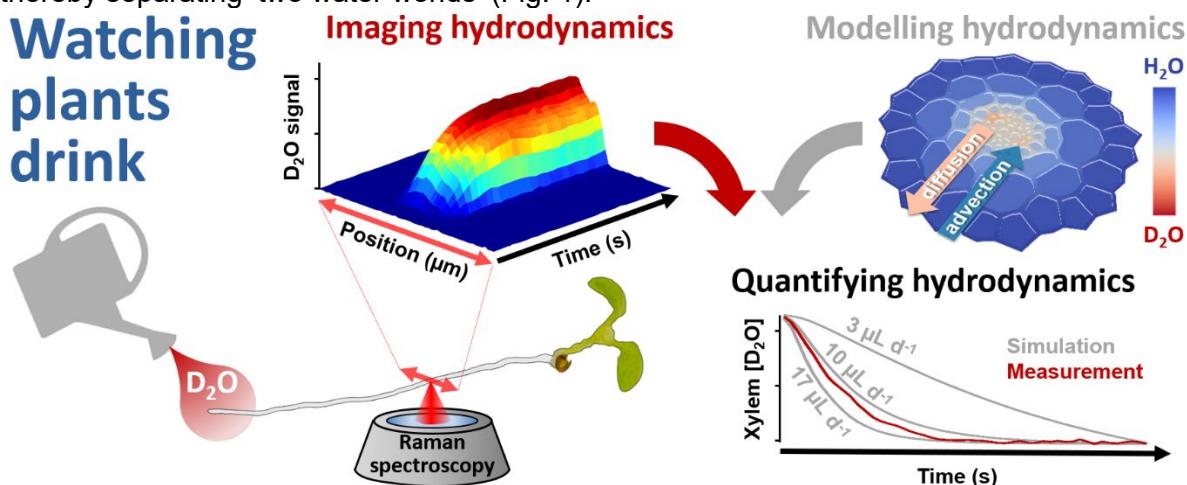


Figure 1: Graphical abstract showing the pipeline of (left) D_2O wash-in spatio-temporal dynamics data acquisition, and (right) comparison with simulated D_2O advection-diffusion during D_2O wash-out phase to estimate xylem water velocity

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Decomposing grass leaf elongation rate: hydraulics, visco-elasticity and ontogeny

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Keywords: grass growth, sink strength, hydraulics, visco-elasticity

Introduction

To increase crop productivity, we need to improve our understanding on how growing organs (sinks) utilize photoassimilates, nutrients and water, and thus we need to better grasp the mechanisms underpinning growth.

In grasses, leaf and tiller initiation and appearance are remarkably coordinated with the onset and cessation of cell division in the leaf meristem. Therefore, the growth kinetics of a specific leaf have important consequences on the development rate of successive leaves and, consequently, on plant and crop productivity. Based on Lockhart's equation (1965), (linear) cell growth has been described as the wall extensibility (ϕ ; in MPa⁻¹ h⁻¹) times the difference between turgor pressure (P ; in MPa) and a threshold for wall yielding (Y ; in MPa):

$$\frac{1}{L} \frac{dL}{dt} = \phi \cdot \max(P - Y, 0)$$

In the growth zone of grasses, turgor has been reported to be rather constant across day and night, and even under progressive drought (Michelena and Boyer, 1982). This low variability in turgor does not map onto the recorded growth dynamics of grass leaves, which show very strong day-night variations and strong effects of withholding water. To explain this mismatch, it has been proposed that ϕ and/or Y should be variable, or that the water potential gradient (and not turgor) is the actual driving force of growth. However, in these analyses, the augmented growth equation by Ortega (1985), which includes elastic effects, is often overlooked. This model describes the 'Maxwell-type' visco-elastic behaviour:

$$\frac{1}{L} \frac{dL}{dt} = \phi \cdot \max(P - Y, 0) + \frac{1}{\varepsilon} \frac{dP}{dt}$$

where the second term is purely elastic, using the elastic modulus (ε ; in MPa).

To improve our understanding of growth, we aim (1) to decompose the short-term dynamics in grass leaf elongation rate into meaningful components, using a model based on hydraulic, visco-elastic and ontogenetic components, (2) to translate insights from short-term dynamics to overall leaf growth, and (3) to infer the impact on the coordination system of grass tillers.

Materials and Methods

We have developed a grass leaf model, parameterized for *Festuca arundinacea*, that scales short-term growth dynamics (minutes-to-hours) to the whole leaf growth period (days-to-weeks). Thereto, the growing leaf is split into four zones, differing in hydraulic, visco-elastic and meristematic properties. Closest to the leaf base, there is the cell division zone (DZ), which is meristematic, highly elastic, a strong sink for carbohydrates and not transpiring, as it is fully enclosed by the sheaths of the leaves on the tiller. Distal to the cell division zone, there is the cell elongation-only zone, where cells have stopped dividing, but are still highly elastic, are elongating, are strong sinks and fully enclosed. In the third zone, cell elongation has stopped, and cells have become less elastic, but are still enclosed and not transpiring. In the fourth zone, cells are mature (and thus no longer growing and less elastic), but are exposed to the atmosphere, and thus transpiring and photosynthesizing. Using the hydraulic architecture presented by Martre et al. (2001) flows of water between connecting zones are modelled according to gradients in water potential. Flows of cells through the different consecutive zones are modelled via the ontogenetic model of Durand et al. (1997). That latter

model has been extended with the functionality of triggering cell division cessation by leaf tip appearance. This growing leaf is inserted on a tiller with three older leaves.

Results and Discussion

Under a day-night regime (Fig. 1A), our simulations show a rather stable growth zone turgor pressure compared to the mature zones turgor (Fig. 1B). The model also allows to decompose grass leaf elongation rate into cell growth and the size of the growth zone components (which results from the newly produced cells via division), but also into the elastic component due to the response of maturing tissue to transpiration (Fig. 1C). This suggests that the actual, irreversible growth rate is masked by substantial elastic dynamics. This may provide a (partial) explanation for the stored growth phenomenon. Because cessation of cell division in the model is triggered by leaf tip emergence from the whorl, leaf growth is enhanced by (artificially) lengthening the pseudostem (Fig. 1D), as has been shown experimentally.

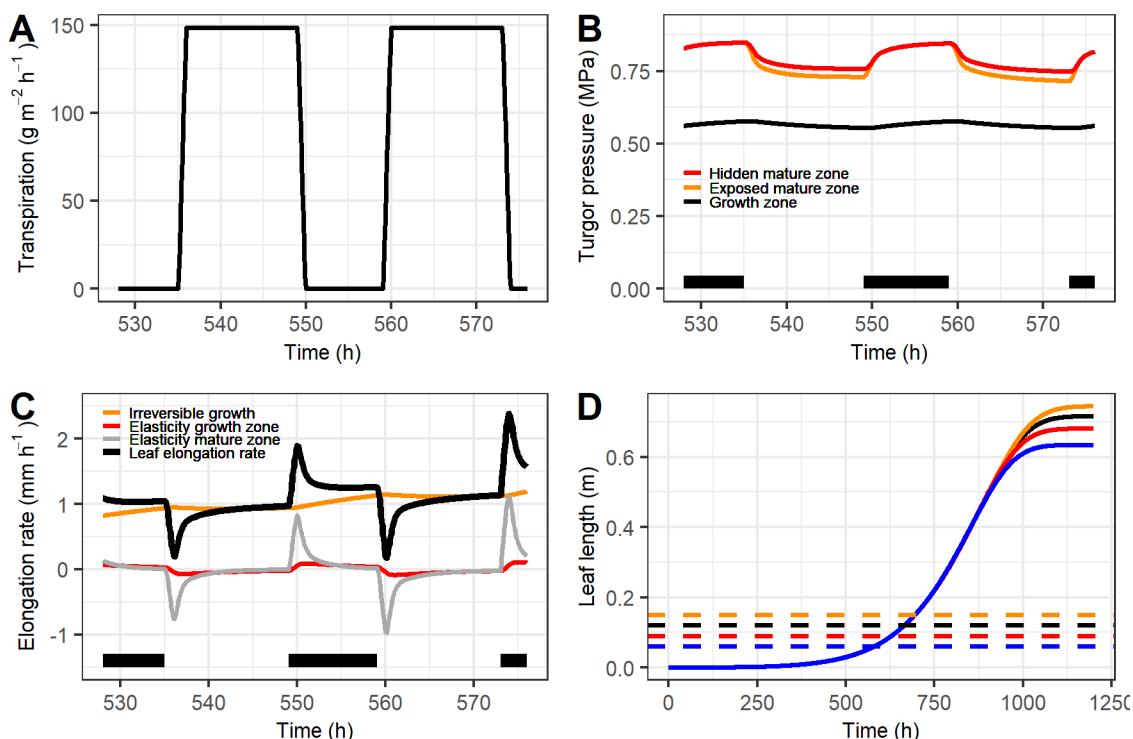


Figure 1: Two-day pattern of the input signal (Transpiration; panel A), turgor pressure simulation in three compartments (panel B), and components of the leaf elongation rate (panel C). Panel D shows the effect of changes in pseudostem length (dashed lines) on the final leaf length.

Conclusion

We provide a hydraulic framework, that predicts constant growth zone turgor, while showing strong day-night dynamics in leaf elongation rate. As such, this model predicted short-term fluctuations in leaf elongation rate without the need for rapid adaptations in cell wall extensibility or turgor threshold, while turgor was still the driver for growth. Furthermore, this model is compatible with the coordination rules in grasses for leaf initiation and appearance, facilitating its inclusion in a full FSPM.

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Simulating common bean in a three sisters polyculture using FSP modelling

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Keywords: Complex intercrop, Milpa, Climbing plants, XL

Introduction

The three-sisters polyculture is the combination of maize (*Zea mays* L.), bean (*Phaseolus* spp.) and a third crop, often squash (*Cucurbita* spp.). While the three-sisters system is an ancient system dating back millennia, millions of subsistence-farmers in current day Mesoamerica still depend on it in some form (Govaerts et al., 2019, Nigh and Diemont, 2013). It is not simply a means for food security, as the three crops are nutritionally complementary (Mann, 2005); polycultures like the three sisters can lead to overyielding (Postma and Lynch, 2012). Studying the contribution of plant traits and mechanisms of complementarity responsible for overyielding in this system will allow us to increase resource use efficiency and enhance selection of improved genotypes, thereby improving the livelihoods of Mesoamerican farming communities. In addition, it may act as a catalyst for modelling complex intercrops in general.

In this work we aim to test the following hypothesis: architectural facilitation in the bean/maize polyculture leads to enhanced light capture (hence improved yield) when compared to growing these crops in isolation.

Methods

Despite the untapped potential in studying spatially complex polycultures, little modelling work on the three-sisters system has been done so far. Postma and Lynch (2012) investigated overyielding in maize/bean/squash polycultures by considering root architecture complementarity. To our knowledge, no attempts have been made at modelling the above-ground processes in such intercrops. Moreover, while climbing plant functional-structural plant (FSP) models exist (e.g. *Hedera Helix* (Smoleňová and Hemmerling, 2008)), as far as we are aware no FSP model for common bean is currently available.

We therefore developed an aboveground FSP model based on (Evers and Bastiaans, 2016) to simulate development in a three-sisters system, using the GroIMP platform (Hemmerling et al., 2008) to simulate complementarity in light capture. We pay special attention to two characteristic phenomena: firstly, the bean plant typically climbs up the maize stalk (Fig. 1), creating a complex physical interaction between the crops. Secondly, maize is usually left on the field to dry, and eventually folded down to minimize damage to the cobs by rain and pests, thereby changing the canopy architecture. Bean continues to grow in this new configuration.

Results

We present a proof of principle, focusing on describing the complex physical bean-maize interaction in the XL language (Hemmerling et al., 2008). When a bean apex is sufficiently close to a 'climbable' object (e.g. a pole or maize stalk), the stem coils in a helix-like way

around said object. In this talk we will highlight how such behaviour can be described in the XL language, and show some preliminary results, including bean growing on a fixed pole and simple bean/maize interaction. In the future we plan to assess how differences in the aboveground layout of the polyculture compared to monocrops under different environmental conditions (e.g. light levels) can lead to increased light capture and yield.



Figure 1: a) Maize and bean form a spatially and temporally complex intercrop, with bean climbing up the maize stalks (photograph adapted from (AnnaJB, 2014)); b) Maize monocrop simulated in GroIMP; c) Coiling around cylinders with varying orientation.

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Unravelling drivers of local adaptation through evolutionary functional-structural plant modelling

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Keywords: *Dianthus carthusianorum*, elevational gradient, model validation, natural selection

Introduction

Local adaptation to contrasting environmental conditions is a widespread phenomenon in plant populations, resulting from divergent selection pressures imposed by variation in environmental conditions on populations occurring across a species' range. The outcome of local adaptation can be documented in field experiments that assess the performance of alternative ecotypes in contrasting environments, where local ecotypes are expected to outperform foreign ecotypes. A wealth of experimental work has shown the pervasiveness of local adaptation, yet we often lack a mechanistic understanding of how individual agents of selection contribute to local adaptation along environmental gradients (Wadgymar *et al.*, 2017). This is caused by individual drivers of selection acting on multiple plant traits, either directly or indirectly, and by individual traits being affected by multiple drivers of selection. The interactions between drivers of selection, such as between abiotic and biotic factors, further complicates disentangling the role of any individual driver in shaping local adaptation. Here, we aim to disentangle the relative contribution of temperature, competition and pollination in elevational adaptation of *Dianthus carthusianorum*.

Methods

To this end, we developed a novel evolutionary-FSP (E-FSP) modelling approach that simulates the combined selection pressure imposed by multiple selective agents on a population of individually distinct plants that interact with each other and with the environment (de Vries *et al.*, 2022). This individual-based perspective is of particular importance to mechanistically simulate natural selection, as key mechanisms that drive selection (e.g. competition for resources) are not only driven by absolute trait values, but also by trait values relative to those of neighbouring plants (de Vries, 2021). The model simulates a population of competing plants over generations, with the performance of individual plants within a generation being determined by multiple plant traits that are subject to selection.

To validate this modelling approach, we use empirical data of two elevational ecotypes of *D. carthusianorum* that occur along an elevational gradient in the Swiss Alps, growing at low (~1000 m.a.s.l.) and high (~2000 m.a.s.l.) elevation. These environments are characterised by commonly reported differences in (a)biotic conditions along elevational gradients (Halbritter *et al.*, 2018), resulting in a tall grassland vegetation at lower elevations, and typical alpine (i.e. shorter) vegetation at higher elevations. These two elevational ecotypes of *D. carthusianorum* are adapted to their elevational ranges and display genetically based phenotypic divergence (Walther, 2020).

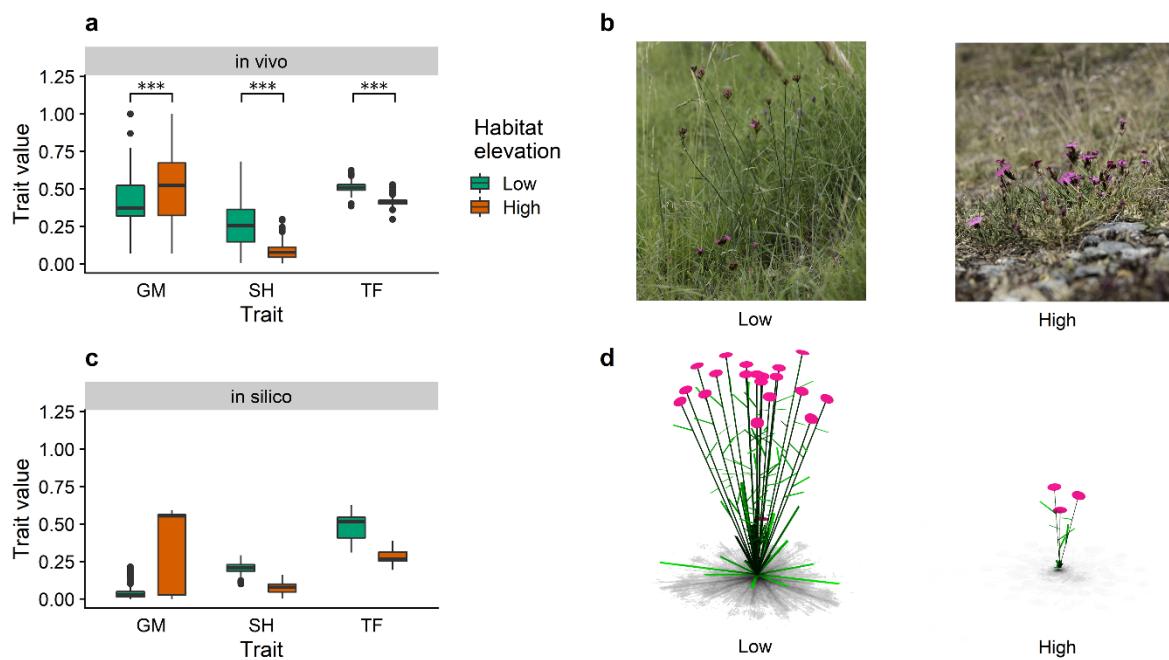


Figure 1. Comparison of trait variation of in vivo (a,b) and in silico (c,d) populations of *D. carthusianorum* in their low and high elevation habitats (Low: Green, High: Red). These elevational habitats select for different phenotypes (b,d), resulting from divergence in three plant traits (germination (GM), stalk height (SH) and time to flowering (TF); normalized trait value (0-1)). Significance is shown only for the *in vivo* data (* P<0.05; ** P<0.01; *** P<0.001).

Results and Discussion

The model reproduced the qualitative differences in three plant traits that differentiate the two elevational ecotypes of *D. carthusianorum* (germination time, time to flowering, and stalk height; Fig. 1). The model was also able to reproduce qualitative differences in four variables related to plant performance that emerge from genotype x environment interactions (flowering time, number of stalks, rosette area and seed production). Additional simulations that isolate the effect of individual agents of selection further suggested that the abiotic environment is the most important driver of elevational adaptation in *D. carthusianorum*, with results matching commonly reported trends in adaptation along elevational gradients (Halbritter *et al.*, 2018)

Conclusion

This study highlights the potential for E-FSP modelling to simulate the emergent behaviour of a complex natural system that includes abiotic and biotic agents, and integrates physiological, ecological and evolutionary mechanisms. E-FSP modelling is a promising and versatile tool that is capable of simulating more complex and dynamic systems than is common in FSP modelling, while integrating more physiological and spatial detail than commonly used eco-evolutionary modelling approaches.

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Modelling the impact of intraspecific genetic diversity on the botanical composition of forage mixtures

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Keywords: grasslands, intraspecific variability, individual-based model, competition, stability

Introduction

Increasing intra-specific genetic variability (IV) has been identified as a potential factor stabilizing productivity and botanical composition in wild and cultivated plant communities. In intercropping systems, this could be a lever to handle the consequences of environmental uncertainty induced by global change. However, little is known about the mechanisms at play and the growing conditions where such effects could be maximised. To do so, mechanistic modelling of plant community functioning is a tool of particular interest (Becker et al., 2022). In this study, the objectives were to use a generic individual-based model (IBM) to assess the impact of increased IV in theoretical bi-specific mixtures and to analyse how variability on different traits involved in resource acquisition affected short term competition at population and community levels.

Methods

The Virtual GrassLand model (VGL, Louarn and Faverjon, 2018; Faverjon et al., 2019) is an individual-based model that simulates plant-plant competition for resources (light, water, nutrients) in a spatially-explicit environment. It was adapted from a previous version (Louarn et al., 2020) to handle within species variability through a multivariate gaussian distribution of plant parameters. This model was used for a simulation experiment to assess i) how the degree of functional similarity of species (i.e. the mean trait divergence between species) and the effect of intraspecific trait variability (IV) modified the annual yield and relative abundance of species and ii) whether the kind of environmental limitations (light versus nitrogen) affected the sensitivity and major traits involved in the observed responses. A total of 63 binary plant mixtures was defined to account for a gradient of functional divergence between species regarding light and nitrogen (N) acquisition. The growth and dynamics of these communities was simulated with three possible levels of IV (very low, moderate and high) into two contrasting environments (high and low soil N fertility; N+ and 0N). Model outputs were analysed in terms of overall community performance (productivity, species balance), population demography, and ultimately, individual plant access to resources.

Results and Discussion

In the range of situations tested, the model anticipated a positive impact of IV on maintaining a stable balance between species over time, but no marked effects on mixture overyielding. The stabilizing effects increased with higher IV levels and under conditions of low soil N fertility. It also tended to be more pronounced in communities of intermediate functional divergence, offering large possibilities of overlap between the parameter values of both species (Fig. 1). The major traits involved differed depending on the most limiting resource, as indicated by the within-population selection of both light and N acquisition parameters under 0N and only light acquisition parameters under N+. The simulation results did not support the hypothesis of IV favouring complementarity between species. Rather, it demonstrated a role of higher spatial heterogeneity on the partitioning of resources within plant communities and suggested more frequent patches with reduced effect of the dominant species over the subordinate species in resource acquisition. At the community level, this lead a ‘competitor release’ effect and a higher probability of recruitment of the dominant individuals within the subordinate species.

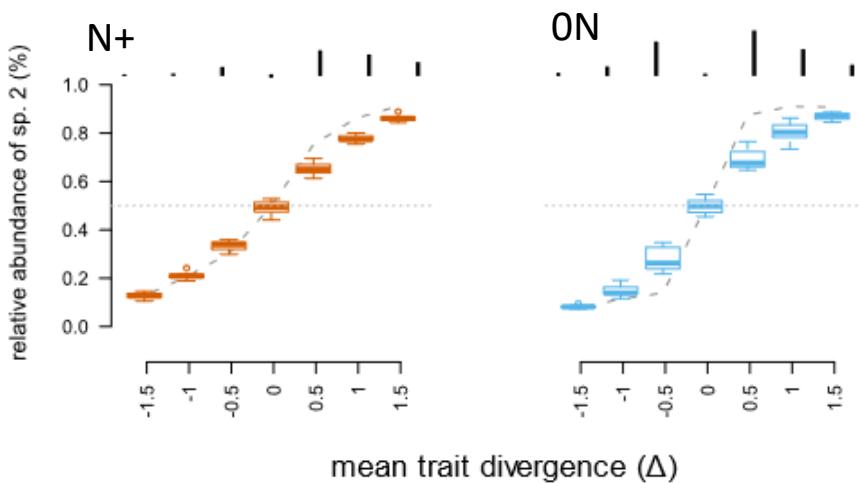


Figure 1: Response of species proportion to the gradient of mean trait divergence (Δ) in T3L (differing by 3 light parameters) communities with high within-species variability ($CV=0.30$). Blue and brown boxes stand for simulations under ON and N+ environments, respectively. Grey dashed line: average species proportion at low within-species variability. Black vertical bars: stabilizing effects of IV, representing the reduced distance to a 0.5 initial proportion.

Conclusion

These results highlight the potential interest of IV for designing improved intercropping systems and illustrate how IBMs can be helpful to specify the advantageous trait combinations and IV range to target for breeders.

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Enabling High-Throughput Field Phenotyping of Whole-plant Physiology via FSPM

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Keywords: Helios, machine learning, sensor emulation

Traditionally, traits that can be feasibly considered in breeding for crop improvement are limited to quantities that can be measured by hand in a reasonable amount of time (e.g., plant height, stand count, flowering time, yield, “health” score), which are useful indicators of plant performance but provide an incomplete picture of plant function. More recently, high-throughput phenotyping methods, usually based on proximal remote sensing approaches, have been developed to automate and accelerate the measurement of traits such as plant height, leaf area, leaf angle, ground cover, among others. However, these traits still often provide a highly incomplete picture of overall plant function in relation to crop performance. For example, the effect of leaf angle on overall plant performance is complex, and depends on a myriad of other interacting traits such as leaf area distribution, growth stage, photosynthetic capacity, stomatal physiology, and water and nutrient status.

We present an approach for estimating whole-plant physiological traits from light-based proximal remote sensors (RGB camera, depth camera, multi/hyperspectral camera, thermal camera, LiDAR) by fusing FSPMs and machine learning models. The Helios 3D plant modelling framework (Bailey 2019) was enhanced to allow for realistic prediction of these sensor outputs as a function of the following sub-models:

1. The 3D biophysical state of the plant system (rates of gas exchange, water status, nutrient status, temperature, 3D structure, phenology, etc.) is simulated using Helios sub-modules.
2. Relevant state variables are input to a leaf optical model (PROSPECT-D) to predict the 3D distribution of tissue spectral reflectance and transmittance as a function of the state of the system.
3. Based on models of camera/sensor intrinsics and light spectral distribution, the model domain is sampled from the point of view of the sensor for arbitrary wave bands as a function of the predicted spectral radiative properties.
4. The simulated sensor data is automatically annotated based on the state of the system, such as locations of elements, geometric parameters, and physiological state.

Parameters of the system can be systematically varied to generate simulated data across a broad parameter space, which can then be used to supplement training of machine learning based models in cases where insufficient physical data is available (Fei et al 2021). Thus, the machine learning model becomes an effective inverter of the 3D biophysical models in order to extract holistic plant-level trait information from proximal remote sensing data. This approach can be used to determine functional and structural traits, which can also provide FSPM inputs that allow for prediction of plant performance across a range of potential environment × management regimes. Example applications are given for integration with a field-based robotic sensing platform.

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Use of LiDAR Data for the Design of Functional-Structural Plant Models of Tropical Trees

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Keywords: Terrestrial Laser Scanner, Quantitative Structural Models, tree parameters

Introduction

Functional-Structural Plant (FSP) models are useful tools for understanding plant functioning and how plants react to their environment. Developing tree FSP models is data-intensive and measuring tree architecture using conventional measurement tools is a laborious process (Surový et al., 2011). Light Detection and Ranging (LiDAR) could be an alternative non-destructive method to obtain structural information about tree architecture (Malhi, et al., 2018). This research aimed to investigate how TLS LiDAR-derived tree traits could be used in the design and parameterization of tree FSP models. A total of 90 papers on FSP tree models were screened and 8 papers fulfilled all the selection criteria. From these papers, 45 structural parameters used for FSP model development were identified, from which 26 parameters were found to be derivable from LiDAR.

Materials and Methods

The tropical tree FSP model of Petter et al. (2021) was selected and parametrized with LiDAR-derived parameters in GroIMP (Hemmerling et al., 2008). The model inputs were compared with the results of the systematic literature review to identify parameters derivable from LiDAR pointclouds. Two parameters, branch angle and internode length were identified and derived through Quantitative Structural Models (Raumonen et al., 2013). The foliage was first removed from the individually segmented pointclouds before running the QSMs. The QSM results were compared to field measurements of height and Diameter at Breast Height (DBH), and for the branch angle and internode length, direct measurements were done from the pointcloud for the first branches of the first and second order. A total of 37 LiDAR-scanned tropical trees were used for the study, scanned in the East Berbice-Corentyne Region of Guyana (10 *Chlorocardium rodiei*, 5 *Gouania glabra*, 4 *Mora excelsa*, 9 *Mora gonggrijpii*, 5 *Eperua falcata*, 4 *Swartzia leiocalycina*). The FSP models were run with the LiDAR-derived median, minimum, maximum and normal distribution of the selected parameters and compared with the default model output.

Results

The LiDAR-derived parameters were compared to measurements, and the RMSE of height (m) was 3.40 and DBH (cm) 12.96. The branch angle (degrees) was 22.19 for the first branch order and 18.1 for the second. The RMSE for the internode length (cm) was 118.62 for the first-order branch and 79.74 for the second-order branch. The branch angle could be used as FSP model input for the tropical FSP tree model. However, the internode length was not suitable due to the larger value compared to the default value. Outputs of the FSP models with LiDAR-derived branch angles differed quantitatively and visually from the FSP model outcomes with default branch angle (Figure 1). Using the LiDAR-derived normal distribution resulted in a more realistic 3D tree.

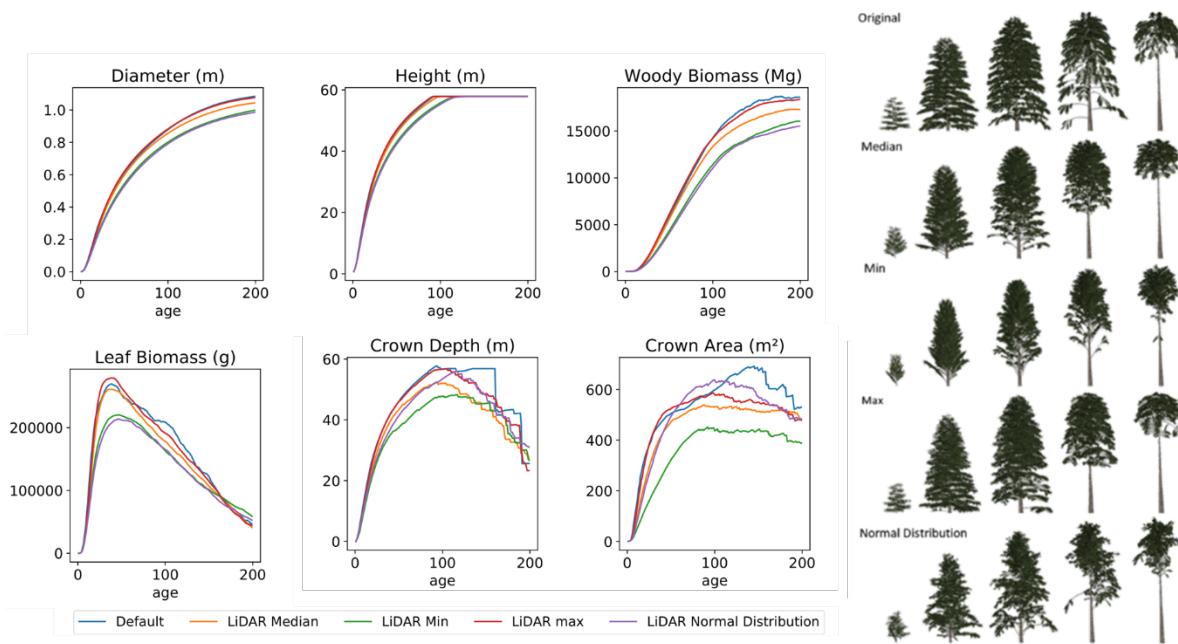


Figure 1: (left) Tropical tree FSP model variable output for different LiDAR-derived parameter inputs. The median of the LiDAR-derived branch angle was used, as well as the 25th percentile (min), 75th percentile (max) and a normal distribution function. The default input settings were used to compare the outputs of the LiDAR-derived parameters. (right) Visual differences over time of the outputs of the tropical tree FSP model with different LiDAR-derived parameter inputs. A total of 37 tropical trees were used to derive the inputs.

Discussion and conclusions

Conclusions from this research have resulted in new insights into considerations and limitations of using LiDAR for deriving structural parameters. Results showed that it is possible to use LiDAR for FSP model inputs, although with caution as this has implications for the model variable outputs. In the future, LiDAR could help improve efficiency in building new FSP models, increase the accuracy of existing models, add metrics for optimization, and open new possibilities to explore previously unobtainable plant traits to include in the models.

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Using FSPM to understand the physiological mechanisms that reduce fruit yield in high planting density orchards

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Keywords: virtual plant, fruit growth, light interception, photosynthesis, carbon availability

Abstract

In fruit tree orchards, fruit yield increases with planting density when the number of plants per hectare is low and plants are small, but yield can decrease with high planting densities (Auzmendi et al., 2022). In trees growing without water or nutrient stress, different physiological mechanisms can contribute to this yield reduction, e.g., competition for light, imbalance between vegetative and fruit growth. However, it is difficult to define and separate these physiological mechanisms in the field. Models of carbon acquisition and distribution between organs have been used to reproduce the effect of plant density on orchard yield (Auzmendi and Hanan, 2020a). These models can be used as well to understand better these mechanisms and their contribution (Room et al., 1996).

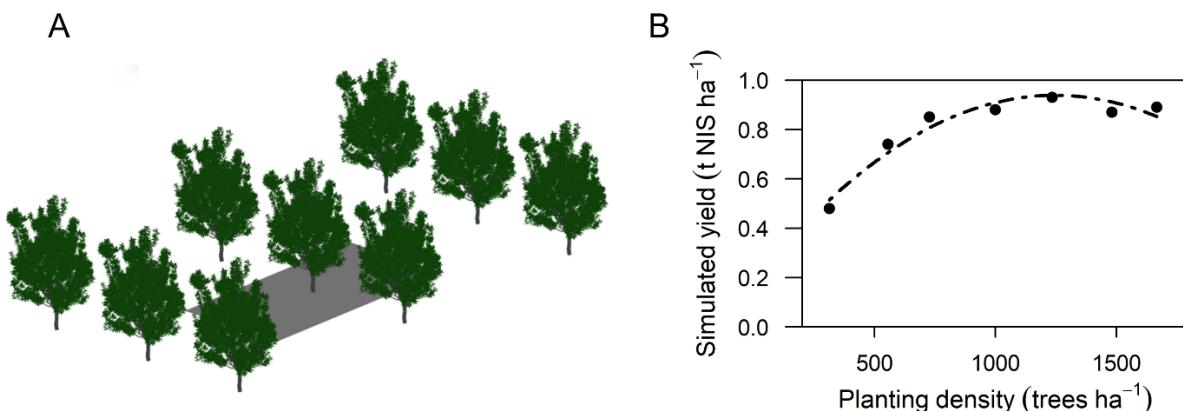


Figure 1: View of a virtual macadamia orchard at the beginning of the simulation with planting density of 313 trees ha^{-1} , corresponding to 8×4 m (A). The ground surface in grey is employed to estimate light interception; and relationship between simulated yield and planting density (B). Macadamia growth during one season was simulated with 7 different planting densities ranging from 313 to 1,667 trees ha^{-1} .

We designed and used a functional-structural macadamia tree model to simulate individual organ growth within the canopy, as well as tree and orchard yield, with different planting distances. This virtual plant incorporated sub-models of light interception, photosynthesis, potential relative growth rates of individual organs and inter-organ competition for carbon (Allen et al., 2005; Auzmendi and Hanan, 2020b). One tree canopy architecture measured in the field was employed to recreate orchard canopies (Fig. 1A) with a range of planting distances, i.e., 313, 556, 727, 1000, 1235, 1482 and 1667 trees ha^{-1} . Individual tree growth was simulated during one growing season, i.e., between flowering and harvest, together with final orchard yield (Fig. 1B) and some physiological parameters, e.g., light interception, leaf area and photosynthesis. A constant photosynthetically active radiation (PAR) value of 33.66 mol $m^{-2} d^{-1}$ for a cloudless sky in north-eastern New South Wales, Australia, was employed

based on data published by Lloyd et al. (1995). Day temperature was 25 °C and night temperature 15 °C.

Our virtual experiments showed how different physiological mechanisms contributed to tree and orchard yield in our simulations. They increased our understanding of and supported our hypotheses about these mechanisms and their role in decreasing yield of high planting density orchards, which can be useful for increasing the productivity and sustainability of fruit tree orchards.

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Integrating the effect of light quantity and quality in the V-Mango model to optimize cultural practices

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Keywords: mango tree, light, vegetative growth, pruning, architecture

Introduction

Plant architecture results from species-specific growth processes and constraints exerted by the environment. In particular, light affects photosynthesis and photomorphogenesis processes. In return, architecture influences light interception, transpiration and water transport as well as carbon acquisition and allocation (Da Silva 2014). Thus, optimization of fruit tree architecture can improve fruit production in terms of quantity and quality. Mango (*Mangifera indica* L.) is the fifth most produced fruit in the world, mainly in tropical and subtropical regions. Its cultivation raises a number of issues such as irregular fruit production across years, and heterogeneity of fruit quality at harvest. To address those issues, the FSPM V-Mango (Boudon et al., 2020; Vaillant et al., 2021) was developed simulating vegetative and reproductive development of mango trees. The model can simulate pruning scenarios, and their effects on subsequent vegetative growth (Persello, 2019). However, the effect of light on the tree development is poorly taken into account, leading to unrealistic distributions of growth units (GU) within the crown. For now, light was mainly considered for photosynthesis, but currently relies on empirical light environments given as model inputs.

This work presents the integration of a radiative transfer model in V-Mango and the implementation of the coupled effects of light environment, pruning and GU characteristics on GU development and mortality. Using these extensions, we aimed to (i) validate the estimation of the vegetative growth following pruning at the tree scale, and (ii) explore the effects of pruning on the light distribution within the crown.

Materials and Methods

To parametrize the developmental rules of V-Mango, data was collected in an experimental orchard of a CIRAD research station located in Réunion Island (20°52'48"S; 55°31'48"E, 125 m a.s.l.). Adult mango trees were pruned with a gradient of pruning intensity (defined at the tree scale as the amount of fresh biomass removed per unit volume of tree canopy) in February 2021. Pruned and unpruned GUs were sampled inside and on the periphery of the canopy and their light environments were estimated from hemispherical photographs. The date of appearance and the number of new GUs appearing on the sampled GUS, as well as the occurrence of mortality of the new GUs and the sampled GUs were collected. Hemispheric photographs were regularly acquired in the center of the crown of mango trees until the end of vegetative growth to record crown closure. 3D scans of the orchard were also acquired with drone after pruning and after vegetative growth, from which volume of individual trees at these different periods were extracted.

The coupled effects of light environment, pruning and GU characteristics on vegetative bud burst and GU mortality were characterized using generalized linear models. Those effects were integrated in the existing developmental rules of V-Mango, detailed in Boudon et al.

(2020), and new functions were developed to simulate GU mortality. Light interception was estimated with the PlantGL library (Pradal et al., 2009). The light quantity variable $TrPPFD$ (the relative transmitted photosynthetic photon flux density), was computed at the GU scale and averaged to obtain hourly values during one simulated day under a clear sky. The light quality variable ζ (ratio between red to far red wavebands) was estimated using a nonlinear relationship linking ζ and $TrPPFD$ (Carrié et al., 2022). The experimental pruning intensities were then simulated on a 3D digitized adult mango tree and vegetative growth was simulated accordingly with V-Mango. To validate such development, different indices such as crown closure and volume were estimated from the generated 3D representations and compared to measurements.

Results and Discussion

Simulation of light distribution within the mango crown was successfully validated in terms of quantity and quality. Implementation of the light dependent developmental rules allowed to simulate realistic crown closure and volume increase due to the vegetative growth induced by tree pruning. Additionally, this new version of V-Mango allows quantifying and comparing the effect of pruning on light distribution and regrowth within the crown. This work opens up great prospects for modeling approaches dedicated to fruit tree systems. However further experiments are needed to simulate the entire growth cycle, taking into account the complex endogenous processes of the mango tree.

Conclusion

In this work, we integrated in V-Mango, a radiative model and implemented the effects of light and pruning on the architectural development of the mango tree. Model simulation accuracy was validated at the tree scale and allowed to quantify pruning effects within the crown. Such a modeling approach makes it possible to optimize cultural practices related to light distribution and thus improve fruit tree production.

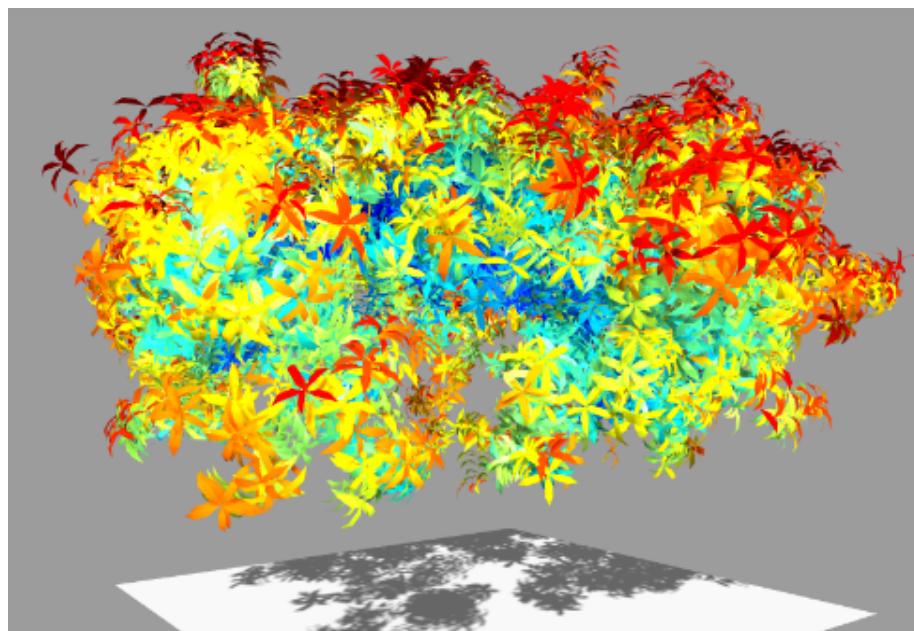


Figure 1: Simulated distribution of the daily average ζ within the mango tree crown in V-Mango

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Testing the capacity of an oil palm FSPM to simulate changes in water and carbon dioxide fluxes under a range of climatic conditions

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Keywords: biophysical processes, climate change, FSPM, oil palm, model assessment.

Functional-structural plant models (FSPM) aim at reproducing the complexity of the ecophysiological and developmental responses of plants to their environment. Such models can be particularly useful to understand and explore plant behaviour in a changing climate, but depend on intensive collection of structural and ecophysiological data. Since errors can rise from different sources such as model implementation, calibration, and coupling, model evaluation can be a major difficulty. Furthermore, some sub-models simulate processes at fine scale (e.g. leaf scale) but the output of interest is an integration at a larger scale (*i.e.* plant or plot scale), which can also add error that is difficult to assess when evaluation is only made at the finer scale. Lastly, very few databases are available for the assessment of FSPM because they require expensive and time-consuming measurements, including plant geometry and sometimes topology, ecophysiological data such as response curves (e.g. A-C_i), and whole-plant measurements to control for the error coming from the upscaling. Consequently, the assessment of an FSPM as a whole is usually omitted because of the lack of such data.

In this work, we first propose a new dataset dedicated to FSPM evaluation at leaf to plant scale. Oil palm plants were placed in a microcosm (Montpellier European Ecotron) where H₂O fluxes, CO₂ fluxes and leaf temperature were measured continuously while air temperature, vapor pressure deficit, photosynthetically active radiation and air CO₂ concentration were finely controlled (Fig 1A). Climate conditions were modified sequentially and independently to obtain eight daily climate scenarios replicated on four plants, allowing the investigation of the impact of climate variables on plant assimilation and transpiration. The dataset also include data for the parameterization of the models, including fine reconstructions of the 3D plant structure from terrestrial LiDAR point clouds (Fig 1B) and measurements of photosynthesis and stomatal conductance using leaf-scale response curves from a gas analyzer, including A/C_i, A/PPFD and Gs/VPD response curves. The three-dimensional reconstruction of the plants and the microcosm were then used to build a digital twin of the experiment.

Secondly, we propose an example evaluation of an FSPM (Treillou et al., in prep., Perez et al. 2022) using this database, and explored how plant transpiration and carbon assimilation were modulated under the contrasted climate scenarios (Fig 1C). Then we tested the accuracy of the biophysical models to simulate these physiological changes, and discussed the discrepancies between observations and simulations. The database presented is unique regarding the complementarity and completeness of the observations made, and would allow testing hypotheses on the spatial integration of physiological processes, and the degree of accuracy required in the representation of plants to properly take into account the relationship between structure and functions in FSPM.

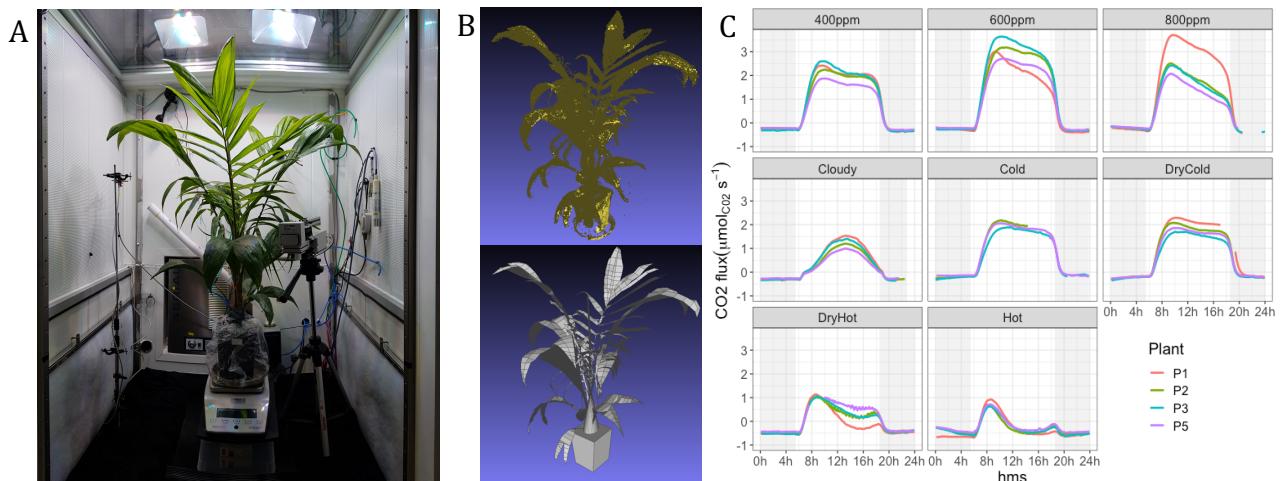


Figure 1: A) Experimental device with monitoring of climate conditions and measurements of physiological processes. B) Reconstruction of the 3D plant structure (bottom) from terrestrial LiDAR point cloud (top). C) Measurements of CO₂ fluxes for the four studied plants (colours) under the eight contrasted climate scenarios.

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Simulating pruning responses in a FSP model of cocoa

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Keywords: branching, model calibration, *Theobroma cacao*, tropical perennial.

Introduction

Pruning in tree crops is the art and science of cutting parts of a plant to increase e.g. production and ease harvest and spraying activities. The impact of pruning on tree architecture and functioning is complex to predict. By removing branches and foliage, pruning directly modifies the architecture of a tree and hence its light interception. At the same time, pruning affects the internal hormonal balance, resulting in altered branching patterns that will influence carbon assimilation and resource allocation in the longer term (Ferree and Schupp 2003).

Functional-structural plant (FSP) models can be used to disentangle the instant and long-term (months to years) effects of pruning on tree functioning and they can help design effective pruning strategies in terms of which branches to prune, at which intensity and when. While some existing FSP models have been used to simulate the direct effect of pruning on tree architecture and light interception (Lescourret *et al.* 2011; Tang *et al.* 2015), studies that include pruning-induced changes in branching patterns to investigate the effect of pruning in the longer term have not been performed.

We developed an FSP model of cocoa trees that incorporates the effect of formation pruning on cocoa branching patterns and biomass accumulation in young (pre-bearing) cocoa trees. Cocoa is an important commodity crop and source of income for millions of smallholder farmers in the humid tropics. In cocoa cultivation, pruning is recommended to farmers, although its effects on early canopy development, cocoa tree growth and cocoa bean production are not well understood (Tosto *et al.* 2022).

Here we present results for parameterization and evaluation using data from two pruning experiments on three years old cocoa trees in Ivory Coast, of a model designed to simulate branching patterns in cocoa.

Methods

Parameterization and evaluation experiments: In the experiment for model parameterization we explored cocoa branching patterns in response to different types of pruning cuts. We applied five pruning treatments: the removal of the branch tip, the removal the branch section containing 66% of axillary buds, the removal of one or two entire branches, and a control (no pruning). Pruning was applied to first-order branches only. Before the cuts and after the first cycle of leaf production, we measured the total number of buds, the number and the position of secondary branches as well as the length of secondary branches.

In the experiment for model performance evaluation, we carried out three contrasting pruning interventions (light, medium and heavy pruning). Before and after pruning we measured stem size, crown size and leaf number. We repeated the same measurements six and twelve months after pruning.

FSP model: Our cocoa model simulates growth and development of young cocoa trees. Architectural and developmental characteristics specific to cocoa plants were included, such as crown layer formation (jorquetting, Fig 1 C) and periodic leaf production driven by thermal time (flushing). Light interception is calculated at the leaf level, driving leaf photosynthesis. In the FSP model, plant growth is the result of source-sink driven allocation of assimilates.

Removal of branches, or portions of branches, modifies the probability of break of dormant buds, affecting the tree crown structure (Fig 1 D). The probability of bud break depends on bud rank and number of secondary branches already present on the primary branch and the pruning treatment, following a logistic curve that was parameterized using data from the parameterization experiment. We simulated the pruning interventions performed in the evaluation experiment and compared the model outcome with experimental data.

Results

Results of the parameterization experiment showed that the emergence of new secondary branches during a flushing cycle was concentrated in the section of the primary branch that had developed before the last flushing event. The pattern of branch emergence was modified by the different pruning treatments, but also varied among branches (Fig 1 A). Probability of branch emergence decreased with the number of secondary branches already present on a primary branch. Results from model evaluation in terms of biomass production and tree architecture, under development, will be presented.

Conclusion

The cocoa FSP model potentially serves as a tool to address relevant issues in cocoa production, such as optimal pruning practice and planting design. In addition, it can be used for screening promising trial options and for ideotyping plant structure for breeding purposes. The 3D visual output makes the model a potential communication tool for academic and non-academic audience.

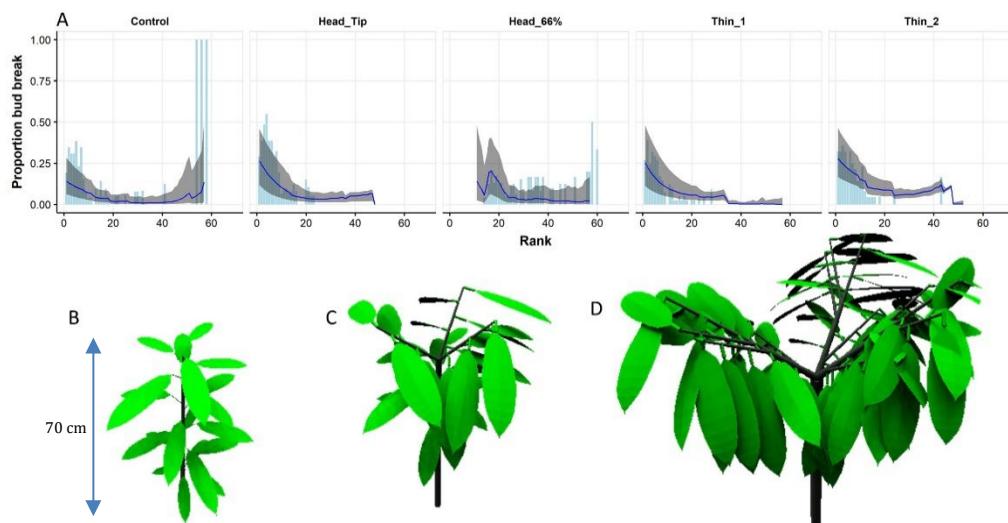


Figure 1 A) Results of the parameterization experiment: Observed proportion of primary branches that had a new secondary branch on a given rank (counting from top of the branch) after one flushing episode per pruning treatment (light blue bars). Blue lines show the predicted probability of observing a secondary branch per rank and the grey areas indicate the 95% confidence interval of model predictions as determined in the experiment. B-D) Visualization of stages of cocoa development simulated with the cocoa FSPM from 6 months to approx. two years, using the GroIMP plant modelling platform. B) Seedling at initiation C) Jorquette formation. D) Secondary branching.

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An evaluation of light distribution and light interception efficiency within Chinese bayberry tree canopy

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Keywords: multi-view images, 3D reconstruction, canopy structure, radiation model

Introduction

Light is the main energy source for plant photosynthesis. Plant architecture and canopy structure determine the internal light distribution and the light interception efficiency, which affect plant growth and development process in turn. Light distribution within fruit tree canopy is one of the important factors to optimize fruit trees architecture and to improve the potential production. The field measurement for light distribution within tree canopy is time-consuming and labor-consuming. Recent advances in image-based 3D reconstruction offer the opportunity of high-throughput tree canopy and the method of high-efficient light distribution (Hui et al., 2018; Zhu et al., 2020). The main aim of this study was to reconstruct Chinese bayberry tree canopy and to evaluate the light distribution and light interception efficiency within the tree canopy based on the multi-view stereo (MVS) approach.

Materials and Methods

There were 700 to 900 multi-view images for one Chinese bayberry tree obtained by moving a camera around the tree canopy. The vertical and horizontal spacing were 20~30° between adjacent camera positions. Three-dimensional point clouds were reconstructed from images based on the MVS-SFM (Multi-View Stereo and Structure From Motion) algorithm. Noisy point removal and point cloud segmentation were based on the Point Cloud Library (PCL), which contains a series of modular libraries, such as filters, registration, segmentation, surface reconstruction and visualization. The encapsulating, smoothing and filling algorithm of Geomagic Studio can automatically transform point clouds into smooth surfaces consisting of triangular facets. The light distribution within the 3D Chinese bayberry tree canopy was calculated by ray-tracing method in a 3D radiation model, which is composed of direct light and diffuse light. Finally, we calculated the light distribution, light interception and potential photosynthetic biomass in different canopy heights. Scenario analysis was used to quantify the effect of tree architecture on the light distribution and potential photosynthetic biomass.

Results

The light is mainly distributed in the periphery of the canopy and in the upper middle layer of tree canopy. Due to the severe occlusion of foliage and branch, the light is less in the inner and in the lower-middle layer of the canopy. The radiation received by the tree canopy showed a single peak change over time, due to the strongest solar radiation at noon and the weakest at morning and evening in sunny days. The light interception efficiency was different significantly among different canopy structures. Chinese bayberry tree with open-center had the highest potential photosynthetic biomass and high light interception efficiency, indicating that its canopy structure is more reasonable.

Discussion

At present, precise automatic segmentation of the leaves and branches from the inside of tree canopy is the bottleneck due to the severe occlusion between leaves in the field environment. Therefore, further algorithm optimization is still needed, particularly for the canopy position with severe occlusions. Quantification of light distribution and light interception efficiency within

Chinese bayberry tree canopy, and exploration of the effect of tree canopy structure on potential production provide reference for pruning and ideal tree architecture design.

Conclusion

The accurate reconstruction of 3D Chinese bayberry tree canopy based on multi-view images provides the possibility for high-throughput 3D canopy structure measurement in the field and allows a better understanding of the relationship between canopy architecture and the light environment.

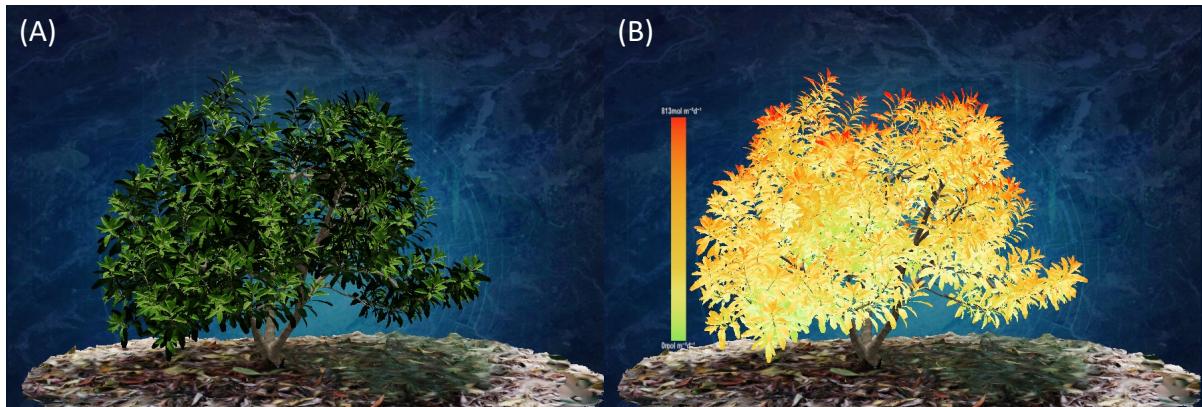


Figure: The Chinese bayberry tree model (A) and light distribution within the tree canopy (B)

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Towards berry sunburn simulations with the functional-structural plant model *Virtual Riesling*

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Keywords: climate change, grapevine, heat, canopy architecture, plant management

Climate change impacts viticulture in different ways. Rising average and peak temperatures, heat waves and elevated CO₂ levels have been observed and are expected to aggravate in the future. This affects the development of grapevines. Temperature-induced changes in phenology have already been observed and plant architecture might respond to higher temperatures and CO₂ levels (Bahr et al., 2021a; Schmidt et al., 2022). Yield and fruit quality could potentially decrease or increase and management may need to be adjusted. The latter is also related to diseases and disorders such as pests or berry sunburn, risks which can increase in future vineyards under changed climate conditions (Bahr et al., 2021a; Gambetta et al. 2021).

In this context, berry sunburn is a risk in viticulture which might increase and become very difficult to predict under the changing environments. A light-boosted heat impact damages the epidermal tissue and this disorder can lead to yield and quality loss. Exposure of berries to sunlight appears to be a key driver of sunburn, along with temperature and berry susceptibility. When berries are suddenly exposed to sunlight, for example after leaf removal followed by high temperatures, the risk of sunburn can increase significantly. On the other hand, sun exposure can also cause berries to adapt to sunlight over time while increasing berry age may again increase susceptibility to sunburn (Gambetta et al., 2021). This highlights the importance of the time course of local light conditions on berries which depend strongly on plant architecture and plant management (e.g. row orientation, row height, leaf removal). It is, however, a challenge to predict such conditions.

Grapevines in vineyards show strong architectural heterogeneity (Schmidt et al., 2019). Thus, each berry is exposed to sunlight differently. While growth of shoots is driven by genetics and environmental conditions, the architecture is also strongly determined by plant management. The trellis system, shoot positioning, leaf removal or pruning for instance, greatly influence the light penetration into canopies (Bahr et al., 2021a; Bahr et al., 2021b). Both, growth and management result in constantly changing local environmental conditions throughout the season. Therefore, to assess the effect of climate change on berry sunburn occurrence it is necessary to consider interactions between plant growth, management and the effects of future environmental conditions.

Such complex interactions can be simulated with functional-structural plant models (FSPM). The FSPM *Virtual Riesling* simulates the daily growth of Riesling (*Vitis vinifera* L.) canopies in a vineyard scene based on temperature and descriptive growth functions. It is coupled with a light model and considers vineyard setup such as row orientation, and in season plant management such as shoot positioning, for instance. Morphological processes are temperature sensitive and allow the model to capture year-to-year variability (Schmidt et al., 2019). This makes the model suitable for accounting for local light environments during the simulation period.

In this study, we assume that modelling of berry sunburn should be possible if local light exposure, berry surface temperature and susceptibility of berries are known (Bahr et al.

2021a). The focus of the model input is initially on morphological and phenological characteristics of grapevines. Accordingly, we show how to extend the model *Virtual Riesling* with such a berry sunburn model based on these assumptions to investigate the risk of berry sunburn under future climate conditions. The extended model includes calculations of the surface energy balance of the individual berry based on local radiation and heat fluxes that vary with the canopy architecture. Berry surface temperatures, thus also predicted berry sunburn occurrence, hence depend on changing local environments.

We then show the first results on the occurrence of sunburn in a virtual vineyard. Since the model is ultimately intended to identify management strategies that minimise the risk of berry sunburn in future vineyards (Fig. 1), we conclude by discussing open questions regarding model development and parameterization.

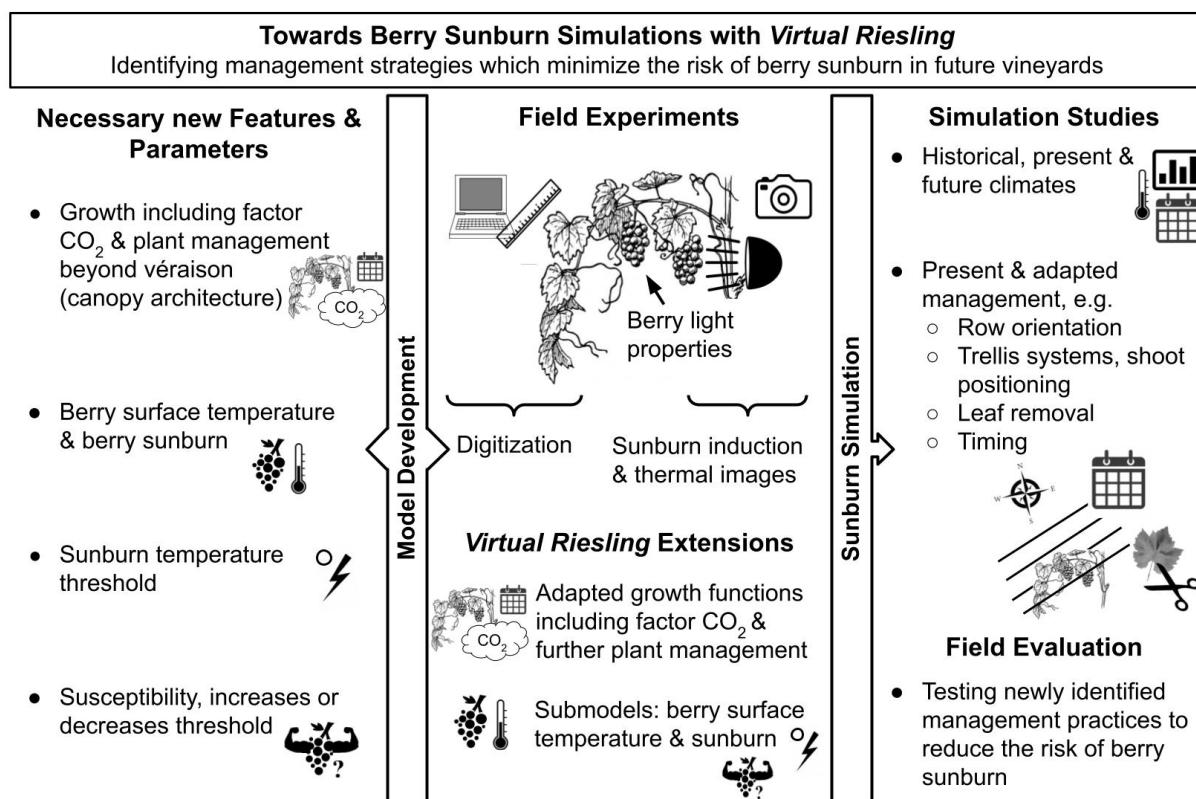


Figure 1: Brief overview of the model development and the planned simulations on the occurrence of berry sunburn in a virtual Riesling (*Vitis Vinifera L.*) vineyard under different environments and management practices. The model *Virtual Riesling* must first be extended with new features and parameterization. This requires field experiments and model implementation. *Virtual Riesling* will then be used to simulate the occurrence of berry sunburn in a virtual vineyard under different environments and management practices. Newly identified management practices that potentially reduce the risk of berry sunburn are going to be tested in field trials.

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Digital Twin of an indoor plant phenotyping facility: use of high frequency aerial biomass monitoring for improved data assimilation between measured and simulated point cloud data in the CPlantBox FSPM

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Keywords: data simulation, controlled environment agriculture, digital phenotyping

Introduction

This work falls in the scope of the booming development in automated phenotyping platforms. In this field where sensors measure large amounts of data in live experiments and models such as FSPM are more and more developed, the Digital Twin paradigm is really the next step.

We present a Digital Twin infrastructure of a controlled environment facility designed to conduct phenotyping experiments on leafy greens, such as lettuce (*Lactuca sativa* L.), with the main purpose of studying the response of photosynthesis and more broadly plant development to varying lighting conditions. Our Digital Twin takes inspiration in all 6 variations of the term as defined by Verdouw et al. (2021). Its physical counterpart comprises the growth facility, sensors, actuators and measured data; while its virtual counterpart is based on the CPlantBox FSPM (Zhou et al., 2020) for the modeling of plant growth – as well as automation routines used for the regulation of environmental parameters.

The phenotyping infrastructure was designed to image plants with a nadir-pointing camera. This design choice comes with the advantage of having a fixed view point during whole growth cycles, offering consistency over time. But also the main shortcoming that results from a fixed point of view located above the plants: occlusions of lower parts of the plants as new leaves grow.

Through the fine tuning of the twinning process in the form of data assimilation (Liu et al., 2019), we aim to automate the parametrization of the CPlantBox model of the plants of interest and therefore solve the issue of occlusions. At this stage, the focus is on the twinning between RGB-D data acquired through a Microsoft Kinect Azure camera and the plant architectures simulated with CPlantBox. Plant biomass was also measured as supplemental data to improve model parametrization.

Materials and Methods

The *in vivo* experiment was conducted on 8 *Lactuca sativa* L. plants in a hydroponics facility with controlled environment (logged and regulated parameters were: irradiance, ambient temperature and relative humidity, ambient CO₂ concentration, hydroponics solution's pH and fertilization level). Observations of the plants were in the form of imaging data through a Microsoft Azure Kinect RGB-D camera, providing RGB images, depth maps as well as 3D point clouds at an hourly frequency. A custom weighing system made of load cells was designed to measure aerial biomass at high frequency: mass data was logged every 10 minutes as a compromise between high temporal resolution and data volume.

To constitute the virtual counterpart of our Digital Twin, a new functionality was added to CPlantBox in the form of a virtual time-of-flight camera, designed to capture 3D point clouds of simulated plants and thus mimic the 3D point clouds from the physical counterpart of the Digital Twin. The virtual camera was designed to produce 3D point clouds representative of the real data, and the point cloud acquisition process is based on a ray casting algorithm so as to reproduce point clouds presenting the same shortcomings as real data in terms of occlusions of the lower parts of the plants' architecture.



(a) Point cloud from a Kinect Azure RGB-D camera in nadir view of a young *Lactuca sativa* L. plant. The color scale is mapped on the green intensity value of each point.

(b) Point cloud simulated by reproducing a virtual RGB-D camera within a CPlantBox modeling. Darker areas represent occlusions due to leaves being hidden from the camera by other leaves.

Figure 1: Measured and simulated point clouds of *Lactuca sativa* L.

Conclusion

The virtual camera provides simulated 3D point clouds at a computational cost very low compared with the duration of the plant simulation itself. The proposed method provides a tool to compare plant structure and geometry with simulated data, paving the way for future developments where *in silico* experiments will mitigate the need for *in vivo* experiments.

The captured point clouds contain rich information (plant projected area, texture, color, 3D structure, volume of convex hull, ...) that can be compared to features of the simulated data. Finally, the simulated 3D point clouds will help solve the issue of occlusions through data assimilation. The biomass measurements will prove useful as supplemental information for the twinning between virtual and physical counterparts of the Digital Twin.

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From functional-structural tomato model to tomato digital twin

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Keywords: virtual greenhouse, greenhouse climate, *Solanum lycopersicum* L., phenotyping

Introduction

Digital twin is a concept used in many areas with applications in prototype design, production optimisation, monitoring, predictions, or virtual testing. It is also an emerging trend in greenhouse horticulture (Ariesen-Verschuur et al., 2022), which is increasingly data-driven, also due to rapid technology developments and the availability of sensors in the area of plant phenotyping. A digital twin is a virtual and dynamic representation of a real object that mirrors its states and behaviour (Ariesen-Verschuur et al., 2022). Although the exact definition seems to vary in different application areas, there are 3 important parts of a digital twin: a model, an evolving set of data relating to the object, and a means of dynamically updating the model based on the data (Wright and Davidson, 2020).

We designed a proof-of-concept digital twin of a tomato crop with the aim to help increase resource use efficiency of greenhouse tomato systems. At the core of this digital twin is a dynamic functional-structural plant (FSP) model. FSP models can simulate plant development and growth in 3D and can be used to predict crop response to environmental factors and management decisions. Dynamic changes in tomato shoot architecture in response to temperature treatments can be well captured by using an FSP model (Chen et al., 2014). In this study, we built on the concepts from their model and added functionality to be able to simulate growth and yield for different cultivars and explore strategies in tomato cultivation, e.g., in lighting and leaf pruning. To make the FSP model suitable for a digital twin application, further functionality was added to support model updating based on data collected from climate sensors and camera images (see van Daalen et al., Xin et al. in this Book of Abstracts).

Materials and Methods

The FSP model was developed in the GroIMP platform (gitlab.com/grogra/groimp), version 1.6. In order to simulate light distribution inside the greenhouse compartment, the model incorporates the tomato plants, planting pattern of the crop, and greenhouse construction. An interface was developed to link the FSP model to a greenhouse climate model Kaspro (de Zwart, 1996), which simulates indoor climate using outdoor climate data and greenhouse properties. To present the results of model simulations to the stakeholders, a new application in Unity was developed that enables interactive visualisation of different scenarios.

To collect data for model development, experiments were conducted in 2021 in the Netherlands Plant Eco-phenotyping Centre (www.npec.nl) facility with four tomato cultivars: 'Merlice', 'Brioso', 'Moneymaker', and 'Gardener's Delight'. A plant-to-sensor system was used to image all plants approximately every 3 days. To calibrate the model for different cultivars, additional manual measurements were performed on optical properties of leaves, photosynthesis light and CO₂ response curves, as well as biomass and size over time.

Results and Discussion

Our FSP model of tomato allows for the simulation of light distribution. It takes into account shading patterns caused by the greenhouse construction, the planting pattern, 3D plant architecture, and optical properties of leaves to quantify light capture by individual leaves. Leaf carbon assimilation is done using the light absorbed by the leaves, and assimilate allocation is calculated based on the concepts of source/sink balance. Organ production and sink duration are temperature driven. The environmental inputs used by the model (incoming light, temperature, CO₂) are calculated by the climate model.

Simulation results can be imported into a Unity application (Fig. 1). Currently, this application allows for the comparison of two scenarios, illustrated by a selection of climate variables and model outputs. Sliders can be used to interactively visualise the daily and seasonal change in sun position and to show the evolution of 3D plant architecture at daily intervals, also in reverse order.

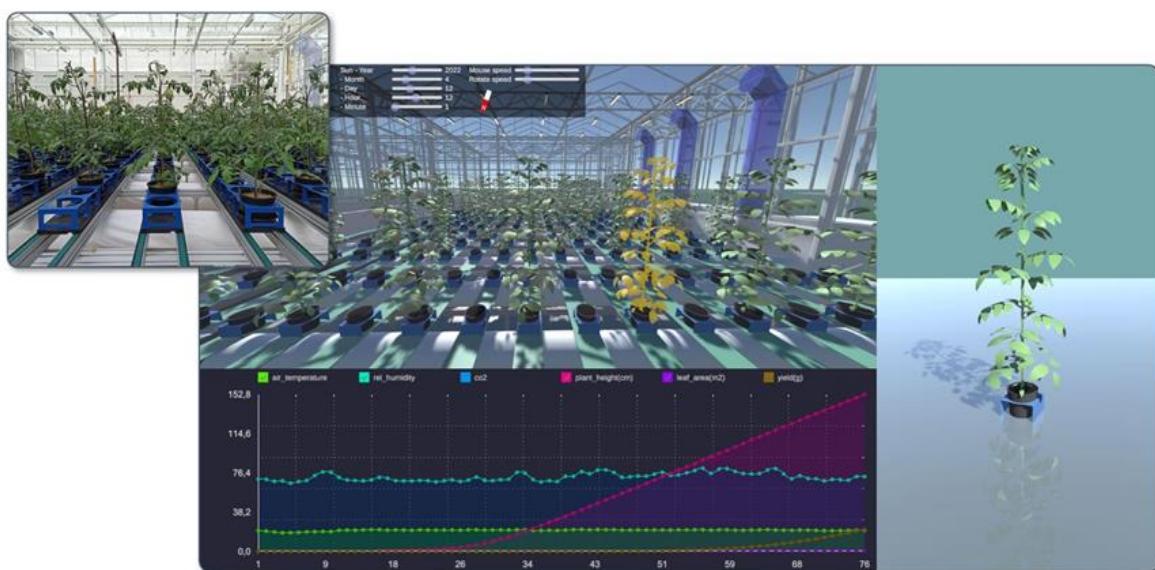


Figure 1: Digital twin application with virtual representation of a real crop inside a greenhouse.

Conclusion

The model can simulate feedback between light absorption by leaves and assimilate production, allowing to run scenarios for different cultivars and cultivation strategies. Our model is especially useful in a digital twin framework when the role of individual plant traits or the effects of manipulation of plant architecture (e.g., pruning) are relevant. A forthcoming analysis will show which model parameters, and thus which sensor data, are minimally required for a digital twin relevant for a greenhouse tomato cultivation.

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A turgor-driven functional-structural model of spring wheat development for vertical farming and extra-terrestrial life support systems

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Keywords: Turgor pressure, photosynthesis, plant architecture, light distribution, *Triticum aestivum* L.

Green plants in extra-terrestrial habitats have many benefits such as converting carbon dioxide to breathable oxygen, providing food, and improving the mental wellbeing of the inhabitants. Wheat is a favourable candidate to grow in these extra-terrestrial life support systems because of its efficiency in converting energy into a high grain yield, its capability to grow well in continuous light condition, and its familiarity for both producer and consumer. However, optimizing wheat growth in these systems is still a challenge due to the complex interaction between the plant and its environment. This is particularly important, since these systems require a substantial amount of energy to provide artificial lighting in an environment where energy and space are limited. Addressing these challenges also helps solving terrestrial challenges of growing wheat in vertical farms. FSPMs are particularly well-suited for simulating 3D light interception by plants. Hence, it can be applied to optimize growing conditions, investigate growth and yield potential for wheat in the aforementioned applications.

In the present study, we developed a dynamic functional-structural plant model for dwarf spring wheat, which relies on a turgor-driven growth approach. This model incorporates a photosynthesis–stomatal conductance–transpiration (P-SC-T) sub-model to estimate transpiration and photosynthetic rates of the plant. Both are used by the turgor-driven growth sub-model as inputs for the available carbon and total transpiration of each organ. Carbon allocation is based on the common assimilate pool concept, where the sink strength of each plant organ is determined by the organ's extensibility and age. Plant growth rate is based on the turgor-time concept, which normalizes growth patterns to water availability (Coussement et al., 2021). To calibrate the growth and physiological parameters, an experiment in controlled environment with two light regimes has been carried out.

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Hierarchical Developmental Timeline Warping: a generic method to design realistic plant architecture models

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Keywords: Organ development synchronization, L-systems, virtual plants

Virtual models of plant architecture are needed for diverse applications in developmental biology, agronomy, botany or computer graphics. They can be used for hypothesis testing, data annotation and augmentation associated with deep-learning training or for producing photorealistic rendering of plants. To match the increasing needs of these applications in precision and realism, virtual plants with increasing realistic details are required. However, the design of such detailed models remains a complex task and new techniques are required to ease this process.

L-systems (Prusinkiewicz 1990) is now a standard procedural approach to model plant architecture development. Their use has been eased by efficient modeling environments (Prusinkiewicz 2018, Boudon 2012) and over years, these systems have incorporated solutions to better capture plant growth dynamics, such as positional information to describe gradients of characters along plant axes (Prusinkiewicz 2001) or multiscale descriptions of plant architectures (Ferraro 2002, Boudon 2012). However, one aspect is still partially lacking: a conceptual strategy to naturally orchestrate in time the growth of different plant parts.

A first step in this direction was proposed in (Prusinkiewicz 2018) where all the parameters controlling the various aspects of organ state or growth are described by functions of a normalized time between 0 and 1. This normalized time is then mapped on either the absolute time of the simulation, or the organ age (i.e. a relative time), using a timeline that stretches each parameter normalized time onto absolute/relative time. Thanks to a timeline editor, the variation in time of the different functions is graphically controlled and the different parameter timelines are adjusted to absolute or relative time. Illustrating the flexibility of this timeline-based strategy, (Cieslak 2021) showed very realistic virtual plant architectures reconstructed by visual and interactive calibration on 2D photographs of real plants.

In this approach, however, all plant parameters are controlled at a unique level of organization, making it difficult to handle the complexity of a possibly important number of control parameters and to design modular components. To tackle these issues, we developed a complementary timeline-based approach, where the hierarchy of plant parts is described by a corresponding hierarchy of developmental timelines. For each simple or composed organ, a reference (normalized) timeline is defined. Different stages of development of the organ are associated with different time-points of this reference timeline between 0 and 1 (Fig 1A). These stages are characteristic morphological steps, which can be easily and reproducibly defined across different individuals, genotypes, or even species, but do not occur at identical time points. In composed organs, the timelines of the component organs are therefore mapped onto that of the parent organ using user-defined warping functions, reflecting genetic or environmental regulations. At the plant level, this builds a hierarchy of timelines warped onto each other in a nested manner (Fig 1B,C,D). At the top level of the hierarchy, the timeline is itself warped onto the real chronological time (Fig 1A). Hence, the developments of all organs are synchronized with each other as well as with the absolute timeline. To model different genotypes or growth conditions, the component

models can be tuned independently (e.g. changing their size or shape) while their synchronization with the parent organ is adapted using timeline warping functions.

We tested our HDTW strategy in order to reproduce realistic virtual architectures of the model plant *Arabidopsis thaliana*. For this, we grew real plants in standard indoor conditions and manually collected various quantitative information on the plant at different scales, focusing on the relative and absolute developmental dynamics of many plant parts and organs. Depending on the trait, hierarchical timelines were either calibrated by measuring the same plants over days (Fig. 1I), or from snapshot pictures, taking advantage of the repetition of the same developmental sequences along the plant axis (Fig. 1F,G). Models constructed with this strategy can reproduce precisely plant architectural dynamics at different scales (Fig. 1E,H).

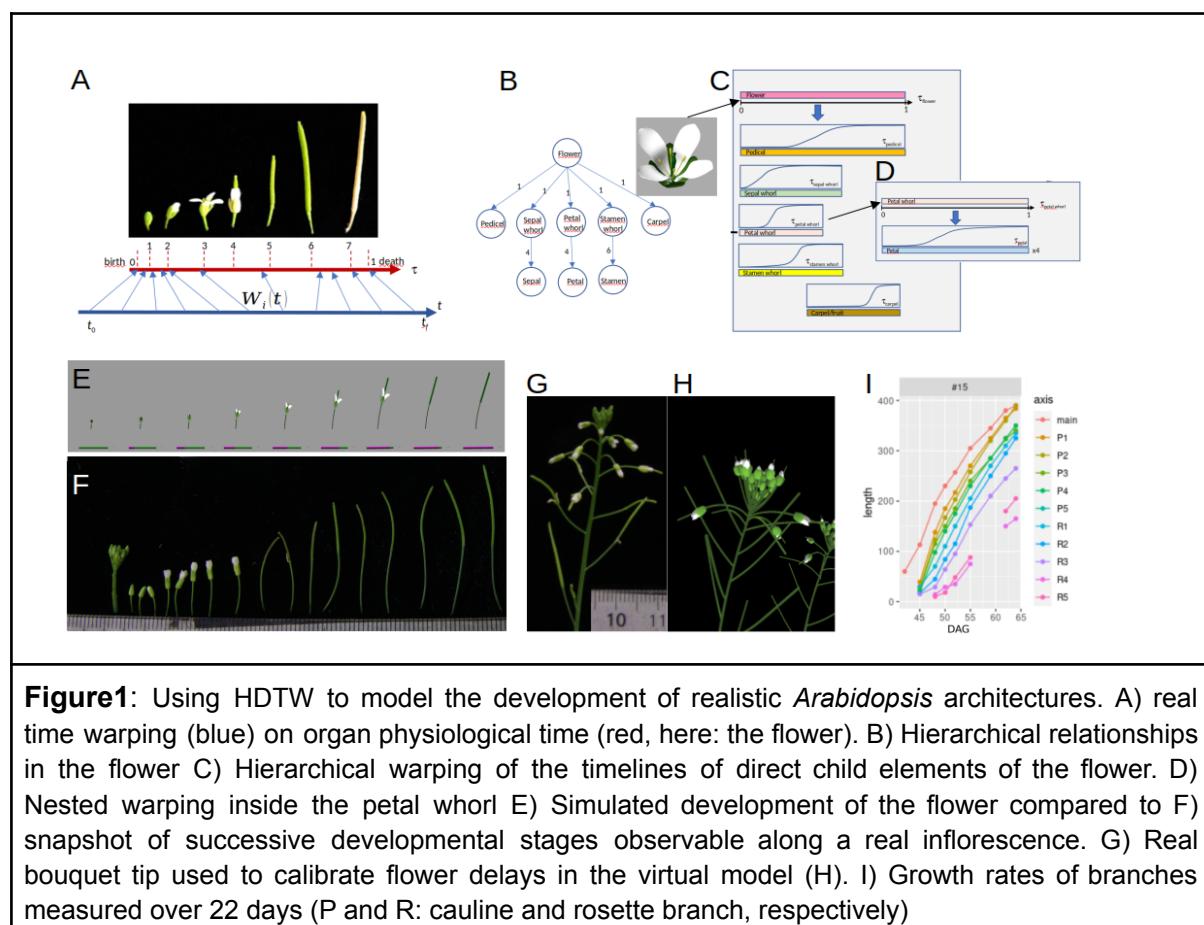


Figure 1: Using HDTW to model the development of realistic *Arabidopsis* architectures. A) real time warping (blue) on organ physiological time (red, here: the flower). B) Hierarchical relationships in the flower C) Hierarchical warping of the timelines of direct child elements of the flower. D) Nested warping inside the petal whorl E) Simulated development of the flower compared to F) snapshot of successive developmental stages observable along a real inflorescence. G) Real bouquet tip used to calibrate flower delays in the virtual model (H). I) Growth rates of branches measured over 22 days (P and R: caudine and rosette branch, respectively)

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Benchmarking of Functional-Structural Root Architecture Models

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Keywords: virtual plant, root system, water uptake, model improvement

Introduction

This work follows up on the call for participating in the collaborative benchmarking of functional-structural root architecture models (Schnepf et al., 2020): “Call for Participation: Collaborative Benchmarking of Functional-Structural Root Architecture Models. The Case of Root Water Uptake”. The call includes benchmark problems for root growth models, soil water flow models, root water flow models, and for water flow in the coupled soil-root system. All the benchmarks and corresponding reference solutions were published in the form of Jupyter Notebooks on the GitHub repository <https://github.com/RSAbenchmarks/collaborative-comparison>. Here, we show results and solutions to the benchmarks problems provided by several groups that develop functional-structural root architecture models.

Materials and Methods

The benchmark problems are outlined in Fig. 1. The first set of problems aims to test individual modules of the overall system, including root architecture development (M1), water flow in soil (M2), and water flow in roots (M3). The second set of problems tests the coupled system for static (C1) or growing (C2) root systems.

The focus of this contribution is on water uptake from a drying soil by a static root architecture and thus specifically looks at results to benchmark problems M2, M3 and C1. The reference solutions are described in Schnepf et al. (2020). The numerical solutions of the different participating simulators as compared to the reference solutions are shown here. The participating simulators are CPlantBox, DuMu^x, R-SWMS, OpenSimRoot and SRI. They have in common that they simulate water flow in the 3D soil domain, water flow inside the root system that is represented as a mathematical tree graph, and the coupling between the two domains in form of a volumetric sink term that describes the transfer of water between the two domains. The simulators differ in the numerical schemes used for solving the water flow equations in roots and soil domains, as well as in the way the sink term is formulated, in particular in the way the possibly increased rhizosphere resistance to water flow is accounted for.

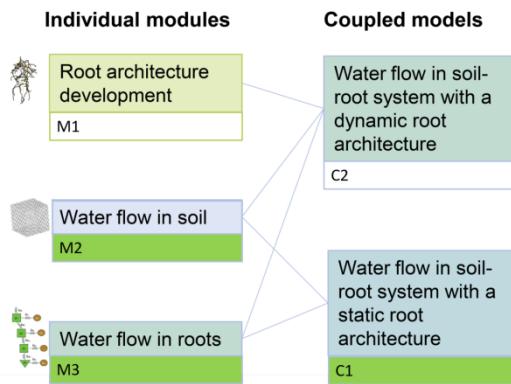


Figure 1: The benchmarking includes problems to test the individual modules for root architecture development (M1), water flow in soil (M2) and water flow in roots (M3), as well as problems to test differently coupled systems (C1, C2). Results of M2, M3 and C1 are presented here.

Results and Discussion

The results to the water flow in soil benchmarks show how the different simulators perform against the analytical solution to a problem of infiltration into an initially dry soil, as well as a problem of evaporation from an initially moist soil. All of the simulators could accurately predict the infiltration front in different soil types as well as the actual evaporation curves.

The coupled problem of root water uptake by a static root architecture from an initially already dry soil posed a bigger challenge to the different simulators and revealed some diversity between the different solutions. The Benchmark with an initially rather dry soil defined a potential transpiration that immediately induced water stress of the plant. The simulators had to simulate the consequent rhizosphere drying and associated increase in rhizosphere resistance. All of the soil simulators smoothed the gradients in the rhizosphere at the soil grid size such that root water uptake was significantly overestimated unless the rhizosphere resistance was explicitly accounted for in the root water uptake model. As a result, all simulators came close to the reference solution (that itself is a numerical solution, see Schnepf et al. 2020 for details).

Conclusions

In this study, we showed that all simulators are generally able to solve the benchmark problems but minor differences occur amongst the simulators when simulating different soil types. Benchmarking led to model improvements and helped interpret model results in a more informed way. The availability of “reference solutions” made modellers aware of the range of validity of their numerical solution and encouraged them to improve either their numerical solution or to introduce new processes Future efforts may aim to extend the benchmarks from water flow to further processes, such as solute transport or rhizodeposition.

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The FSPM platform GroIMP, its ongoing upgrading and some new extensions and plugins

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Keywords: GroIMP, simulation software, Java, plant structure, interactive selection, grouping, scene editing, point clouds, clustering, RSML

GroIMP (Growth-grammar related Interactive Modelling Platform) is a software tool designed to develop functional-structural plant models based on parallel graph transformations, generalizing L-systems (Kniemeyer, 2008; Kniemeyer and Kurth, 2008) and offering various possibilities for interactive editing of scenes and for exchange of data. We will present our recent progress in upgrading the software to the latest Java versions and in improving the internal organization of its code, with the aims of better efficiency and transparency. Furthermore, extensions and plugins will be demonstrated which solve the following tasks:

- Interactive selection and grouping of objects (e.g., plant organs) using geometrical constraints or arbitrary choices of the user and employing multiscale representations (cf. Ong et al., 2014),
- editing and segmentation (using density-based cluster formation, Ester et al., 1996) of point clouds representing parts of plants,
- insertion of measurement-based leaf shapes into structural plant representations embodied in the dtd file format,
- import and export of root system representations given in the RSML format (Lobet et al., 2015).

We will demonstrate these and some more features of GroIMP and discuss the further development of the software.

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MaCS4Plants: A mathematic & computer science network for FSPM

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Keywords: FSPM, Computer Science, Modelling workflow

Introduction

Since the early 90's, AMAP lab (Montpellier, France) has developed multiple software applied to plant architecture modelling. AMAPstudio embeds models and applications to simulate the structure (AmapSim, RoCoCau), the function (ARCHIMED), and visualize (Xplo, Simeo, Scan) plant architecture and functional outputs (e.g., light interception, carbon assimilation). These tools were first developed in collaboration with researchers doing in-field traits and architecture measurements, for plants species studied in natural forests, agroforestry systems and crops. More recently, AGAP Institute developed the OpenAlea platform (Pradal et al., 2008) to answer the growing need for computational resources coming from the increasing complexity and scale of applications of plant models, and for data analysis associated to new data acquisition techniques such as high-frequency phenotyping platforms or LIDAR measurements. Both AMAPstudio and OpenAlea are designed for providing modelling tools for the FSPM community, they share common formalisms for plant representation (*i.e.*, MultiScaleTreeGraph, mtg; Godin et Caraglio, 1998) and similar 3D edition and visualization tools. However, these tools have largely diverged for multiple reasons: language source code, integration in different platforms, plants with different architectures studied for specific research topics but also different laboratories with distinct needs and directives. Therefore, although many human and financial resources were mobilized, they were organized in an inefficient way that led to a duplication of work and hindered the tackling of important scientific questions and upcoming challenges mobilizing the FSPM community.

Materials and Methods

In this context, researchers and engineers specialized in mathematics and computer science from AMAP and AGAP decided to gather their expertise into the Mathematics & Computer Science (CS) network For multiscale functional structural modelling of Plants within their agroecological systems (MaCS4Plants). This network aims at providing an extensive library of generic functional models (e.g. Albasha et al., 2019, cf. also Vezy et al., 2022, talk in this conference) as well as tackling scientific problems in the math and CS domain applied to agroecological transition and resilience to climate change: big data analysis, hybrid modelling, multiscale and structure-function studies or full plant modelling (*i.e.*, root and shoot). The technical objectives are: i) to offer a coherent and integrated modelling offer to the community based on OpenAlea platform, ii) develop scientific workflows to automatically and efficiently integrate, develop, test and distribute models, iii) provide an extensive documentation and a large set of example notebooks, from a short demo of a model to a full workflow for reproducible paper. The aim of these notebooks is to ease reproducibility and offer training material for FSPM modelling to young students, researchers and collaborators.

Results and discussion

In this study, we will present the first achievements of the MaCS4Plants network:

- An extensive catalogue of modelling software developed and their integration into OpenAlea (<https://openalea.rtfd.io>).
- The proposal of a standard format that integrates both topology and geometry at multiscale of plants, and the possibility to export it toward common 3D visualization software.
- A set of online didactic interactive notebooks on FSPM.

An example application with the PalmStudio project will be presented (cf. Fig. 1) to showcase a complex FSPM application integrating multiple models written in different languages (C++, Fortran, Python, Java, Julia), and interacting at different space and time scales. PalmStudio models shoot and root architecture development in interaction with the environment.

Conclusion

Finally, we advocate for the need to facilitate interoperability of models via easy integration into existing platforms but also via development of standard formats. Therefore, we emphasize the fact that this network is open to anyone willing to collaborate and aims to be a first step toward a similar initiative at international level.

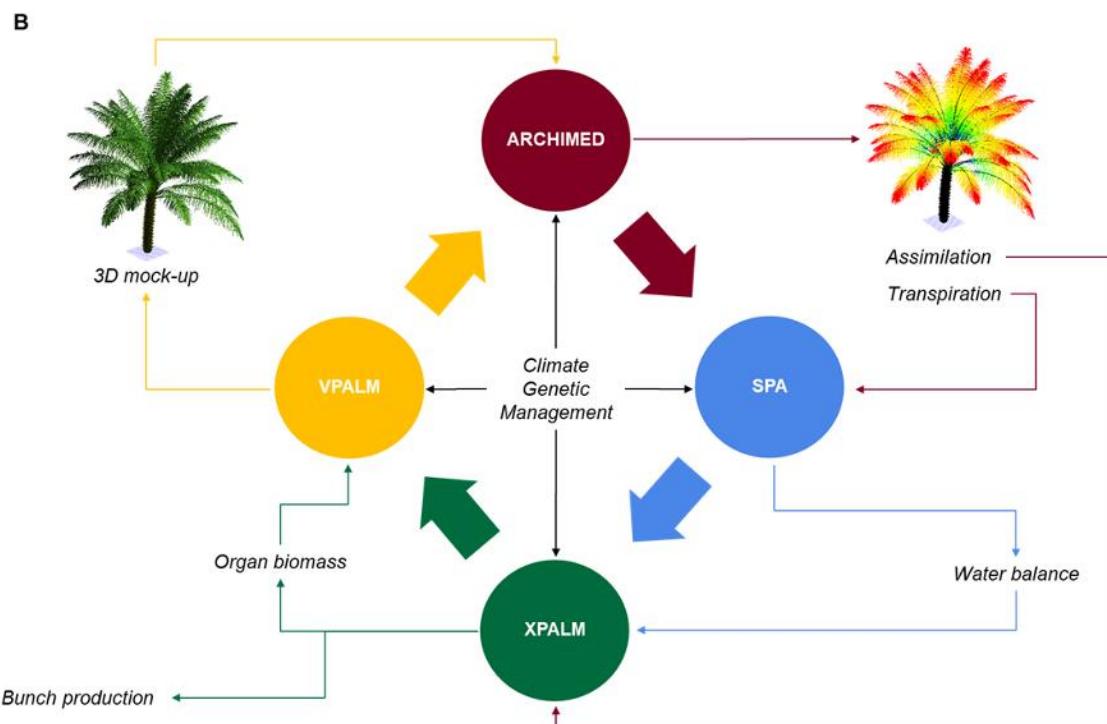


Figure 1: Diagram of the PalmStudio FSPM workflow. This final workflow aims at simulating the growth of palm plants, representing a realistic system based on in-situ architectural and geometrical measurements, and simulating biophysical processes such as light interception, energy balance, CO₂ and H₂O fluxes in interaction with the root system and the soil, and finally allocating assimilates for organs growth and development and eventually plant yield.

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PlantBiophysics.jl: a Julia package for fast and easy calibration, prototyping and simulation of biophysical models

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Keywords: FSPM, crop model, energy balance, photosynthesis, stomatal conductance

Biophysical processes are important factors to account for in the soil-plant-atmosphere continuum to predict the fluxes of energy, CO₂ and H₂O in the system. They include processes such as photosynthesis, evapo-transpiration, energy balance, temperature, or stomatal conductance. Biophysical models have been continuously developed for several decades to better understand and predict those processes, but they are still either complicated to use (e.g. compiled monolithic models) or slow to compute (e.g. implemented in R or Python), and very often the sub-processes included in those models are complicated to extend and evaluate independently. Furthermore, there are often many implementations to simulate the same process (e.g. see stomatal conductance models reviewed in Buckley (2017)), mostly only differing by a slight correction or improvement in their formulation. For example, Schymanski and Or (2017) corrected the model of Penman-Monteith by clarifying the number of sides exchanging sensible and latent fluxes in leaves. Those model implementations are developed for various reasons, including improvements in the knowledge about a process, different constraints for the simulation scale, data availability, or computational intensity. In this context, it can be difficult to choose one model over another, or even to evaluate their accuracy or applicability considering the particular objectives of the simulation. Besides, current tools only propose a limited set of models, without the possibility to easily add or compare external models.

Consequently, a tool that allows both user friendly code development (*i.e.* calibrating, prototyping, switching, extending and coupling models with the ease of an interpreted language such as R or Python), and fast computation to put the model in production (*i.e.* with the speed of a compiled language such as FORTRAN or C) would be useful for the community. We propose a new software, **PlantBiophysics.jl** (Treillou et al., in prep.), that implements such requirements including:

- Soft learning curve and ease of use thanks to the extensive documentation: <https://vezy.github.io/PlantBiophysics.jl/stable/>;
- Easy model evaluation thanks to a fine control over model coupling and degrees of freedom (*i.e.* variable forcing)
- Easy parameterization with automatic fitting methods for the models
- Scaling of the models from a simple organ to an entire plant, or any other 3D object;
- Strong composability that allows e.g. error propagation with no effort
- Extendability with a clear, simple and standard way of adding models and processes
- High code readability, with a unique language (Julia), and code close to the scientific article thanks to Unicode symbols such as T₁, φ or R_s
- Scalability: fast to compute, easy to integrate into other models and distribute on computer clusters

PlantBiophysics is well tested with unit, integration and evaluation tests using measured data. It was compared to the plantecophys (Duursma, 2015) and LeafGasExchange.jl (Yun et al., 2020) packages and its computation time was several orders of magnitude faster with a computation time of 7 × 10⁻⁷ seconds for one simulation (median value) of the coupled energy

balance – photosynthesis – stomatal conductance models, compared to the slower 4×10^{-2} seconds for plantecophys and 2×10^{-2} seconds for LeafGasExchange. PlantBiophysics also presented a lower prediction error thanks to its state-of-the-art and careful implementations of the models for energy balance and photosynthesis (Fig. 1). **PlantBiophysics.jl** opens new ways to easily couple and apply models at large scales without giving up user-friendliness for prototyping, calibration, and simulation, which is an important aspect for many scientists in biophysics, ecophysiology and climatology.

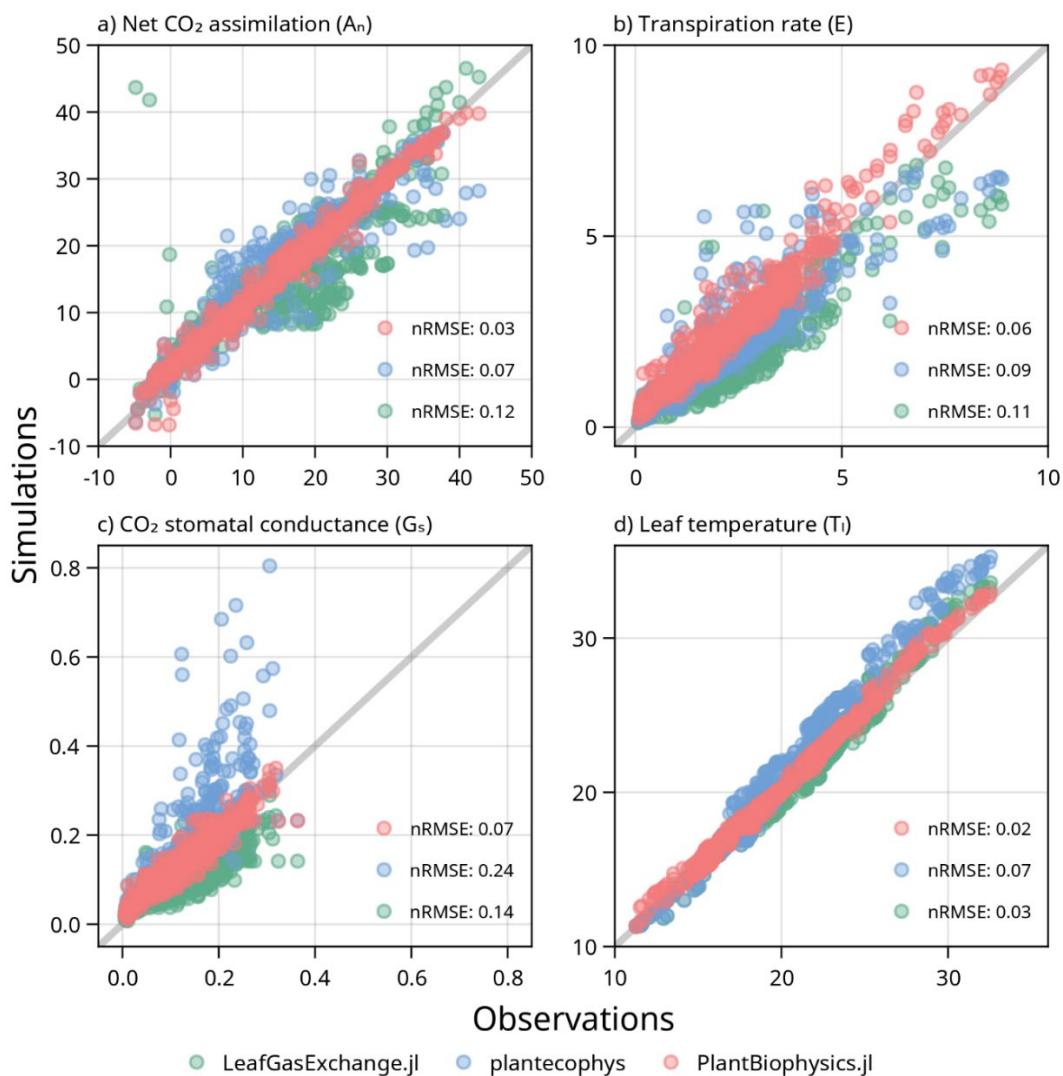


Figure 1: Measured data for *Eucalyptus delegatensis* (Medlyn et al., 2015) plotted against simulations of: net carbon assimilation (a), net transpiration rate (b), stomatal conductance for CO₂ (c) and leaf temperature (d). All simulations were performed using a photosynthesis-stomatal conductance-energy balance coupled model with LeafGasExchange.jl (green circles), plantecophys (blue) and PlantBiophysics.jl (red circles). Grey line represents $x=y$. All simulations were done with $\text{Ca} > 150 \text{ ppm}$, and were fitted using the fitting methods from PlantBiophysics.jl.

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Comparing FSPMs using unconventional computing methods

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Keywords: reservoir computing, sim-to-real, plant research, computer science

Introduction

Over the past two decades, FSPMs have seen tremendous progress in modelling capacity, scope, and applicability. However, studies involving FSPMs are often focussed on the scope of a biological question. As such, it is difficult to evaluate the general effectiveness of FSPMs when they are applied with conditions that were not accounted for initially. Moreover, comparing different FSPMs is not trivial. We proposed an initial framework based in reservoir computing in (Pieters et al., 2020), and want to extend upon this work here.

Reservoir computing (RC) is an unconventional computing paradigm. This paradigm entails using a high-dimensional, nonlinear dynamical system as a computational resource to solve a task, illustrated in fig. 1 (a). The tasks should be dependent on the input, but the underlying relationship need not be known. The readout is combined such that the desired target is approximated. Suitable systems for RC must satisfy multiple requirements, such as high-dimensionality, nonlinearity, fading memory with respect to past inputs, and sufficient separation of targets with respect to recent inputs (Nakajima, 2020). We believe plant models such as FSPMs to be good systems for RC due to their complexity and embedded memory. *In vivo* physical RC (PRC) was recently demonstrated by Pieters et al. (2022) on strawberry plants. Here, the simulated system is replaced with a physical medium (plant) that performs the computation, as illustrated in fig. 1 (b).

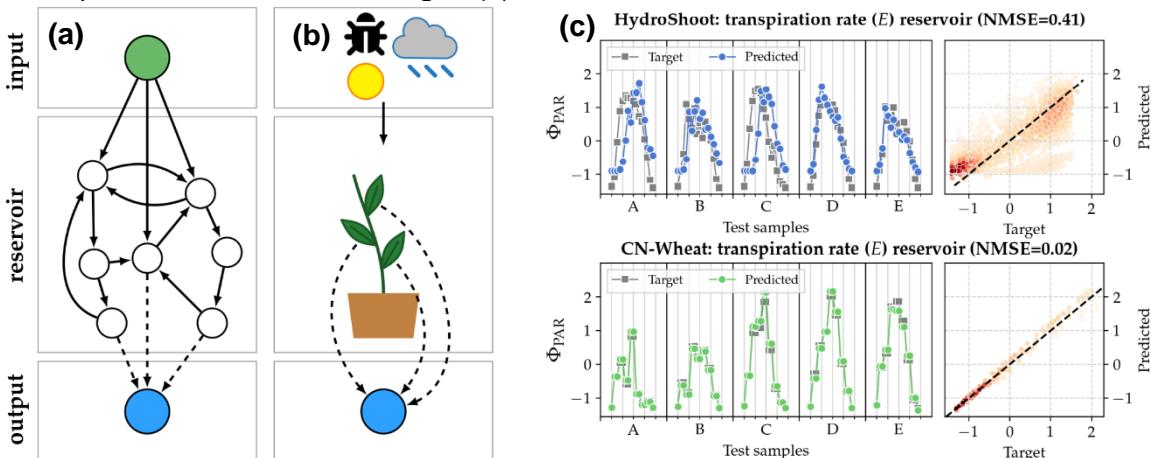


Fig. 1: (a)-(b) Illustration of a PRC system (licence: CC-BY, Pieters et al., 2022) and (c) simulation results for Hydroshoot and CN-Wheat. (a) A (simulated) reservoir computing system. The input (e.g. temperature, relative humidity and irradiation data in the case of an FSPM) is fed into the model, which is a complex system with recursion. Information is thus embedded into the system, based on current and past states through the internal dependencies. A readout function is used to map the internal state to a desired output signal. The performance of this mapping can be used as evaluation metric for computational power.

(b) A plant-based PRC implementation. The plants' state is used to estimate a target. (c) Time series prediction of photosynthetically active radiation (Φ_{PAR}) using an E -based reservoir. The left plot shows predictions for five days randomly sampled from the test set. the right shows correlation between target and predicted values. Darker colors indicate a greater density of points.

Methods

To evaluate the application of RC to FSPMs, we selected two models for evaluation: HydroShoot (Albasha et al., 2019) and CN-Wheat (Barillot et al., 2016). HydroShoot is an

FSPM of common grapevine. It has been conceived to study gas exchange in large plant canopies under water deficit conditions and to compare the effectiveness of different canopy shapes. CN-Wheat, on the other hand, is a mechanistic model of common wheat that simulates the effect of fertilization regimes on carbon (C) and nitrogen (N) metabolism in wheat culms during the three post-flowering stages of development. Currently, the RC framework is limited to the reservoirs that are unchanging over time. Plants are not static reservoirs in the general case because they go through several growth phases that drastically change their structure and behaviour. Because of this, we specifically selected plant models with a static plant structure (*in casu* HydroShoot) or a dynamic structure in a stage of post-vegetative growth (CN-Wheat). Additionally, both models operate at an hourly rate, which is necessary to generate sufficient data for training and evaluation of the readout model. For *in vivo* scenarios, stationarity can be approximated by investigating reservoir dynamics within a time window for which the growth rate is negligible (Pieters et al., 2022).

We selected transpiration rate (E) as model readout and photosynthetically active radiation (Φ_{PAR}) as target variable. E is highly variable within a plant, based on the incident light intensity and water availability. Φ_{PAR} directly influences E in a non-trivial manner, resulting in sufficient dependency and variability between target and observation. Φ_{PAR} is estimated based on a linear combination of E from different elements in the FSPM. The ridge/L2 regression loss (Tikhonov, 1963) is minimised to train the model parameters. The readout of CN-Wheat and HydroShoot consists of seven (70%) and thirty-two (10%) independent respectively. These represent the partial observations of the system (fig. 1 (a)), the percentage in brackets indicates the relative number of observations of the entire reservoir. Increasing the readout size further of HydroShoot did not improve performance (results not shown).

Models are visually compared and using the normalised mean squared error metric: $\text{NMSE} = \frac{1}{N} \sum_{i=1}^N \frac{(y[i] - \hat{y}[t])^2}{\text{var}(y)}$. This normalised version MSE allows tasks from different reservoirs to be compared.

Results and Discussion

Figure 1 (c) depicts the main results for both models: a time series prediction of (normalised) Φ_{PAR} using an E -based reservoir. HydroShoot cannot reproduce finer details, underpredicting the highest targets and overpredicting the lowest. Moreover, HydroShoot's predictions are sometimes delayed compared to the target (fig. 1 (c), samples A and C), and other times lead the target (fig. 1 (c), sample D). In contrast, CN-Wheat's transpiration rate captures finer details much better. This is also reflected in the NMSE score (0.41 vs. 0.02). This test indicates that in the context of reservoir computing and this specific metric, CN-wheat is more performant than HydroShoot. However, additional validation will be needed with additional tasks and readouts to form more coherent benchmark for the comparison of FSPMs.

We hope to improve upon these results in the future by including additional benchmark tasks, a more formal mathematical framework and more FSPMs. Moreover, we hope to guide *in vivo* PRC using *in silico* estimations of promising readout-task combinations and as such speed-up PRC research.

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Exploring symmetries in plant architectures

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Keywords: symmetry, plant architecture, tree edit distance, algorithmic clustering

Symmetries and invariance

Symmetries are ubiquitous in living forms and often reflect repetition in the mechanisms of morphogenesis. They are closely related to the mathematical concept of invariance. An object x is said to be invariant under a certain operator T when it remains unchanged under the action of the operator, i.e. $Tx = x$. Observing symmetries means identifying operators under the action of which an object remains invariant. However, in living forms, because of intrinsic biological noise and environmental effects, symmetries are often imperfect and correspond to $Tx \approx x$. Here, we investigate how these concepts can be applied to identify symmetries in plant architectures.

Symmetries in plant architectures: the swap operator

A plant architecture can be modeled as a mathematical rooted tree (Godin and Caraglio, 1998), i.e. a connected graph with no cycle in which a node, called the root, has been selected. In addition, each node in the tree may carry some additional pieces of information such as the type and the geometry of the elementary component of the plant, or even its physiological state. A subtree is a subpart of a tree made of a node and all its descendants in the tree. Macroscopic parts that are susceptible to be similar in plant architectures are often subtrees (Arber, 1950; Ferraro et al., 2005; Godin and Ferraro, 2010). In order to identify the symmetries of plant architectures, we therefore introduce the swap operator that swaps two subtrees (see Fig. 1).

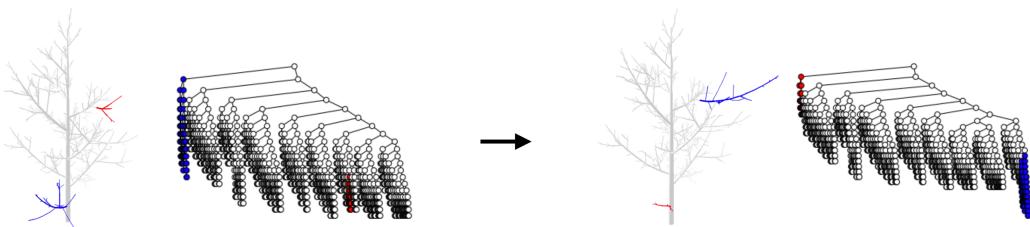


Figure 1: Illustration of the swap operator: red and blue subtrees in the original data (left) are swapped both in the mathematical tree and in the 3D plant architecture it models (right).

However, not every pair of subtrees can be swapped: if a subtree appears as a descendant of another, their swap does not make sense. A set of subtrees that can be swapped pairwise forms an antichain for the inclusion partial order: these subtrees are not related to each other by parent-child relationships. Now, we are going to see how antichains can be used to formalize the idea of symmetric (or close to symmetric) structures in trees.

Maximal symmetry antichain

A symmetry antichain is an antichain of subtrees such that their swap preserves the architecture of the plant, i.e. for any pair of subtrees t and s in the antichain, the tree T' obtained after their swap is equal (or at least very similar) to the original tree T . Such a symmetry antichain is said maximal when there is no other subtree within T that can be

swapped with one of the antichain while preserving the general architecture. Detecting the symmetries actually means identifying all the maximal symmetry antichains.

In a real plant architecture, one does not expect to observe exact symmetries. One must therefore be able to quantify the similarity between subtrees. For this, we use the tree edit distance developed in (Zhang, 1996) and already used for the comparison of plant architectures in (Godin and Ferraro, 2010). We have thus developed an algorithm to build all maximal symmetry antichains of the plant architecture that proceeds through a clustering of all its subtrees based on the above tree edit distance, instead of an exact match.

Visualization of symmetries

Within an antichain, the subtrees are not related, but from one maximal symmetry antichain to another, this may be the case. We can therefore consider the graph of maximal symmetry antichains: two maximal symmetry antichains are linked by an edge when subtrees of one appear as descendants of subtrees of the other, and the weight of the edge corresponds to the proportion of such links. Using this graph, we can therefore not only observe all the symmetries of a plant architecture but also their nesting, which represents a major difficulty when dealing with tree data (see Fig. 2). This symmetry graph actually represents the symmetry signature of the tree architecture.

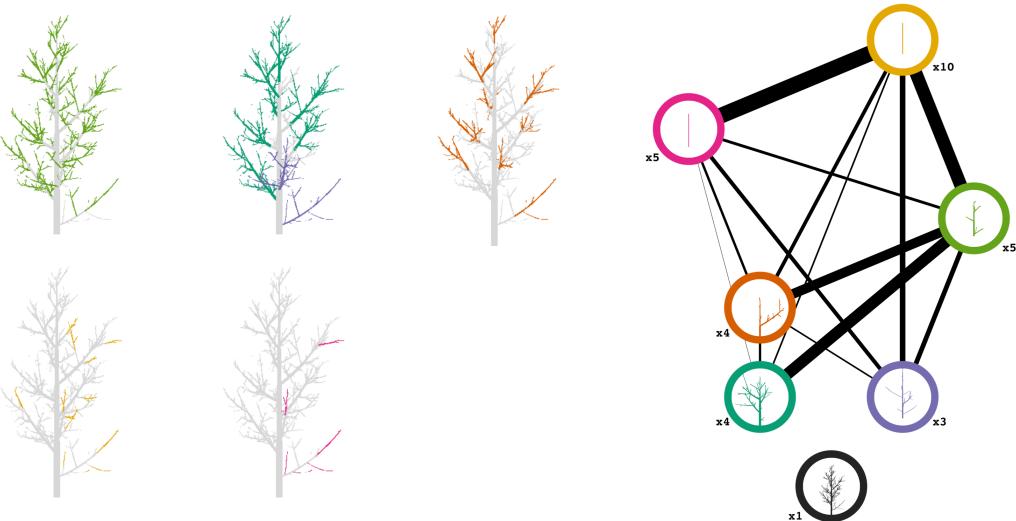


Figure 2: This 3D plant architecture presents 6 maximal symmetry antichains (identically colored subparts of the plant) which nesting links are given by the graph on the right. At the top of the graph, we find the smallest subtrees of the plant. At the bottom, we have the largest structures that contain all the others.

Towards reverse engineering?

By observing the symmetries of a plant, we can better characterize its structure but also study the production and growth mechanisms that generated it. The maximal symmetry antichains we have identified in this work were probably generated by identical biological, chemical and mechanical processes. This can be verified on simulated plants for which the construction rules are known. This also provides a new conceptual tool for the analysis of the functional origin (molecular, biophysical) of structure repetitions in plant architectures.

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Realtime input of sensor-based phenotypic traits for functional-structural plant modelling of tomato

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Keywords: Functional-structural plant modelling, Phenotyping, Point cloud, Tomato plants

Introduction

Functional-structural plant (FSP) modeling has been widely applied to study plant performance by simulating 3D plant architecture and functioning in response to environmental drivers (Evers and Marcelis, 2019). To develop an accurate plant model and track the interaction between the plant growth and the environment, quantification of phenotypic traits of plants at different growing stages is required (Cieslak et al., 2022), we call it a “phenotype-to-model” approach. Currently, phenotypic traits of plants are generally measured manually, which is exceptionally time consuming. 3D high-throughput automatic phenotyping techniques provide feasible solutions towards this problem through sensor-based data acquisition and processing. However, the complexity of tomato plant architecture and serious occlusion among organs make this phenotype-to-model approach challenging. To further investigate the performance of this phenotype-to-model pipeline applied to tomato plants, four types of phenotypic traits (stem internode length, stem internode diameter, leaf branching angle and leaf phyllotactic angle) were quantified using point cloud processing techniques. These estimated traits can be used to update related parameters and states of an FSP model developed for tomato plants.

Materials and Methods

The overall mechanism is revealed in Figure 1. An FSP model was developed to simulate growth of a tomato plant. An automatic phenotyping pipeline was developed to acquire the phenotypic traits by taking point clouds of tomato plants as the input. An imaging system in the Netherlands Plant Eco-phenotyping Centre (www.npec.nl) was used to acquire tomato plant point clouds. The imaging system contains 15 cameras mounted in a cylindrical-shape black box from different perspectives. Fifteen synchronised images of the object were captured with these cameras at each imaging moment, and a coloured point cloud was then reconstructed with the shape-from-silhouette method (Golbach et al., 2016).

The phenotyping pipeline contained two parts: 1) a deep-learning-based point cloud segmentation to identify and localise the plant skeleton; 2) a tree quantitative structural modeling (TreeQSM) algorithm (Raumonen et al., 2013) to achieve the morphological analysis of the skeleton point cloud and the calculations of relevant parameters. To segment the point cloud into plant parts, we employed one of the top-performing deep neuron networks – PointNet++ – as the backbone (Qi et al., 2017). Together with data augmentation techniques, a clean plant skeleton point cloud was obtained, and was then taken as the input of TreeQSM algorithm. TreeQSM performed a morphological analysis of the input point cloud to divide individual points into morphological orders, i.e. stem, secondary branches (petioles) and tertiary branches (petiolules). Cylinder fitting was applied to the point cloud using least square algorithm, where parameters of each meta cylinder, including cylinder length, cylinder diameter and cylinder orientation vector, were calculated. Relevant plant traits were finally obtained by combining relevant cylinder candidates within the same internode.

Four tomato plants from two commonly used tomato plant cultivars (Merlice and Briosco) were used to test the preliminary performance of the proposed phenotyping pipeline, where three of them were Merlice and one was Briosco. Destructive measurements were conducted on those plants in order to obtain the ground truth values.

Preliminary Results and Discussion

The average absolute error of stem internode lengths, stem internode diameters, leaf branching angles and leaf phyllotactic angles were 22.5 mm , 3.1 mm , 15.3° and 23.2° respectively. A potential reason for the bias was the limitations on point cloud density. Within a point cloud, the separability of parts close to the morphological top of a plant was poor, which resulted in a relatively poor segmentation of the plant skeleton. This can be further dressed by employing a higher resolution during the point cloud reconstruction from the images. In the next steps, the performance of the FSP model with the interaction with the real sensor data will be measured by comparing predicted shoot dry mass with the actual destructive measurements.

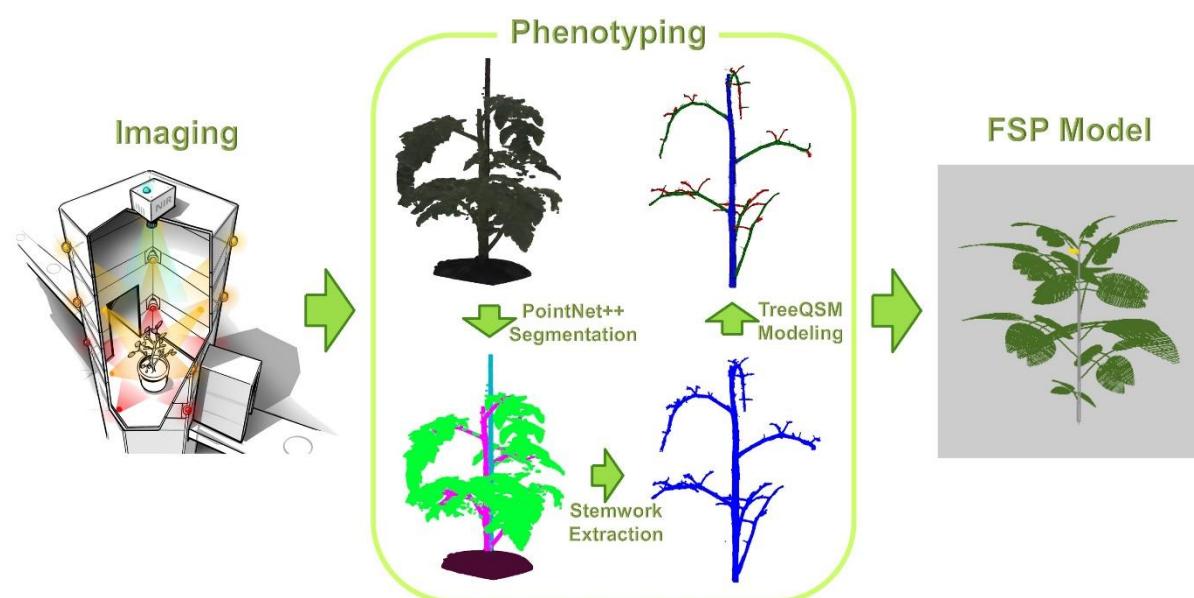


Figure 1: Pipeline of the proposed phenotype-to-model approach for tomato plants.

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High-throughput 2D+t root system architecture reconstruction and modelling from time-lapse phenotyping data

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Keywords: spatio-temporal plant model, root system architecture, high-throughput phenotyping, time-lapse tracking, computer vision

Background: High-throughput phenotyping is crucial for modelling root system development. In recent years, imaging automata have been developed to acquire Root System Architecture (RSA) of many genotypes grown in Petri dishes to explore the Genetic x Environment (GxE) interactions. Time-lapse phenotyping offers novel possibilities to characterise RSA and a golden path to build and fine-tune “digital twins” of root systems, by coupling mechanistic functional models and root system architectures characterized in both space and time. Such goals require methods for acquiring dynamic parameters such as the organ apparition rate or the growth rate of individual organs or inferring latent parameters from observations, and feeding geometrical and topological models with such parameters to simulate root system development. However, getting an accurate description of the topology, geometry, and dynamics of a growing root system remains a challenge.

Materials and Methods: We designed a high-throughput phenotyping method, combining an imaging device and an automatic analysis pipeline based on registration and topological tracking (see Figure 1). First a registration pipeline is built to address the alignment issue. Then root systems are segmented and labeled with root segments apparition time. A novel root topological tracking algorithm is applied that combines temporal and spatial information and solves ambiguities introduced by root crossing. This pipeline reconstructs the full RSA parameterized with development time, saved in the standard format RSML (Lobet et al, 2015). The method was tested on a challenging *Arabidopsis* seedling dataset, including numerous root occlusions and crossovers.

Results and Discussion: The pipeline allows to accurately characterize the topology and geometry of observed root systems in 2D+t. Static phenes are estimated with high accuracy ($R^2=0.996$ and 0.923 for primary and second-order roots length, respectively). These performances are similar to state-of-the-art results obtained on root systems of equal or lower complexity. The main result of our pipeline is to estimate the development of root architecture accurately and automatically ($R^2=0.938$ for lateral root growth estimation). The estimated architecture and development is captured into a model that allows us to simulate the whole RSA growth. We illustrate this capability by building a realistic time-lapse movie, and generate synthetic observations intended to feed deep learning models.

Conclusions: We designed a novel and fully automated 2D+t architecture reconstruction method. It has been used to characterize developing patterns of root systems grown under various environmental conditions and dissect structure and development to simulate a continuous spatio-temporal architectural model from a sparse time-series of images. It provides a unique geometrical and topological substrate for mechanistic models of root

systems and can be used for testing new hypotheses on actual time-lapse data. The architecture parameterized in space and time could be used further to simulate additional observation time-points in order to train segmentation models for improving phenotyping pipelines.

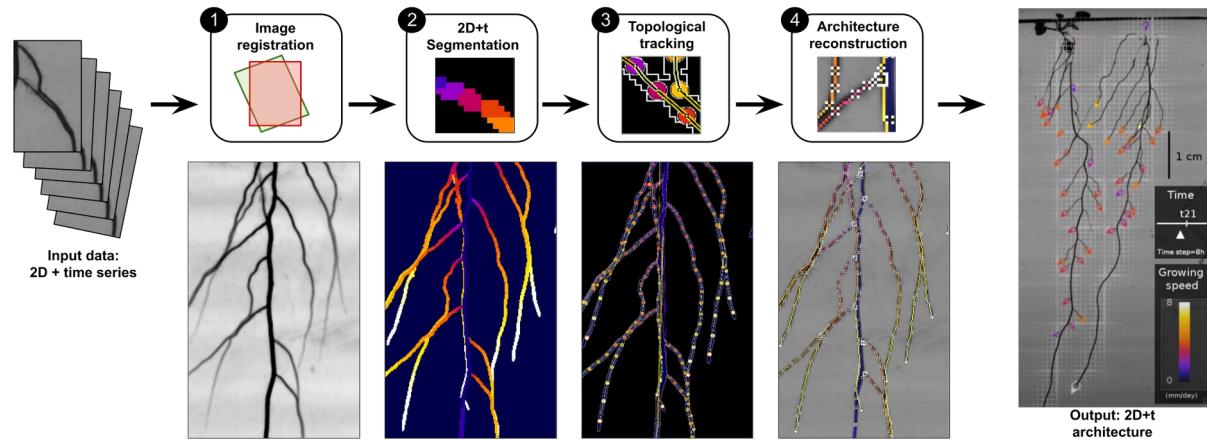


Figure 1: The automatic processing pipeline. Upper line: pipeline steps, bottom line: outputs of the successive steps.

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From tree growth modelling to synthetic point clouds: Applications to data science

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Keywords: species modelling, tree architecture, remote sensing, forestry, automation

Introduction

Deep learning is increasingly becoming an effective technique for automated quantification of unstructured data such as 3D point cloud data (PCD) and skeletons. Past work has tried to leverage point clouds for extracting and analysing individual trees from point cloud for forestry stock assessment (Hartley et al., 2022). However, deep learning usually requires large and diverse training datasets with associated ground truth labels for model training. Collecting ground truth labels for forest phenotyping can be highly laborious and not realistic at scale. We propose a pipeline for fully automated generation of tree point clouds and their associated skeletons based on user selected tree growth parameters to support model-assisted functional phenotyping. Using the pipeline, we demonstrate creating synthetic training datasets by generating realistic tree point clouds at individual tree level and associating tree growth parameters used as ground truth labels.

Materials & Methods

Our pipeline fully automates the generation of 3D PCD from growth models that can be used as training data for deep learning by leveraging multiple open-source tools (Figure 1). The Grove 3D tree growing software (van Keulen 2021), a commercial open-source Blender add-on, was chosen for its ability to generate high-quality tree models and realistic-looking architectures reacting to the light and mechanical environment. Growth and form is controlled by over 100 user specified parameters. Varying parameters and tree architecture is automated using the blender-python scripting functionality. For botanical applications, the growth model used by the pipeline could be replaced by a classical FSPM if it can generate 3D mesh objects (.obj file).

The exported Blender objects are converted to high density tree point clouds using Helios++, a software specifically developed for simulated laser scanning surveys. Helios++ (Winiwarter et al., 2022) offers a range of scanners (TLS/UAV) and platforms (tripod, UAV and fixed wing plane). The positioning and trajectories of these platforms can be specified dynamically in our pipeline. A separate, optional stream of the pipeline takes the exported mesh files to produce high-fidelity tree skeletons using the skeletor python package (<https://navis-org.github.io/skeletor/>). The last stage of the pipeline uses either those skeletons or PCD converted to a PyTorch Geometric (https://github.com/pyg-team/pytorch_geometric/) dataset for Graph Neural Network (GNN) deep learning for automated tree growth parameter quantification. The combined skeleton and point cloud training dataset also allows for the development of automated skeleton extraction algorithms.

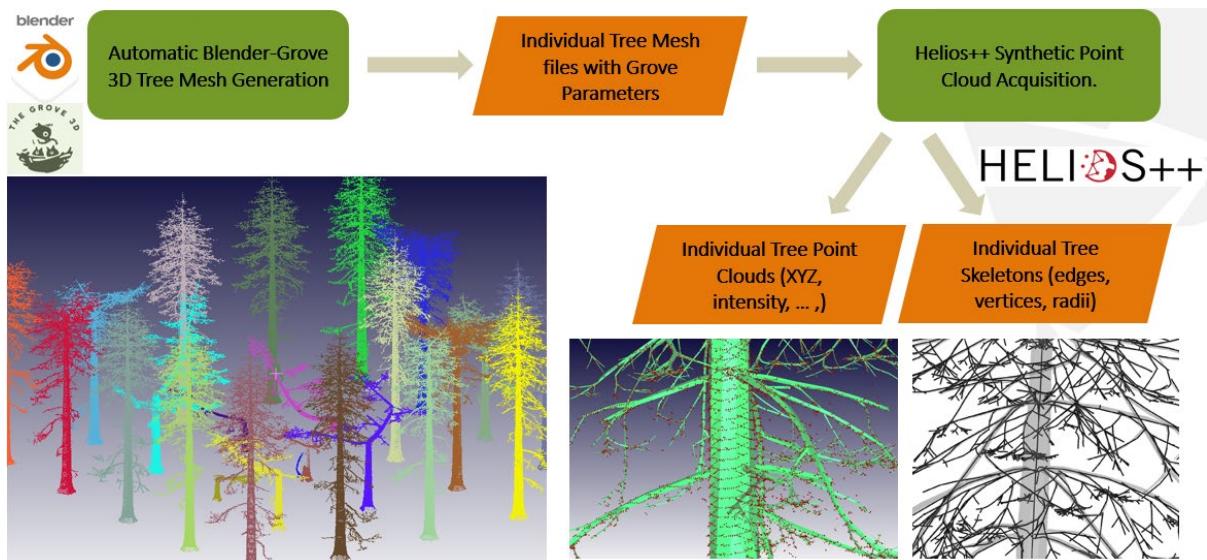


Figure 1: Overview of the synthetic point cloud data generation pipeline.

Results and Discussion

To demonstrate how the generated PCDs can be used to train deep learning models for estimating tree growth parameters, synthetic PCD were generated with the pipeline by varying three Grove parameters: branch angle, branch weight, and turn up. For each of the three parameters, ten unique values ranging from 0 to 100 were used, resulting in a full factorial design of 1000 trees. 100 randomly sampled trees were held out for the validation and testing sets, with the remainder used to train a GNN multitask deep learning regression model. All other Grove parameters were held constant. PCDs ranged from 75,000 to 275,000 points. Results on the test dataset were; branch angle RMSE=7.79, R²=0.97, branch weight RMSE=5.70, R²=0.98, and turn up RMSE=13.38, R²=0.92. Results highlight the strong ability of the approach to estimate various Grove parameters and that some parameters are more challenging to estimate than others. Future studies will focus on increasing the number of growth parameters that the GNN model can extract from PCD.

Conclusion

A fully automated software pipeline has been built to generate synthetic PCD by varying the parameters of a tree growth model to train deep learning models to identify those parameters for arbitrary PCD, including remote sensing datasets.

Acknowledgement

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Towards automated Functional-Structural Plant Model parameterisation

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Keywords: FSPM, model updating, automated phenotyping

Over the last years, big advances have been made in the field of artificial intelligence and optimisation, with applications in autonomous greenhouse control (Hemming et al., 2020) and plant phenotyping. In plant phenotyping, 3D plant architecture can be reconstructed and used to estimate, e.g., light interception (Chen et al., 2019), or to train neural networks (Cieslak et al., 2021). Here, we explore the use of phenotyping data to extract parameter values for functional-structural plant (FSP) models.

FSP models have been connected to greenhouse climate models, making it possible to simulate trials and different cultivation strategies under greenhouse microclimate conditions (Zhang et al., 2022). Recently, in the 'Virtual Tomato Crops' project, we developed an FSP model that predicts growth and development of tomato plants in response to greenhouse climate conditions and management decisions. In the model, the plant height is calculated as a function of air temperature and is a result of the appearance rate of new internodes and speed of internode elongation (described by a logistic function). An important step in the model creation is the parameterisation (Cournède et al., 2011), which is a time-consuming process for complex FSP models. Optimisation algorithms can save modellers valuable time in the development.

In this work, we studied how the parameters of a dynamic FSP model can be updated during the crop cultivation, when plant traits are measured with automated phenotyping. We chose plant height as a test attribute because it can be estimated directly from 2D images. We developed a pipeline for model updating which consists of 3 automated steps: 1) extraction of the plant height from the images, 2) fitting of p-spline mixed model to estimate plant height per genotype, 3) execution of an optimiser to parameterise a tomato FSP model at specific time steps, using the values from step 2.

Materials and Methods

An experiment with 3 tomato cultivars ('Merlice', 'Brioso', 'Moneymaker') was conducted in autumn 2021 in the Netherlands Plant Eco-phenotyping Centre (NPEC) at the Wageningen University and Research (www.npec.nl). Plant-phenotyping sensors were used to collect data on climate and plant development of 282 plants.

All plants were imaged every three days from 6 sides by an RGB camera. The plants were segmented from the images (Fig. 1), and a pixel to mm conversion was used to extract the plant height from the images. The plants were imaged by a plant to sensor system which needs multiple hours to scan all plants. Therefore, a 1-D p-spline was used to predict plant height at the same time points for all plants. Then a linear mixed model was used to adjust for potential spatial variation in the greenhouse,



Figure 1: Image segmentation. Left: camera image. Right: segmented plant without the supporting stick.

predicting an average plant height value per genotype per timestep. A bayesian optimiser was used to find parameter values of the FSP model which control the simulated plant height. This was done by minimising the Mean Absolute Percentage Error between the modelled plant height for the set parameters and the statistical output for the average plant. In practice the parameter values for different cultivars and experiments with the same cultivar are related. Using the parameter values found in previous experiments could therefore be used to lower the computation time.

Results and Discussion

The FSP model simulation started on day 26 (after emergence) of the experiment, on which the first manual measurements were taken. To test the performance of the Bayesian optimiser, we compared the results with model parameter values estimated through a parameter fit on manual measurements for a subset of plants (Figure 2).

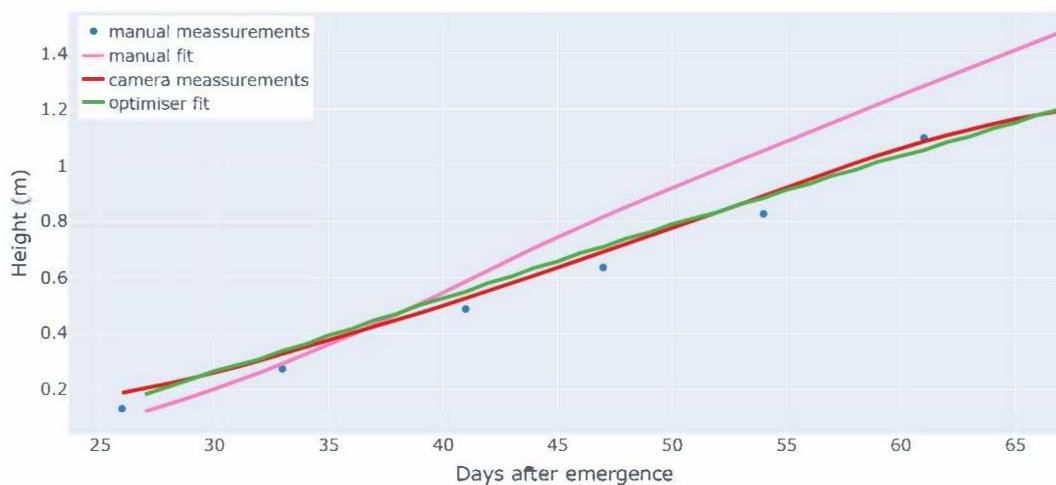


Figure 2: Manually measured mean values of plant height for cultivar 'Merlice' (blue), FSP model simulation of plant height using parameter values manually fitted on a subset of data (pink), predicted plant height from camera images using linear mixed model (red), and the result of the optimisation in respect to the camera images (green).

In the future work, the proposed pipeline will be tested on more complex plant traits.

Conclusion

The developed automated imaging equipment, segmentation and statistical analysis pipeline enable us to capture high quality data. In combination with the automated parameterisation, this enables us to accurately parameterise the model. Furthermore, it generates enough data to perform model updates during the experiment, making the approach suitable for digital twin applications which require state updates to improve predictions. A model is a simplification of reality, and thus external or unmodelled effects can influence the real plants generating a gap between predictions and reality, which would enable better simulations of control strategies during the cultivation.

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Species model parameterisation

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Keywords: point cloud, tree skeleton, parameter extraction, optimisation

1 Introduction

Species modelling from remote sensing data for digital twin cities (Gobeawan & al., 2018), is increasingly important to enable digital tree management, environmental simulations and analysis for urban planning. Species modelling for large, city scale involves parameterisation of various traits of individuals and species into an individual profile and species profile, respectively.

A species profile is used to generate individual tree models of certain species, whereas an individual profile is used to generate a unique individual species model. Both profiles are derived from extracting or estimating parameter values (known parameters) from field observation and remote sensing data (such as LiDAR point cloud) and solve for unknown parameters by optimisation. This abstract aims to describe and demonstrate a workflow of species model parameterisation from point cloud data to optimised individual species model (Figure 1).

2 Methods

To generate an individual species model representing an actual tree, we start by processing individual tree point cloud for a woody/non-woody classification in order to reconstruct the tree skeleton (in MTG format) and then derive some basic measurement parameters. Together with the measurement parameters, a known species profile and the growth space that envelope the tree point cloud form the constraints to solve for unknown parameters. The complete parameter configuration is then an individual profile that generates a representative model similar to the actual tree.

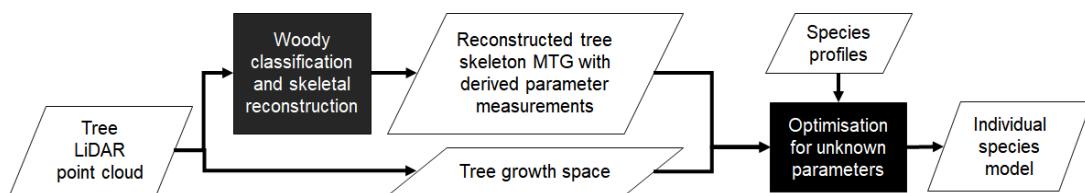


Figure 1: From LiDAR data to parameterised species model

Based on (Lim & al., 2020), we use point sparsity and intensity for classifying woody points. The woody points are then sorted into groups of nodes (binning slots) by their traversal distance to the lower root point at the tree base. We then infer the radial thickness of each node and form a node network of branching structure. This branching network is used to derive the tree skeletal MTG data, from which some initial parameter values can be derived: trunk angles, trunk diameter, trunk height, number of first order branching, number of second order branching, first order branching angles, etc..

Initial known parameter values, growth space information, and species profiles are used as constraints to generate 3D tree species models (Gobeawan & al., 2021). Unknown parameters will be solved by optimisation (genetic algorithm) to generate target species models that fit within growth spaces. Parallelisation is applied to the optimisation module to improve the system efficiency and running time.

3 Results and Discussion

We present results of species model parameterisation from LiDAR point cloud to optimised species models in Table 1 and Figure 2. As a work in progress, up to ten parameters with unknown values are being optimised. We aim to optimise for all parameter values to achieve a better fit.

Table 1: Species Profiles (all parameters solved)

Parameter	<i>K. senegalensis</i>	<i>P. pterocarpum</i>	<i>T. rosea</i>
bud lifespan	5	10	5
rhythmic growth period	1	2	0
initial diameter	0.01	0.05	0.01
branching delay	1	2	1
monopodial/sympodial	M	S	S
number of apices	1	many	1
branch arrangement	alternate	alternate	opposite
divergence angle	137.5	137.5	90.0
age	12	48	21
trunk pitch angle	12.9400	0.4400	1.6400
trunk roll angle	43.2400	217.7700	0.0000
trunk height	4.3400	1.6900	2.2500
number of 1 st order branches	2	1	3
branch pitch angle	30.0000	20.0000	15.3773
branch roll angle	167.1365	137.7591	257.4362
number of new nodes/year/bud	145	14	9.0000
internode length	0.0262	0.0240	0.0680

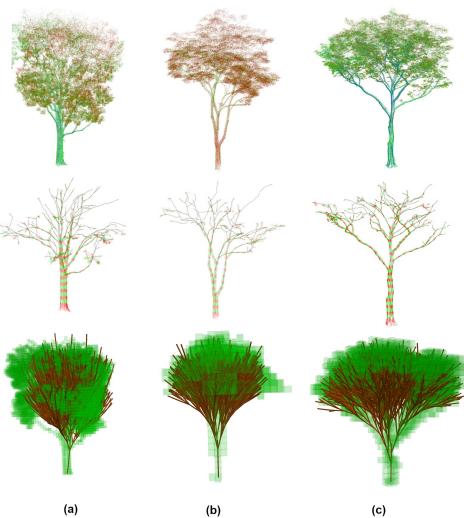


Figure 2: Row 1: tree point clouds, Row 2: tree skeletons, Row 3: optimised species models within growth space, (a) *Khaya senegalensis*, (b) *Tabebuia rosea*, (c) *Peltophorum pterocarpum*

4 Conclusion

We demonstrate a species model parameterisation from LiDAR point cloud to generate representative models. This is done by processing the point cloud for woody classification and skeletonisation to derive parameter values, and then solving for remaining parameters with unknown values by optimisation.

5 Acknowledgment

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Analysing the architecture of *Corylus avellana* and parametrizing L-HAZELNUT FSPM

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Keywords: hazelnut, Lpy, modelling

Introduction

Tree architecture is a fundamental part of a functional structural plant model. This is particularly evident in perennial tree crops where the structure of the plant influences the position of source and sink organs, as well as light interception inside the canopy, and serves as storage pool for exceeding carbohydrates. Therefore, a precise description of tree 3D structure is essential to realistically allocate carbohydrates in a FSPM (Costes et al., 2006). Hazelnut tree architecture has different characteristics compared to other fruit tree crops that have been modelled (i.e., peach, mango, apple, and kiwi). It is a monoecious species. Female flowers are grouped into inflorescences located into mixed buds, while male flowers are arranged into inflorescences in the apical position of sylleptic shoots. Each node could bear more than one bud and, the following year, the new shoots are much shorter than the shoots from which they were born. The present study aimed to analyse hazelnut one-year-old shoots 'architecture in order to build the structural part of L-HAZELNUT: a functional structural plant model of hazelnut (*Corylus avellana*).

Material and Methods

Own-rooted tree clones of *C. avellana*, cultivar "Tonda di Giffoni", were chosen, during winter, in 2020 and 2021 in Deruta (Italy). Plants were normally irrigated and fertilized. No pruning occurred during the two years. 104 one-year-old proleptic shoots were sampled according to four length categories: short (Sh) when shorter than 5 cm, medium (Me) when they were between 5 and 20 cm, long (Lo) when they were between 20 and 40 cm, and very long (VLo) when longer than 40 cm. For each shoot, diameter, length, and number of nodes were recorded. From the base of the shoot to its tip, the fate of each node was noted. Four fates are distinguished in *C. avellana*: blind nodes, vegetative buds, sylleptic shoots and mixed buds. In the year subsequent to sampling, the same measurements were repeated on the lateral shoots that were born from the buds.

Statistical analyses were done in 2022, using packages from RStudio. First, exploratory analyses were performed to investigate the distribution of the bud types or sylleptic shoots depending on the rank node along the one-year-old proleptic shoots and thus, to address if there were some homogeneous zone (i.e., zones characterized by a stable distribution of the possible bud fates (Guédon et al., 2001)). This led us to draw a flux diagram (Figure 1). Each part of the diagram corresponds to specific logical connections, between FSPM components, which were addressed using specific probabilistic models, inferred from the collected data set.

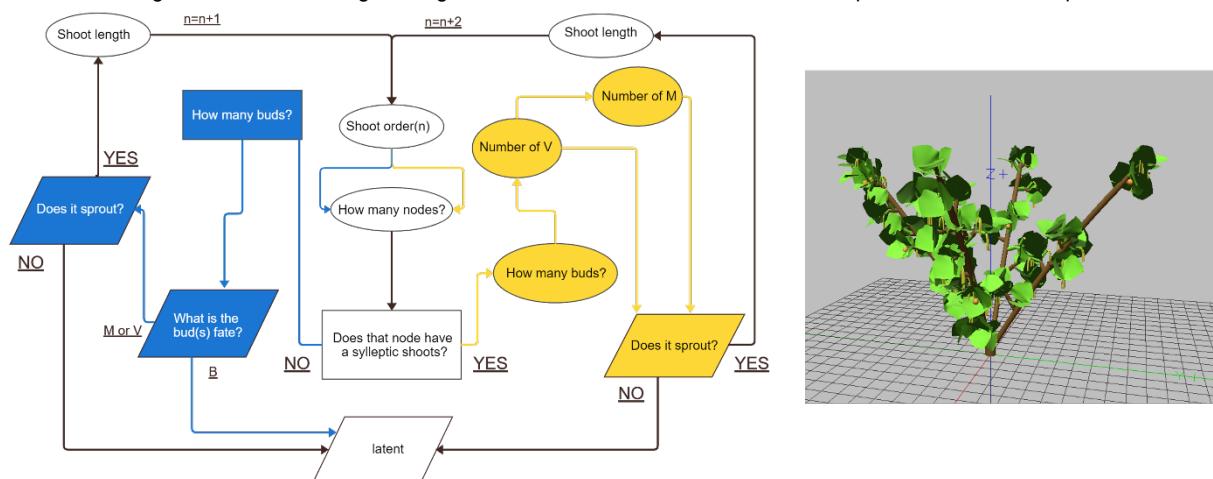
Results and Discussion

During this study new knowledge regarding the architecture of *C. avellana* was acquired. Even though male flowers were stated to be located on proleptic shoots 'nodes (Botta & Valentini, 2018), we instead highlighted the presence of male flowers in the apical position of sylleptic shoots. It was also observed that hazelnut has a sympodial growth. Each statistical model, associated with the FSPM components, was used to define functions to answer each of the questions addressed in the flow diagram. All the functions were coded in L-py (Boudon et al., 2012) to build a L-system program able to generate the architecture of hazelnut (Figure 1).

Conclusion

This led to a first coarse FSPM named L-HAZELNUT, in reference to some previous FSPM for fruit tree crops (Lopez et al., 2010). It simulates the growth of a hazelnut tree over two successive years. The conception of an FSPM is a long and meticulous process that requires having in mind a clear scheme that describes the growing and branching processes. Such a scheme can be acquired by appropriate observations and analyses of how the plant grows and develops. However, as many aspects of the plant have to be considered, the accuracy of the presented 3D structure has still to be evaluated and further studies will be necessary to validate them. Moreover, L-HAZELNUT model should be complemented in the next future with a functional part describing carbon acquisition and partitioning within the tree.

Figure 1: On the left: Logical diagram of the architectural model. Each box represents a model component that had



to be coded in L-py to draw the architecture of hazelnut. Different shapes represent different scales: shoot scale (circled boxes), node scale (squared boxes) and bud scale (rhomboid boxes). The blue and yellow colours represented proleptic and sylleptic shoots, respectively. On the right first 3D output of : L-HAZELNUT architectural model, viewed in PlantGL.

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Optimizing plant traits for efficient nitrogen use in maize using functional-structural plant modelling

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Keywords: FSP model, maize, nitrogen use efficiency, plasticity

Introduction

Maize (*Zea mays*) is the most widely planted crop in China, and is often overfertilized. This causes environmental damage which can be mitigated by breeding for nitrogen-use efficient maize. Nitrogen use efficiency (NUE) is a complex trait, which depends on soil attributes as well as plant architectural, physiological and developmental roots and shoots traits (Chen et al., 2021). The relative contribution of these crop traits to NUE is not well known, but relevant to identifying breeding targets. To increase nitrogen capture, phenotypic plasticity in response to N availability also plays an important role (Schneider, 2022). However, the effect of plastic responses in N uptake and utilization-related traits on NUE is not known. Here, a functional-structural plant (FSP) modelling approach was used to quantify the effects on NUE of differences in plant traits and their plasticity in relation to plant and soil N. We applied this model to quantify maize trait values at a population level by optimizing yield and NUE.

Materials and Methods

We constructed an FSP model of maize to mechanistically simulate the growth and development of root and shoot driven by temperature, light and carbon and nitrogen sink-source relationships with plastic responses to plant N status.

Data from two independent field experiments and a greenhouse experiment were used to develop, parameterize and evaluate the model. In field experiment 1, three nitrogen levels across two years and six maize cultivars were used. We used the data to parameterize the maize plant model. In the greenhouse experiment, a single cultivar was grown at five nitrogen levels. Individual plants were harvested at five stages to quantify the plastic response to plant N status, which was subsequently incorporated into the model. On the data from field experiment 2, model evaluation was conducted for 5 levels of nitrogen treatments across four years.

With the calibrated model, simulation experiments were conducted to identify the importance of variation in plant traits and in plasticity of plant traits with plant N status for NUE. The plant traits selected here were root diameter, root number, root N uptake rate traits, photosynthesis-related traits, leaf number, phyllochron and nitrogen remobilization traits. The plastic responses quantified here were carbon root-to-leaf ratio (RL) in response to leaf N and root emergence rate (ER) in response to shoot N. To identify the importance of variation

in plant traits, simulations were run under high N application (5714 $\mu\text{mol/L}$) and low N application (0 $\mu\text{mol/L}$), increasing or decreasing 10% of target traits. To identify the importance of variation in plastic responses, simulations were run under six N applications with enabling or disabling plastic responses. We assigned random values within defined ranges to traits identified before for individual plants. We then ran simulations and used yield and N uptake as the criteria to select optimal trait ranges.

Results

Model simulations showed that root architectural traits played a more important role than physiological traits related to root N uptake. Developmental traits determined the structure of the shoot through source: sink ratio over time which, in interaction with light and temperature, resulted in a significant effect on physiological efficiency (g DW/ g N per plant). Photosynthesis traits were more relevant to biomass accumulation than to grain biomass, especially under high nitrogen conditions. Simulation results showed both plastic responses can improve nitrogen uptake by adjusting the distribution of root system architecture (Fig. 1). In addition, both plastic responses contributed to improving yield at low N conditions.

Conclusion

Our study identified and quantified the effects of several potential architectural and developmental traits and plastic responses on NUE. In addition, we incorporated plant-to-plant interaction with the understanding of underlying mechanisms for an individual plant to optimize NUE and yield.

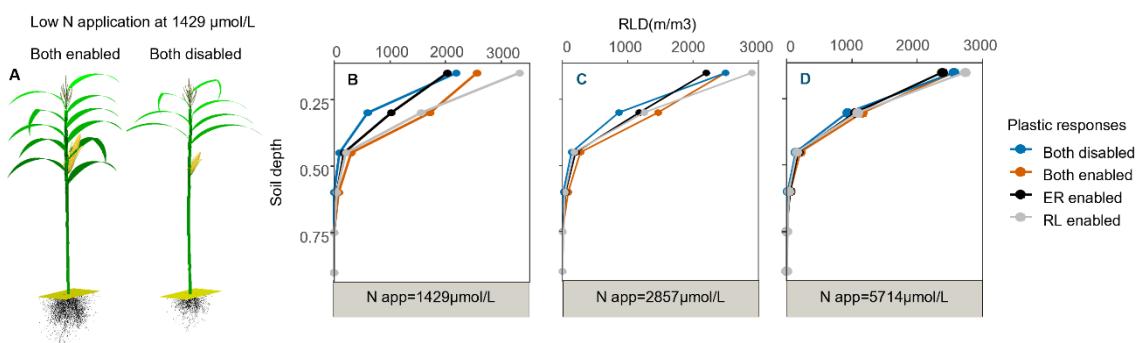


Fig.1 Illustration of effects of plastic responses on root length density (RLD) under various N applications.

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Identification of various supplementary parameters of a recent extended model of C₃ leaf photosynthesis from many CO₂ response curves

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Keywords: A/C_i curves, high dimensional search, outlier, non-smooth optimization

Introduction

Recently, the biochemical model of Farquhar, von Caemmerer and Berry on C₃ leaf photosynthesis (FvCB model) was extended to account for effects of nitrate assimilation (Busch et al. 2018, Yin et al. 2021) and variable mesophyll conductance (Yin et al. 2020). These new developments increase the generality of the FvCB model, but comes at the cost of various additional parameters which might be hard to estimate from classical gas-exchange protocols as A/C_i or A/I curves. Here we test the feasibility to estimate these additional parameters simultaneously with identification of V_{cmax25}, J_{max25} and V_{TPU25}. Additionally we account for the likely non-smooth behavior of the objective function and the presence of outliers.

Materials and Methods

CO₂-response curves of tomato leaf photosynthesis were measured in a greenhouse using a LI-6800 portable photosynthesis system on most recent expanded leaves on 6 cultivars and 4 EC – values of the nutrient solution. Each cultivar x EC treatment combination was repeated over 4 cabins and assessed, resulting in a maximum of 96 A/C_i curves that were fitted simultaneously.

We implemented the solution of the extended FvCB model (Eq. 20) given by Yin et al. (2021) as Matlab® function which accounts for the exported fractions of glycolate carbon as glycine (α_G), serine (α_S) and CH₂-THF (α_T) and implements the variable g_m - model of Yin et al. (2020) with parameters g_{m_0}, m, and d. We adopted m = 0.3 for tomato and fixed g_{m_0} to a constant as results turned out to be insensitive to this setting. Additionally, we implemented variable fractions of $\alpha_G(C_c)$ and $\alpha_S(C_c)$ as function of the chloroplast CO₂-concentration according to the approach of Busch et al. (2018) with the additional requirement to specify the nitrate assimilation rate (N_{ass}).

The basic data structure for all inputs and outputs of the implemented FvCB model was coded in matrix style, where each row was designated for one specific A/C_i curve and each column contained all measured or calculated values at measured C_i. Using Matlab's element wise matrix operators and some matrix restructuring, the FvCB model can be run very efficiently over many A/C_i-curves, i.e. whole experiments. In order to save degrees of freedom we estimated day respiration R_{d25} as being proportional to J_{max25}. After some preliminary tests we devised a gradient free parameter identification procedure, which starts with a rough global search on absolute deviations, a more refined global-local search and an iteratively weighed least square problem with updated weights defined by the Huber function of residuals.

Results and Discussion

Depending on the size of the tested optimization problem (here 24 to 96 A/C_i curves) the optimization procedure converged slowly within 1-24 hours on a high end PC, despite a highly vectorized objective function, but this is related to the choice of gradient free search algorithms and the concurrent estimation of parameters and weights of residuals.

With the tested plant material, we got strong indication, that parameters characterizing a variable g_m assumption (d), serine (α_S) and CH₂-THF (α_T) related carbon losses from the glucolate pathway can be identified whereas glycine losses (α_G) tended to be

negligible. Moreover, it proved to be effective to make $\alpha_s(C_c)$ variable, as the nitrate assimilation rate (Nass) could be identified.

In the literature there is a strong believe, that TPU limitation along A/C_i curves is always preceded by W_j limitation. Here we observed a different picture: Besides the ubiquitous Rubisco limitation at low C_i, TPU limited often A at higher C_i, while RuBP regeneration limited A was frequently absent, making J_{max25} not identifiable.

Conclusion

Auxiliary parameters involved in the analysis of A/C_i curves as parameters related to mesophyll conductance and nitrate assimilation can be estimated from a concurrent parameter identification on a large set of A/C_i curves. Using the latest developments related to leaf C₃-photosynthesis (Busch et al., 2018, Yin et al., 2021), quite different limitation state distributions are becoming apparent.

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Impact of leaf angle orientation on gas exchange and leaf temperature on a grapevine population using HydroShoot, a functional structural model

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Keywords: Leaf orientation, Leaf temperature, Grapevine, Leaf gas exchange model

Introduction

Extreme temperatures can cause dramatic leaf burn symptoms in grapevine (*Vitis vinifera* L.). The repetition of these extreme events underlines the need to grow varieties more adapted to high temperatures (Delrot et al., 2020). Leaf temperature (T_{leaf}) depends, from the one hand on the absorbed radiation, air temperature, humidity and wind speed and from the other hand on the ability of the plant to regulate its temperature by evaporative cooling. Stomatal conductance (g_s) has been shown experimentally to strongly vary among grapevine genotypes (Coupel-Ledru et al., 2014). Nevertheless, no study investigated the potential impact of genotypic variation in architectural traits on leaf temperature, while they are crucial as they determine plant microclimate and the amount of light intercepted by each leaf in the canopy (Da Silva et al. 2014). This presentation aims at studying the existing variability in grapevine architecture traits (mainly leaf angles) and their consequences on gas exchanges and temperature. To reach this objective, we used both an experimental approach and a functional structural plant model to explore the potential impact of architecture on leaf temperature in a set of grapevine genotypes.

Materials and Methods

A panel of 30 genotypes was selected from a core-collection of grapevine varieties covering the worldwide genetic diversity (Nicolas et al., 2016) and prepared as cuttings in pots at Institut Agro Montpellier (France, 3°53' E, 43°37'N). 16 genotypes were identified on the basis of leaf burn symptoms that were induced by the major heat wave of June 2019 (8 genotypes very sensitive and 8 with little or no sensitivity). The other 14 genotypes were selected to maximize the variability in architectural traits (including leaf orientation, leaf shape and internode length). Selected cuttings were maintained in pots and fertirrigated to avoid any water deficit or mineral deficiency. Experiments were conducted at Institut Agro Montpellier in summers 2021 and 2022. Measurements were made on two and one-year old plants in 2021 and 2022 (new cuttings), respectively. We kept only one shoot per plant, with all the secondary axes removed. We digitized all the plants to get an exhaustive representation of plant architecture including leaf orientation (defined with three angles: elevation, pitch and roll). We completed these architectural measurements with a large number of g_s and T_{leaf} measurements performed with a fluo-porometer on 20 different days, displaying large variability in weather conditions (sunny/cloudy days, wet/dry, warm/cold days). This choice was made to assess the repeatability and consistency of the observations whatever the environmental conditions. We then used Hydroshoot (Albasha et al., 2019), a modular FSPM developed in the OpenAlea platform (Pradal et al., 2008) to simulate photosynthesis (A_n), transpiration (E) and temperature (T_{leaf}) at the individual leaf level. All model parameters, except the architectural ones, were assumed constant across genotypes, in order to assess only the impact of leaf orientation and architecture of plant performance.

Results and perspectives

The architectural traits showed high broad sense heritability values ($H^2 = 0.79, 0.96, 0.84$ for internode length, individual leaf area and leaf inclination angle). Similarly, we observed a high heritability for leaf temperature and stomatal conductance ($H^2 = 0.67, 0.76$ for g_s and T_{leaf} , respectively). Nevertheless, we did not obtain an obvious link between the architectural traits and T_{leaf} when performing usual correlation analysis on the genotypic values. These conclusions were in agreement with HydroShoot simulations which showed that the genotypic architectural variability we observed (including the leaf elevation angle) hardly influences T_{leaf} and A_n (Figure 1), although within-plant variability in T_{leaf} was observed. This first result suggests that different combinations of architectural traits and stomatal control gave the same behaviour in terms of leaf temperature. Sensitivity analyses of the model to gas exchange and architectural parameters are undergoing, to further quantify the relative impact of both architectural traits and parameters of the model that drive stomatal conductance responses to temperature and relative air humidity (Leuning, 1995). The expected output of this study is to define new ideotypes with optimal combinations of architectural traits and stomatal behaviour that could maximise water use efficiency and reduce the risk of leaf burn symptoms.

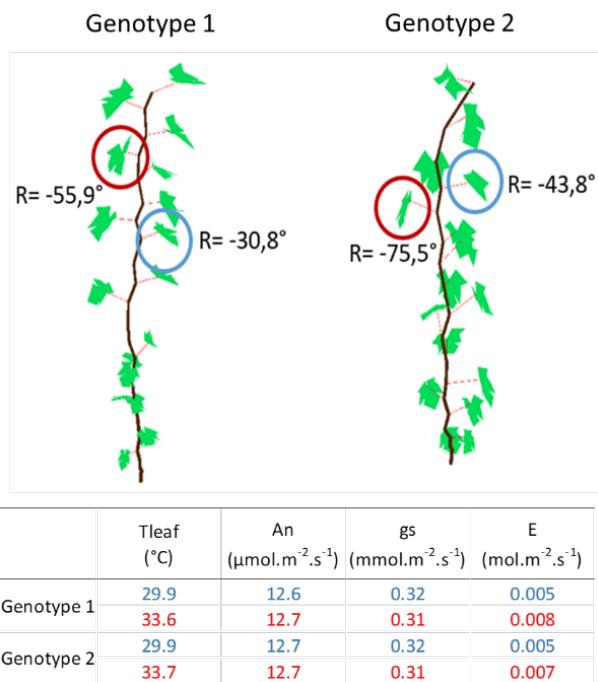


Figure 1: Representation of the two 3D mock ups for two genotypes used in this study. The HydroShoot model was run on these architectures to estimate photosynthesis (A_n), stomatal conductance (g_s), leaf temperature (T_{leaf}) and transpiration (E). Results presented in the tables correspond to the values simulated for the two leaves circled in red and blue. R is the elevation angle of the two corresponding leaves.

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Turgor-driven water flow and carbohydrate storage in wheat stems increase hydraulic capacitance during drought

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Keywords: composite water flow, mechanistic modelling, *Triticum aestivum*

Hydraulic capacitance is an indication of drought resistance as it quantifies how much water a plant can use from its internal water storage pools with a decreasing water potential. Usually, this capacitance declines under drought stress, as the osmotic demand from the storage tissues does not exceed the evaporative demand from the leaves. Yet, in wheat, due to carbohydrate mobilisation, up to 60% of the stem dry weight can consist of osmotically active carbohydrates, exerting a considerable osmotic force.

Recently, a mechanistic wheat model was built and calibrated, simulating water flow and storage in wheat stems (Verbeke, 2022). A flow and storage model for trees (Steppe et al., 2006) was coupled to the concept of composite flow by Steudle and Peterson (1998), in which water flow is subdivided into a cell-to-cell pathway and an apoplastic pathway, including a new compartment, the vascular parenchyma (Figure 1). This was necessary to allow turgor-driven water flow out of the storage parenchyma. The new model was able to simulate a declining stem water content under a decreasing osmotic potential due to the carbohydrate mobilisation, as observed in a dedicated experiment. Both data and simulations showed an increased hydraulic capacitance of the stem under drought stress. By storing osmotically active carbohydrates in the stem, wheat is thus able to increase its hydraulic capacitance under drought stress. Turgor-driven backflow allows this water to flow to the developing grain.

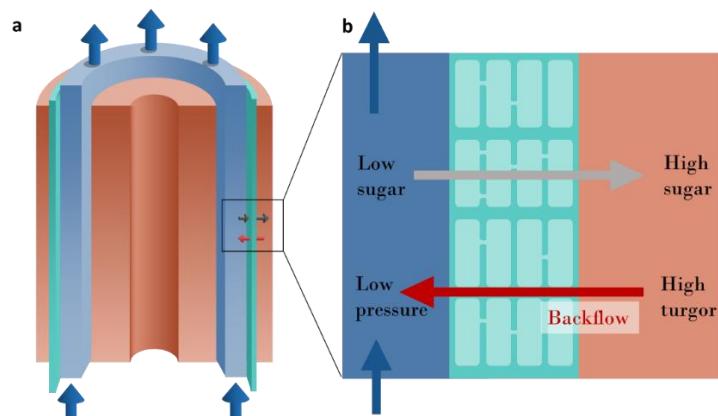


Figure 1: Schematic representation of the water flow in wheat stems, simulated by the flow and storage model for wheat (Verbeke, 2022). (a) 3D-representation of the stem geometry simplification as it was implemented in the model. Xylem vessels are merged into a xylem ring (blue) while vascular parenchyma cells are combined with phloem cells into a vascular parenchyma ring (teal), dividing the storage parenchyma (orange) in two concentric compartments that are still hydraulically connected. (b) Radial flow between the different compartments. Water flow between the xylem and storage parenchyma crosses the vascular parenchyma.

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Simulation of leaf growth response to elevated atmospheric carbon dioxide concentration ($[CO_2]$) using CN-Wheat, a model of morphogenesis driven by trophic dynamics

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Keywords: climate change, morphogenesis, wheat, FSPM, CO_2

Introduction

The Earth is facing an increase in the atmospheric carbon dioxide concentration ($[CO_2]$). Elevated $[CO_2]$ affects plant growth and development by modifying a range of physiological processes. Stimulation of leaf area development by elevated $[CO_2]$ is important in terms of plant productivity because green leaf area determines total biomass and final grain yield. As atmospheric $[CO_2]$ is currently a limiting factor for C3 photosynthesis, it has been demonstrated that the primary effect of elevated $[CO_2]$ is a stimulation of photosynthesis due to both enrichment of substrate for Rubisco carboxylation and an inhibition of competitive Rubisco oxygenation (Long *et al.*, 2006). High $[CO_2]$ also induces stomatal closure leading to a decrease of transpiration per leaf area unit. Elevated $[CO_2]$ has also been shown to reduce plant demand for nitrogen (Dong *et al.*, 2022). The resulting interactions between water, photoassimilates and nitrogen are complex, and the underlying mechanisms by which elevated $[CO_2]$ affects leaf growth are still not clearly understood. To address remaining knowledge gaps and uncertainties in estimating the effects of elevated $[CO_2]$ and climate change on plants, research should expand experiments under a wider range of growing conditions and improve the representation of responses to climate in models. Functional Structural Plant Models (FSPMs), which account for the interactions between biological processes and environmental factors, are among key tools to explore plant responses to climate change and possible adaptation mechanisms. In this work, we evaluated the ability of CN-Wheat (Barillot *et al.*, 2016 and Gauthier *et al.*, 2020), a wheat FSPM, to simulate leaf growth response to contrasting CO_2 concentrations.

Model description

CN-Wheat represents the plant as a collection of tillers. Tillers are considered as a set of botanical modules representing several mature and growing shoot organs (blades, sheaths, internodes and growth zones), a root compartment and a common pool mimicking the phloem and allowing fluxes of metabolites among organs. Each organ includes structural, mobile (sucrose, nitrates, and amino acids) and storage (fructans, proteins) materials. CN-Wheat accounts for the main biological processes occurring in plants: resource acquisition (N uptake, photosynthesis) and allocation within the plant, morphogenesis (leaf and internode growth) and senescence. Leaf growth is represented as a self-regulated system driven by: i) the local concentrations of carbon (C) and nitrogen (N) in the growth zones which regulate the rate of organ elongation, specific structural mass and width, ii) coordination rules linking the timing of leaf extension between successive phytomers. CN-Wheat allows for a dynamic representation of the 3D geometry of plants, which is used to compute light distribution at organ scale. In this work, CN-Wheat sensitivity to $[CO_2]$ was assessed by simulating the growth of wheat plants for ~105 days and exposed to low $[CO_2] = 200$ ppm, medium $[CO_2] = 360$ ppm, and high $[CO_2] = 800$ ppm. Only the morphogenesis of the main stem leaves was considered, the tillering was kept constant between simulations. Except for $[CO_2]$, virtual set-up was similar to Gauthier *et al.* (2020) and come from plants grown in the field in Grignon (France) in 1998 and 1999.

Results and Discussion

Simulation results indicated that $[CO_2]$ increased plant photosynthesis by ~40% between $[CO_2] = 200$ ppm and 800 ppm (data not shown). LAI increased by ~20% between $[CO_2] = 200$ ppm and 800 ppm but was similar between 360 and 800 ppm (Fig. 1a). On the contrary, N content in shoot was lower at high $[CO_2]$ until day 55 (Fig. 1b). N concentration increased on this day, due to particular weather conditions. After that date, N concentration started to decrease drastically at $[CO_2] = 200$ ppm, as a result of complex interactions. At the end of the simulation, cumulated blade transpiration was ~40% lower at $[CO_2] = 800$ and 360 than at 200 ppm. Phyllochron was little affected by $[CO_2]$ (Fig. 1d), except for the last leaf which appeared later at low $[CO_2]$. There was no difference in leaf length across $[CO_2]$ treatments (data not shown), but leaf width increased with CO_2 . On the last leaf, width was ~30% higher at $[CO_2] = 800$ than at 200 ppm (Fig. 1e). The specific structural leaf weight (Fig. 1f) was also greater at $[CO_2] = 800$ than 200 ppm (~25%). Overall, CO_2 effects were greater between 200 and 360 ppm than between 360 and 800 ppm.

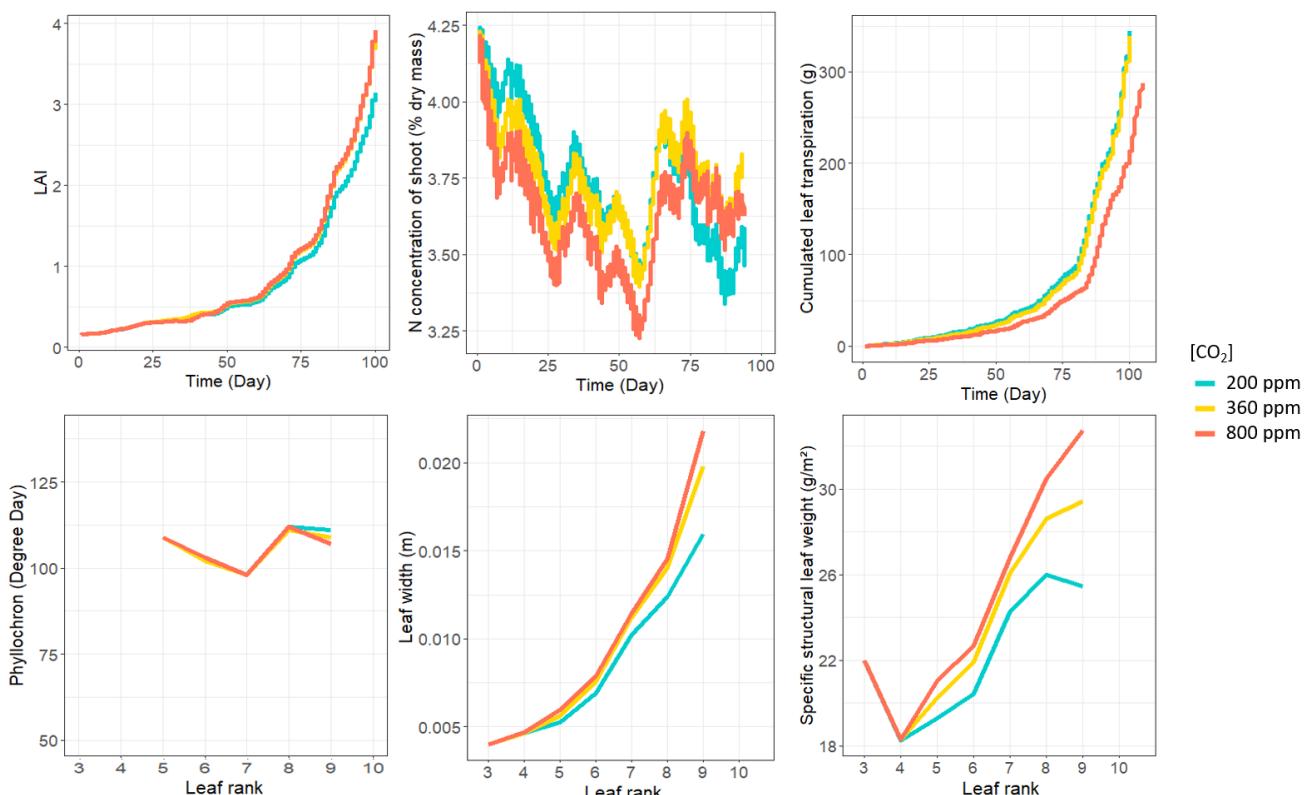


Figure 1: Simulation results of dynamics of LAI (a), N mass of shoot (b), cumulated leaf transpiration (c), phyllochron (d), leaf width (e), and specific structural leaf weight (f) as function of the leaf index, at three different $[CO_2]$: 200 ppm, 360 ppm and 800 ppm.

Conclusion

CN-Wheat showed interesting properties for exploring leaf growth response to $[CO_2]$ for plants grown in optimal water conditions. The further step is the implementation of water dynamics within CN-Wheat to extend the approach in simulating the response of leaf growth to $[CO_2]$ x drought interactions.

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Architectural plasticity in response to plant density increases canopy light interception

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Keywords: workshop, virtual plant, *in silico*, plant research

With rising population levels and increased pressure on our agricultural system due to climate change a key challenge is increasing crop productivity. Recent agricultural practice in winter wheat (*Triticum aestivum*) uses high planting density to increase yield potential per ground area but also enhances intra-genotypic competition, which can cause yield penalty.

To understand the balance between yield potential and penalty under high planting density, we phenotyped 200 winter wheat genotypes and their plasticity in response to three planting densities (30, 89 and 270 plant m⁻², Fig. 1A) using high-throughput phenotyping platform PHENOARCH (INRAE, Montpellier, Fig. 1B). The image data (Fig. 1C) and ground truth measurements allowed to quantify dynamic changes of 10 categories of functional and architectural traits during four weeks experimental period: 1) plant height and plant elongation rate, 2) tiller number and tiller development rate, 3) total leaf area and leaf expansion rate, 4) fresh and dry biomass 5) absolute and relative growth rate of biomass, 6) canopy leaf area distribution, 7) canopy leaf angle distribution, 8) canopy light interception, 9) light extinction coefficient and 10) degree of self-shading.

Interestingly, the development of leaf area was fastest under intermediate density, suggesting competition-driven plasticity in biomass allocation and/or in leaf mass per area. Genome-wide association study showed that genomic regions on the D6 and B6 chromosomes associated with these traits. Biomass and tiller number per plant decreased with increasing density and the degree of this plasticity differed largely between genotypes. High correlation between plasticity of biomass and tillering suggests that biomass of genotypes maintaining tiller development under high density was least affected by planting density, probably by increasing light interception per plant. To prove this, we conducted *in silico* experiments simulating the effects of architectural plasticity (Fig. 2) in response to density on light interception at individual and canopy levels. This was achieved by coupling the 3D plant architecture models obtained from the experiment with a light model. Interestingly, increasing density without architectural adaptation of individual plant reduces canopy light interception in the most studied genotypes. This indicates that architectural plasticity in response to high planting density is not purely a "selfish" behavior, but also beneficial to canopy light interception and therefore productivity.

Our results highlight how non-invasive phenotyping in combination with 3D modelling can reveal the important functions of phenotypic plasticity on canopy productivity.

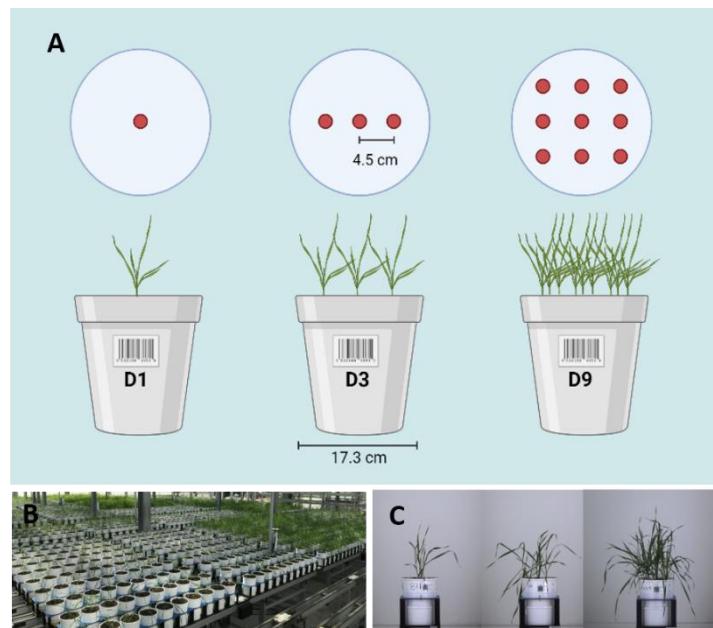


Figure 1: (A) Set up of three different planting density; (B) In total, 2400 pots were images; (C) example of the plant image in D3 treatments.

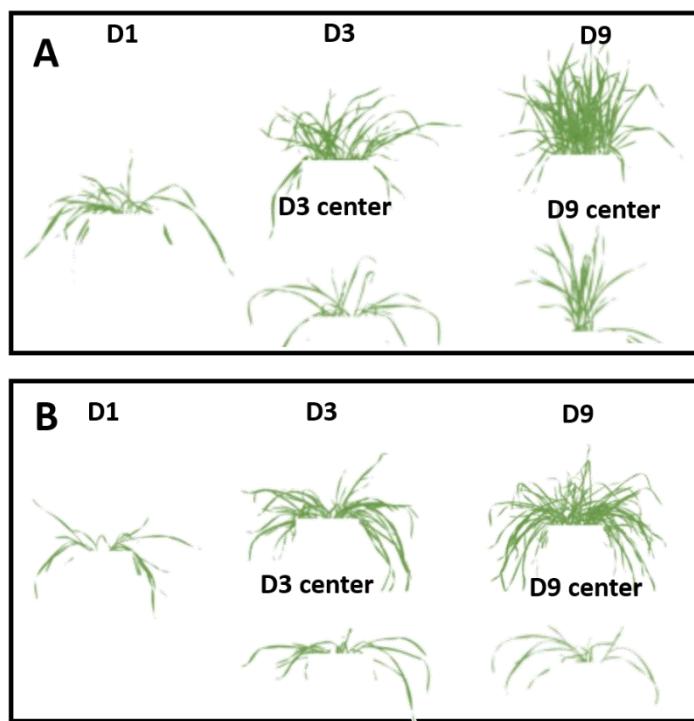


Figure 2: Two-dimensional projection of a architectural plastic (A) and a non-plastic (B) genotype in response to the planting density.

Unravelling the diversity of root morphogenetic parameters within forage legumes using image analysis

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Keywords: Root architecture, phenotyping, image analysis, modelling

Introduction

Establishment of forage legumes is critical to the performance of temporary grasslands and affects the production and quality of multi-species forages in Europe. Root traits are critical in determining the outcome of competition for soil resources and the successful establishment of species. However, up to now, efforts on root phenotyping have been limited, particularly in small seed forage species.

The ARCHISIMPLE model (Pagès et al. 2014) has recently served as a framework for deciphering and modelling the contribution of different root traits to complex root phenotypes in a wide range of species. This includes forage legumes for which contrasting rooting strategies were demonstrated (Faverjon et al. 2019). However, little is known regarding cultivar differences within each species. Furthermore, as forage legumes are allogamous species, each cultivar can contain a substantial genetic variability (i.e. half-sib populations; Julier et al. 2000). The extent to which within-species trait variability might be of interest for resource acquisition, resource cycling and genetic resource for breeding remains to be determined.

In this study, a phenotyping experiment was carried out with the aim to examine the inter- and intraspecific diversity of root morphogenetic parameters in two major forage legumes. A pipeline for automatic image analysis of shoots and roots was tested for the dynamic follow up of shoot - root allocation and root parameters used in the ARCHISIMPLE and Virtual GrassLand (VGL) models.

Methods

An experiment was carried out in 2021 at INRAE's 4PMI phenotyping platform, Dijon, France, using 642 RhizoTubes® (RT; Jeudy et al, 2016). A panel of five contrasting varieties was studied in two forage legumes (red clover and alfalfa) under two nitrogen conditions (N+: high N level preventing nodulation of legumes; ON: zero nitrogen with inoculation of Rhizobium for nodulation). Each RT contained one plant and was imaged three times a week using the high throughput aerial and root phenotyping booths in a RhizoCab® HD (Jeudy et al., 2016).

The high-resolution images of the growth kinetics of root development were analysed by combining two methods. First, high-resolution images (12 000 * 12 000 pixels) were divided into 16 smaller images (3000 * 3000 pixels) and a segmentation was performed on each small image with machine learning software. Then, small-segmented images were reassembled and analysed for counting root pixels and determining root system traits. In addition, a semi-automatic approach was developed to assess parameters from the ARCHISIMPLE model. Root traits as the maximal root tip diameter (Dmax), the maximal elongation rate (ELmax) and the average interbranch distance (IBD) were determined from points records on the primary root of each RT.

Destructive measurements were performed once a week and used to determine shoot and root biomass on a subsample of 15 plants. These regular measurements were used to calibrate relationships between the counting of plant pixels and biomass accumulation above- and below-ground. These relationships were then applied to the dataset of

segmented images for the N+ treatment. Kinetics of root allocation were finally characterised through the determination of two allometric coefficients used in the VGL model (αR and βR , standing for the initial allocation to roots and an allometric coefficient, respectively; Louarn and Faverjon, 2018).

Results and Discussion

Within-species variability of root traits proved significant for all the traits studied. The kinetics of root allocation with respect to shoot growth differed strongly between the two species. Red clover displayed lower total biomass production, but higher relative investment in roots. Alfalfa presented a higher within-species variability of root allocation, both in the initial growth rate of roots and in the variability of the allometric coefficient βR . Significant genetic diversity was demonstrated in the two species, with very different patterns of root allocation depending on the studied cultivars. These differences were more closely related to the initial growth rate of roots (αR) than to βR . The relationships between allocation patterns and root morphogenetic parameters were also investigated. Significant species and cultivars effects were confirmed for most ARCHISIMPLE parameters. Correlations between root trait values appeared relatively low, suggesting a relative independence of their genetic determinism.

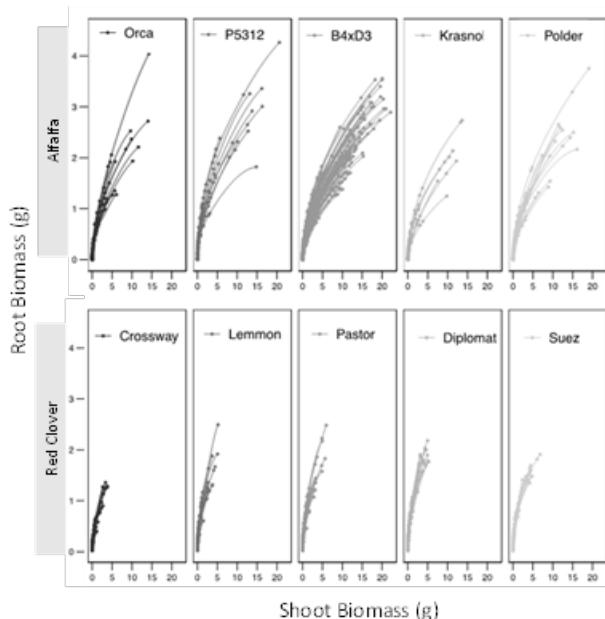


Figure 1: Allometric relationship between shoot and root biomass accumulation in individual RhizoTubes®. Upper and lower panels represent plants from the different varieties tested in alfalfa and red clover, respectively

Conclusion

A high variability of inter- and intraspecific root trait values was confirmed for small-seed forage legumes under potential growth conditions (N+). The pipeline tested here could help simplifying the parametrisation of FSPMs based on the ARCHISIMPLE formalisms.

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Combining the strength of CFD modelling with FSPMs to map phylloclimate heterogeneity in lettuce (*Lactuca sativa L.*)

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Keywords: Photosynthesis, Transpiration, Microclimate, Air flow

Functional-structural plant models (FSPMs) have the unique characteristic of combining mechanistic plant-environment interactions with the 3D morphology of plants. The full potential of this combination shines in applications whereby effects of plant morphology, physiology and environment need to be investigated on a scale smaller than a crop canopy or even smaller than an individual plant. Investigation of effects on such a small scale requires an understanding of the phylloclimate (i.e., the physical environment actually perceived by the plant (Chelle, 2005)) rather than the macro-environment. In this context, FSPMs are especially suited to evaluate light conditions, as the combination of the 3D structure with light conditions allows for a relatively straightforward evaluation of absorbance, reflectance, and transmittance on the scale of individual plant organs. The evaluation of other phylloclimate characteristics, such as air temperature, relative humidity, and air speed, is a more difficult challenge, as these conditions can be highly turbulent and computationally difficult to account for in the context of an FSPM. These conditions nonetheless significantly impact some of the most important ecophysiological processes within the plant, such as photosynthesis and transpiration and have been associated with plant quality characteristics as well. The indoor production of lettuce (*Lactuca sativa L.*), for example, is plagued by the incidence of tip-burn, which is hypothesised to be related to the stagnation of airflows and the associated reduction in transpiration (e.g., Lee et al., 2013). Understanding such dynamics requires accurate mapping of the interaction between the plant and its variable phylloclimate. Computational-fluid dynamics (CFD) modelling allows the bridging of this gap but is conversely not well suited for the incorporation of dynamic 3D plant morphology and ecophysiology.

To unlock the strength of both methodologies we present a direct interface between FSP and CFD modelling, initially applied to lettuce. The combination of both modelling methods is the only way to accurately assess (and eventually optimise) the interaction between phylloclimate and gas exchange: as changes in leaf phylloclimate cause changes in leaf gas exchange, which in turn, changes the leaf phylloclimate. This would effectively allow the creation of a spatio-temporal map of phylloclimate conditions in a closed growing system and, in the case of lettuce, may aid in the identification of problematic growing conditions. Furthermore, the accuracy of these individual methods can improve from the added information provided by the other. CFD modelling can benefit from including the accurate (growing) 3D structure of a plant, forming a physical barrier to air flows. In turn, FSPM ecophysiological calculations benefit from having more accurate phylloclimate estimations.

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In silico investigation on phosphorus efficiency of Zea mays: An experimental whole plant model parametrization approach

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Keywords: CPlantBox, parameterization, phosphorus, workflow

Introduction

Phosphorus (P) is a crucial macronutrient for plant growth and essential for yield development. In 70 % of the globally cultivated land area, P is a limiting nutrient. Yield security is currently only obtained by regular application of plant available P fertilizer. However, the crops use-efficiency of the fertilized P is low. 70-80 % of this P is not utilized and eventually cause eutrophication of open water bodies. Therefore, it is important to increase the P use-efficiency of crops by improving breeding and agricultural management. The first step towards this is the prediction of the effects of P availability and deficiency to relevant crops. Significant changes in plant architecture, like reduced growth and rigid appearance of shoots, inhibition of primary root growth, or changes within lateral root growth have been associated with P deficiency. However, it is challenging to quantify the relevant processes that cause the detrimental effects of P limitation on crop and canopy development and the consequences on relevant physiological processes (Marschner, 2011).

FSPMs are appropriate tools to approach this, since they integrate several processes based on (3D-)simulated plant structures (Schnepf et al., 2018). To parametrize these models for the evaluation of P deficiency effects on plant structure, times-series data of whole plants under P deficiency are required. Specific parameters, related to growth processes, like the elongation rate of stem, leaf, base and lateral roots are important, but often difficult to acquire. This project focuses on the creation of a dataset for the parameterization of a FSPM for *Zea mays* under various levels of P limitation. The data include time-series of photographs of shoot and root of maize until 28 days after sowing, growing at different P levels in soil. Our aim is to parametrize the FSPM CPlantBox to simulate crop structure development under P deficiency. Through the coupling of CPlantBox with water, carbon-flow and photosynthesis modules, we will enable the modelling of structure, water- and nutrient uptake and light-use efficiency of a maize crop with variable P limitation under field conditions (Zhou et al., 2020). This study introduces an easy to implement workflow to acquire dynamical data of root and shoot simultaneously for FSPM parameterization. We aim for a broader understanding of the influences of P deficiency on maize, by using a FSPM, to unravel the effects of P deficiency on plant structure and function.

Materials and Methods

Zea mays cv. B73 was grown in greenhouse-rhizotrons in a P deficient luvisol soil from a long time fertilization trial. The initial plant available P concentration was 2.0 mg P 100 g⁻¹soil (CAL-Method). To obtain the different P treatments, the substrate was additionally fertilized with 2.0, 4.0 and 6.0 mg P 100 g⁻¹. P was the only limiting factor for plant growth.

Images of shoot and root, starting with germination, were regularly taken on a fixed position. Image processing was done in several steps including segmentation, skeletonization and parameter extraction. Above- and below-ground organ segmentation differed. Shoot segmentation was performed by a background color filter algorithm. For root segmentation,

we implemented a combination of automated segmentation with convolutional neural networks and manual correction into the segmentation tool “RootPainter”, enabling the processing of time-series (Smith et al., 2022). The skeletonization was performed by RootSystemAnalyzer, a program originally designed for root parameter extraction, but also usable on shoot segments (Leitner et al., 2015). It directly provided the shoot parameter and RSML-files from which the parameters for the root system were derived.

Results and Discussion

We established a pipeline to extract root and shoot parameters from 2D images, usable for the parametrization of the FSPM CPlantBox. With this, we obtained full parameter-sets for *Zea mays* with corresponding response-curves of key-parameters under various P limitations. First results show that the P level in the soil influences, e.g., leaf and basal root elongation. Diameter of basal roots raise with increasing P supply, while the seminal root count is decreasing. Our plant models indicates that the root system re-organize without a gain in total root length until a P threshold, while the leaf growth is increasing until the same P level. Only with P supply higher this threshold, total root system length increases, while leaf area stagnates. The coupling with photosynthesis, water- and carbon-flow modules will enable investigations on underlying mechanisms.

Conclusion

Our results will facilitate the *in silico* observation of functional and structural crop reaction to various P limitations and help to understand more detailed the architectural and physiological responses of maize to P deficiency. These insights will provide valuable information for breeders on trait selection and management decisions.

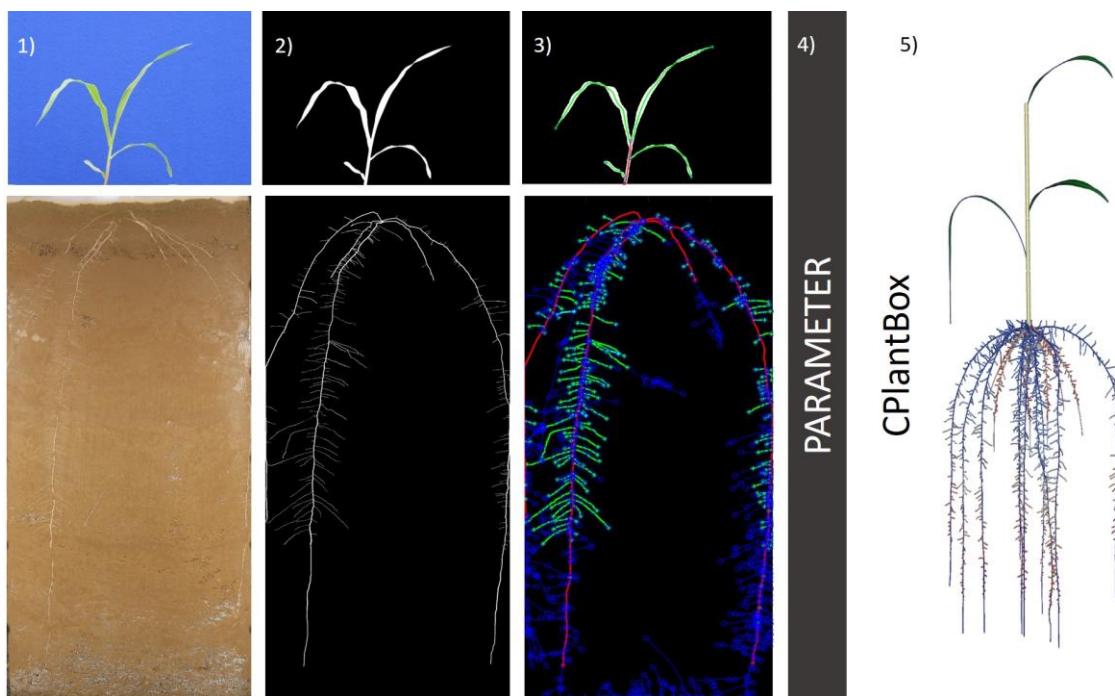


Figure 1: Workflow from 2D- images of shoot and roots to FSPM parameterization: 1) image acquisition, 2) segmentation, 3) feature detection and parameter extraction, 4) assemble parameter set, 5) plant structure from parameter

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How does root anatomy influence water uptake in tomato?

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Keywords: root anatomy, modelling, water flow

Abstract

1. Introduction

Since root it is the place of water and nutrients extraction from the soil, root features are well studied, with a strong focus on root architecture. At a lower scale, root anatomy influences water and nutrient uptake, and anatomical features have been identified as new potential targets for the development of efficient and resilient crops. Combining anatomical and architectural information is thus necessary to fully understand water dynamics in plants. However, studying anatomy is time consuming, and there is lots to do for improving anatomy phenotyping.

To by-pass this experimental gap, computational tools can be used to model plant structures and compute water dynamics at multiple scales. At the anatomical scale, the generator of root anatomy GRANAR (Heymans et al., 2020a) coupled to the anatomical hydraulic solver MECHA (Couvreur et al., 2018) enable the study of the impact of root anatomy on maize water uptake (Heymans et al., 2021, 2020b).

In this work, we extend the capabilities of GRANAR to generate dicotyledonous anatomies, by implementing new functions and calibrating them with tomato root anatomy measurements. More specifically, we focused on secondary growth patterns and maturation stages along the root. This work constitutes the first step for adapting VIPER, the Virtual Phenotyping Pipeline for Root Hydraulic Traits (Heymans et al., 2020b) to dicotyledons.

2. Materials & Methods

Wild (*Solanum pimpinellifolium*) and domestic (*Solanum lycopersicum*) tomato were grown in hydroponic system. The main roots were collected, and cross-section pictures were taken with microscope using multiple colorations and techniques. Each root was divided in segments, and the anatomy of each segment was quantified (Figure 1). In addition, maturation stages were characterized. The measurements were processed into XML files that can directly be used as input parameter files by GRANAR. With these measurements, a new function was configured for GRANAR to generate anatomies with secondary growth patterns.

The virtual tomato anatomies were then entered into MECHA to compute the radial water conductivity k_r . An analysis of the sensitivity was done to investigate the effect of specific anatomical traits on k_r .

3. Results and discussion

The new version of GRANAR with the function *Pack Xylem* is able to simulate root anatomies in secondary growth that are compatible with MECHA (Figure 2). This link can be used to compute the radial conductivity of a given anatomy and investigate the influence of specific anatomical traits on radial conductivity .

The next step will be to connect this new version of GRANAR-MECHA to a virtual root architecture, to use the root water uptake solver MARSHAL (Meunier et al., 2020) and the soil model HYDRUS. This updated pipeline based on VIPER will open the path for studying the impact of specific and/or combined effect of anatomical and architectural traits on global water dynamics of dicotyledons.

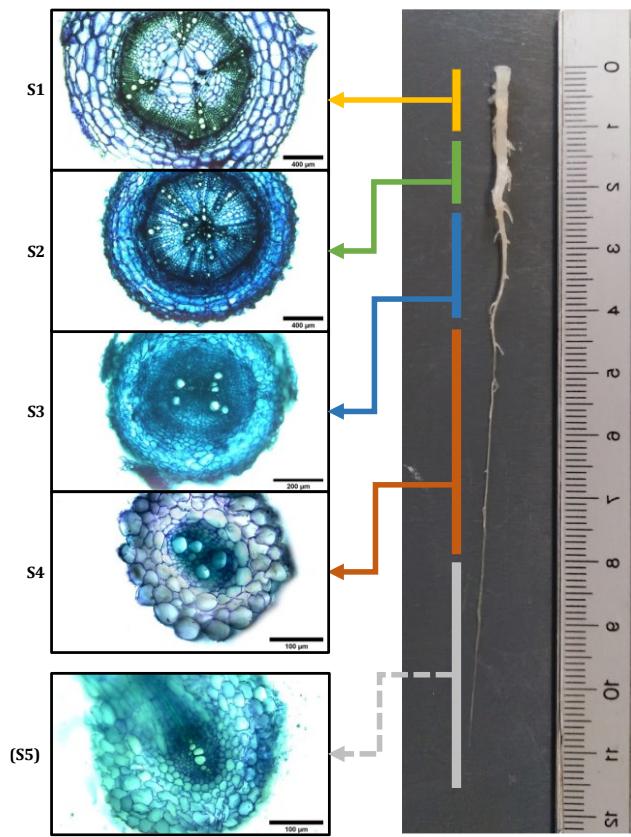


Figure 1 : Each root was divided into segments, and each segment was quantified.

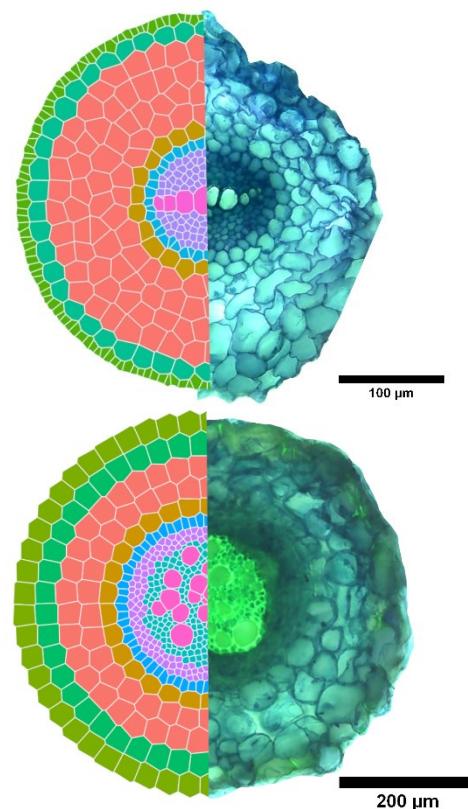


Figure 2 : Comparison side by side between generated cross section and corresponding anatomy picture. Top : Initial version of GRANAR vs. primary growth cross section. Down : Update of GRANAR vs. secondary growth cross section.

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Towards fully automated semantic and morphological labelled point clouds from FSPMs – a plant morphology-based pipeline in GroIMP

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Keywords: GroIMP, virtual plant, synthetic training data, 3D, segmentation

Introduction

The determination of topological and physiological plant characteristics is a time consuming, labour-intensive task, regarded a bottleneck in the crop breeding cycle (Song et al., 2021). In this process, there is the opportunity to automatically determine architectonic and morphological traits by segmenting structural parts of 3D point clouds generated using 3D-scanners, allowing for high-throughput non-invasive phenotyping. Advances in the field of deep learning on point clouds have the potential to extract relevant local and global features, but the lack of labelled 3D plant data with organ labels as well as topology information is hindering the exploration of this possibility.

Therefore, in the present work, the potential of functional-structural plant modelling to fill this gap of missing 3D datasets is explored. GroIMP is extended by the possibility to act as a data generator for synthetic 3D plant point clouds with an automatic generation of labels and morphological information. The aim is to help accelerating the scientific progress in developing algorithms for an automatic extraction of morphological traits from 3D point clouds. The feasibility of synthetic plants from FSPMs to improve leaf counting tasks (Ubbens et al., 2018) in images as well as semantic segmentation tasks in point clouds have already been demonstrated (Mirande et al., 2022, Turgut et al., 2022).

Materials and Methods

In this work the cucumber *Cucumis sativus* in a five-leaf stage is used as a reference plant. The growth rule defining the phytomer consists of an internode I, a petiole P and a lamina L, following the community convention (Kahlen, 2006).

Cylinders are used to model internodes and petioles, which require the morphological parameters length and diameter. For leaf modelling, GroIMPs possibility to design BSPlines using a vertex list is used. Leaves were modelled statically based on the geometry of a cucumber leaf with rank five. Depending on the leaf rank, the mesh is scaled by an empirically determined scaling factor, which is another morphological parameter.

A high diversity is necessary for machine learning approaches to enable a good generalization. In other words, the segmentation algorithm to be trained does not benefit from seeing the same deterministic plant often, but morphologically varied architectures. To achieve this, the deterministic SPM must be augmented with variability. This is done by varying each morphological parameter with a uniform distribution based on a literature review of Cucumber FSPM modelling. To create a point cloud from a mesh described by a L-System, GroIMP provides a module called ‘scanner’, which is implemented using a ray tracing approach. However, the generated point cloud is just an unordered set of 3D coordinates without any semantic information. The semantic information for each point is generated by making use of the RGG language of GroIMP. Each organ is a node with attributes in the graph structure. The scanner can query every organs attribute that is part of the imp3d-class. The ‘layer’-parameter of GroIMP objects can be used to set them visible or invisible during the scan processes.

In this work therefore, for each petiole, internode and mesh an own module, assigned to a specific layer, is created. The order in which the modules are arranged in the turtle logic is critical, otherwise incorrect assignments will be made. Note that switching a layer to visible or invisible renews the coordinate system in the graph scene. E.g. if layer 4 gets isolated, its coordinate system is set to the origin. All point clouds generated in this way are therefore in their own coordinate system and thus lose spatial reference to the other organs. To solve this, a small reference sphere is introduced into the scene. This sphere is kept for each organ. However, to remove it in the generated point clouds, a post-processing using a Python script is performed. This script also adds a label to the remaining points. Thus, semantic labelling is implicit in the layer mapping of the modules used to construct the SPM. The structure of the plant must therefore be determined a priori. The data creation of segmented point clouds is further extended with morphological information (e.g. length, diameter, spatial orientation, leaf area) using queries implemented in GroIMP. Point clouds and morphological information are saved in a csv file.

Results and Discussion

Creating synthetic data sets requires an FSPM (or an SPM) to represent the structure of a plant as realistically as possible. This work presents a processing pipeline that can generate large datasets of semantic segmented 3d point clouds with morphological information about each organ within the capabilities of GroIMP. Using the presented approach, an automated generation of labelled point clouds based on virtual plants was successfully performed. In first tests, data was created and partly modified with displacement noise to train a segmentation algorithm. It was found that, due to the highly simplified geometry, there are significant deviations from point clouds of real scans. Future work should therefore improve the geometric modelling and adapt it to new plant types.

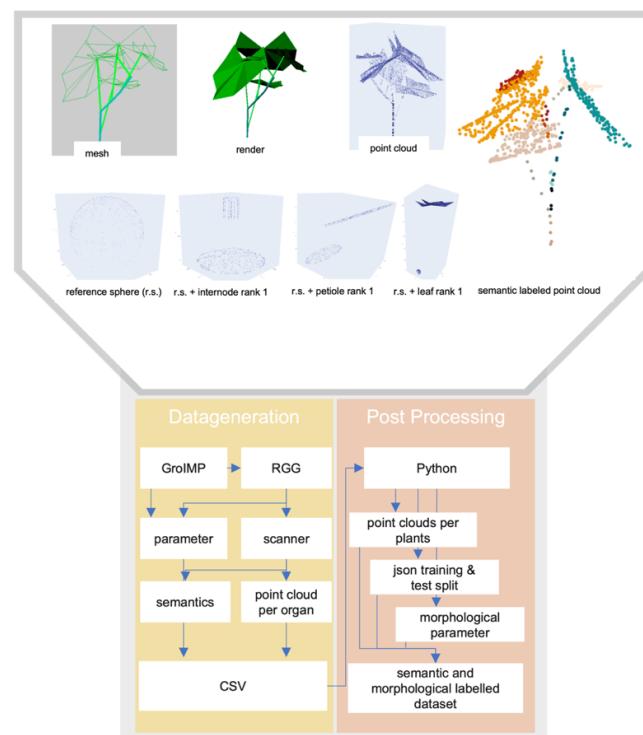


Fig.1: This work presents a processing pipeline that can generate large datasets of semantic segmented 3d point clouds with morphological information about each organ within the FSPM modelling capabilities of GroIMP

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The design of a reusable FSPM to unravel the intertwined relationship between Lettuce (*Lactuca sativa L.*) and phylloclimate in vertical farming systems

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Keywords: Photosynthesis, Transpiration, Validation techniques,

Currently, agriculture is facing a lot of challenges. The sector is expected to produce more in an everchanging world, under the pressure of more extreme weather events due to climate change. At the same time, consumers attach more importance to quality and safety of products. Due to these challenges, the agricultural sector is pressured to look for alternative production systems. In recent years, multi-layer production systems have gained a lot of interest. Vertical farms make it possible to increase productivity per square meter and bring production closer to the consumer (Vatistas et al., 2022). Vertical farming is a relatively new field of research with a lot of challenges including energy usage and efficient operating systems. Another important challenge, being the focus of this research, is the environmental conditions in these dense production systems. Environmental conditions will differ greatly from field conditions, and even greenhouse conditions. The environment, experienced by the plant as the phylloclimate, will have an effect on plant morphology, physiology and quality while the plant itself will also influence the phylloclimate (Chelle, 2005). Therefore, it seems relevant to study the interaction between the phylloclimate and lettuce, in this study used as model plant for vertical farming production.

An FSPM for lettuce was developed. Morphological parameters were retrieved from a large dataset of manual measurements. Physiological parameters were based on gas exchange measurements on leaf level. Model validation was performed using a set of innovative measuring techniques including whole-plant gas exchange. Special attention was given to minimize the amount of input to realize a functional, accurate FSPM for the goals discussed below. Therefore, a minimal amount of practical solutions were developed which will allow for a straightforward recalibration of the FSPM under different conditions. Both climate and phylloclimate were measured continuously in order to allow a better understanding of the complex and intertwined relations between the phylloclimate and the morphology, physiology and quality of lettuce plants. The investigation of these relationships will only be preparatory as they are too complex to fully grasp using common statistical methods. The developed FSPM will thereafter be coupled to a CFD model (Computational Fluid Dynamic) to further unravel the relationship between phylloclimate and plant (Presented separately).

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A root hydraulic database: the link between experimental data and modelling

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Keywords: hydraulic conductance, literature review, CPlantBox, root system age

Root water uptake is a central component in the modulation of water fluxes in the soil-plant-atmosphere continuum. As plants lose water during transpiration, roots are responsible for transporting water from the soil to the leaves, avoiding desiccation. In wet soil conditions, (i.e. when soil does not represent a major resistance for water flow), the root water uptake is directly affected by the hydraulic conductance of the root system, a key trait that might determine the water use of plants under changing environmental conditions (Vadez, 2014). Root hydraulic conductance depends on root traits such as root architecture (Doussan et al., 2006), root anatomy (Strock et al., 2021) or aquaporin expression (McLean et al., 2011), but a systematic analysis of its variation among species or plant functional types (PFT's) is still missing.

Here, we present an open access root hydraulic database based on an extensive literature review of more than 200 studies published between 1973–2021. This included 148 studies of the whole root system (K_{rs}), and 55 studies of the radial conductivity and 33 of the axial conductance of individual roots. The purpose of the database is twofold: (1) to determine the range of variation in root hydraulic properties across species and PFT's observed experimentally; and (2) to calibrate/parametrize functional-structural models such as CPlantBox (Zhou et al., 2020), which can then be used to improve our mechanistic understanding of the main factors causing variation.

The database shows a very large range of variation in reported K_{rs} values ($3 \times 10^{-11} – 8 \times 10^{-7} \text{ m MPa}^{-1} \text{ s}^{-1}$), which cannot be explained by systematic differences among PFT's or species, alone, but rather by factors such as root system age, experimental treatments or the driving force used for measurement (hydrostatic or osmotic). We investigated the relationship between root system age and K_{rs} in more detail and observed an asymptotic behaviour (very fast increase in K_{rs} with age at early stages, saturation at older ages) in various crop species. Simulations in CPlantBox using root segment scale parameters extracted from the database confirmed this behaviour, indicating a decrease in the total conductance per unit root surface area at later stages of development, associated with a larger proportion of less conductive old root tissues.

This analysis exemplifies the role of the root hydraulic database as a link between experimental data and functional-structural models and its potential as a key input for the mechanistic description of the factors affecting root hydraulic properties across species and under contrasting environmental conditions.

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Integrating phenomics and genomics to predict plant architecture across the temperature gradient

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Keywords: crop niche modeling, climate change, plant architecture, genomics, phenomics

Introduction

Climate change is a global issue for agricultural production. Facing climate change and more frequent and extreme weather events, it is urgent to breed vegetables with tolerance to heat, flooding, and drought and with resistance to new emerging pathogens. Additionally, vegetable crops have small and fragmented markets requiring many different market types, making market-driven breeding of climate-resilient varieties challenging. High throughput phenotyping and cost-effective next-generation sequencing techniques are critical to speed up vegetable breeding programs. This study aims to integrate phenomics and genomics into predicting plant architectures under different climatic conditions.

Materials and Methods

A pepper core collection was developed by the G2PSOL project, representing pepper's genetic diversity among worldwide genebanks (Tripodi et al., 2021). This study evaluated a subset of this core collection, three hundred *Capsicum annuum* L. accessions, in three seasons: one cool, one mild heat, and one severe heat season in Taiwan. Genotyping-by-sequencing of this core collection was performed by the G2PSOL project, resulting in about ten thousand single nucleotide polymorphisms (SNPs). High throughput phenotyping was conducted with Phenospex PlantEye F500, a sensor that automatically collects 3D multispectral reflection in the field and transforms the plant architecture into morphological and spectral parameters. This facility serves as a real-time monitor to capture the phenotyping changes across the environmental gradients. We integrated all the digital phenotypes among the three trials and harvested over half-million data points. Each data point described the plant architecture under a specific climatic condition. A machine learning algorithm, gradientForest, was applied to evaluate the association (r^2) between the digital plant architecture and the temperature gradient (Ellis et al., 2012). The genome-wide association study was done with the GEMMA software after filtering out SNPs with minor allele frequency < 0.05 (Zhou and Stephens, 2012).

Results and Discussion

We used the normalized differential vegetation index (NDVI) as an example to illustrate the results of this study. NDVI is a vegetation index that reflects plant health; NDVI close to 0.8 suggests a healthy plant; it drops when temperature increases, which means the plant becomes less healthy (Moges et al., 2004). For this sub-core collection, NDVI showed a heat sensitivity of final cumulative $r^2 = 0.44$; the cumulative r^2 of NDVI increased dramatically (from 0.15 to 0.42) from 26 to 28°C, suggesting NDVI became more sensitive to the temperature above this stress threshold. With this association, the NDVI values of this pepper core collection can be projected to the world under different temperatures. Meanwhile, seven thousand SNPs were used to identify the quantitative trait loci (QTL) associated with the plant architecture. Significant signals associated with NDVI per degree Celsius were detected from 16 to 35°C. The QTL of NDVI per degree Celsius presented one similar pattern from 16 to 26°C, which involved 18 candidate SNPs. Only one QTL was detected from 27 to 35°C. The

heritability of NDVI from 16 to 35°C ranged from 0.13 to 0.50, implying that the genetic variation within this core collection may contribute to the variation of plant architecture across the temperature gradient. The putative performance of every accession under different temperatures suggested the adaptability of accession in different regions. More studies are required: validate the candidate accessions in the target regions, involve more environmental variables in the models, and link these digital traits contributing to other characteristics of interest, such as yield and disease resistance.

Conclusion

Omics data is growing and accumulating worldwide, opening a gate for precise breeding vegetables for various niche markets. Abiotic tolerance is required universally while facing global warming conditions. Phenomics and genomics data can be integrated with the climatic conditions while conducting field trials to predict the plant architectures in different environments.

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End-to-end coupling of FSPM visualization with image analysis methods on high-performance compute systems

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Keywords: visualization, plant data analysis, image analysis, high-performance computing

Introduction

Plant image analysis is an established method to obtain architectural parameters of crops (Minervini et al. 2015). In order to get reliable results, accuracy is required. Accuracy depends on many factors, including image quality, environmental conditions, setting (lab or field) and the frequency of measurements.

Synthetic data is a promising option for not only enabling a higher order of correctness, but also for validation of results (Cieslak et al. 2022). Plant images have to be realistic as well as rich in relevant information. However, labor intensive processing steps are necessary to arrive at sufficient image quality. Many of these steps still need to be done manually or semi-automated. Reducing sample and consequently information density is often the only way to make processing feasible. This inherently reduces scalability, which is detrimental to accuracy. For synthetic data to be impactful, it must be almost costless to produce, enabling scalable workflows. Synthetic data must also be meaningful, i.e., provide objective measurements, be reproducible, and mutable. Game engines like Unreal Engine (UE) provide easy to operate, state-of-the-art tools and technologies to achieve realistic images (Hu et al. 2020).

FSPMs can provide parametrized geometries that enable the creation of augmented data. In combination with UE, it is further possible to alter the environment regarding perspectives, lighting, and weather scenarios. This provides a potential input for deep neural network (DNN) training or as a validation of the original data. However, the creation of this synthetic data is complex and requires expert knowledge in Computer Graphics, Visualization and High-Performance Computing (HPC).

Materials and Methods

We are addressing this by introducing a framework (see Fig.1) that allows users to train algorithms on streams that equal live footage in an HPC compatible way. WebRTC is a peer-to-peer streaming method, typically used for video conferencing. In the case of UE, it enables streaming the final image composition of the rendering pipeline for remote visualization, while user devices only need to display the stream. In our case, running UE remotely means that it can run on a powerful visualization compute node, while DNN approaches can be delegated to specialized hardware.

Results and Discussion

Using WebRTC media streams to deliver images or videos of virtual plants, and training a DNN with those images, yields a very powerful pipeline that can potentially achieve unrivaled accuracy. However, WebRTC utilizes hole-punching, a network communication technique, making it unusable in HPC environments, due to firewall and connectivity restrictions. Our framework circumvents this by introducing mediators (Helmrich 2022), that allow the use of streamed virtual scenes in supercomputing environments. The resulting service is able to continuously produce realistic images of plant data or FSPMs, while also facilitating the training of DNNs.

This enables the use of pipelines directly targeting the parametrization of FSPMs under different conditions. A more general and robust parameter estimator may be trained using a large data stream that encompasses random FSPM parameter sets, implemented in a virtual lab or field experiment, or a combination of both. In contrast to real plant images, augmented images resulting from this approach are free of measurement error. Present approaches that use image data to facilitate parametrization can not only become more robust through costless training, but can also be evaluated based on synthetic data with known parameter configurations, and reproducible virtual camera setups.

Furthermore, this framework is not limited to pixel-level algorithms, such as segmentation. Users will be able to train image-to-geometry algorithms and statistical estimators that compute, e.g., leaf-area index. Our implementation integrates different ways of accessing different types of data and sample workflows are convenient to set up.

Conclusion

Our work makes synthetic data workflows accessible for plant science analysis, while retaining its most impactful properties, like scalable workflows with infinite data streams. The result is a pipeline to easily access realistic synthetic data of plants with already parameterized geometry under various environmental conditions. The conditions and perspective of the scene are defined by the user. Resulting data can be used for DNN training, to increase parameter robustness, for further plant trait detection and validation of original parameters.

We enable a user-friendly introduction to the training of DNNs by offering ready-to-use pipelines, providing virtual field visualizations, a python-binding library to access synthetic data, and a ready-to-run container to train a model.

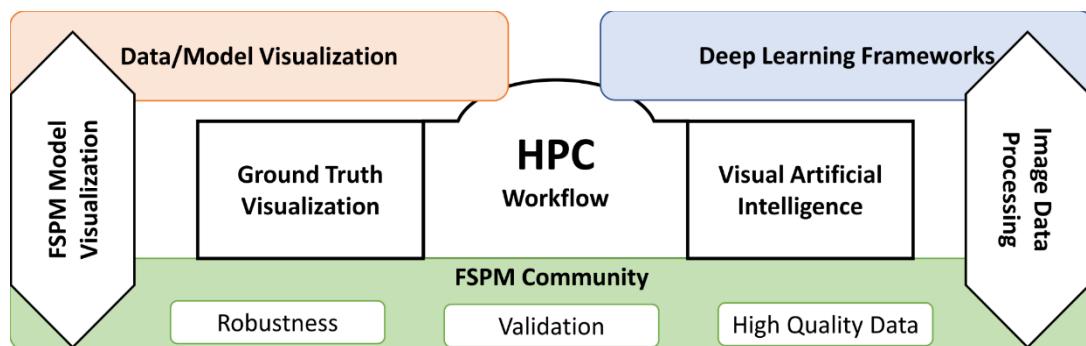


Figure 1: Conceptual overview of components and integration concept, building on an HPC structure to enable better performing workflows.

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Upscaling of functional-structural root models to simulate plant water uptake

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Keywords: root hydraulic architecture, soil water balance, rhizosphere, water uptake.

Introduction:

Water uptake by plant roots is determined by the water demand from the atmosphere and limited by the supply of water from the soil through the root system to the canopy. This supply function depends on water potential difference between the soil, the root system, and the leaves and on the conductances or resistances along the water flow paths. To represent the variety of flow paths and associated conductances in the soil-root system, functional-structural root models, which represent the structure of the root network and the conductances of the root segments, have been coupled to three-dimensional soil water flow models, which simulate water flow in the soil and the rhizosphere. With these models, water flow and water potentials in the soil-root system can be simulated as a function of the soil/rhizosphere and root system hydraulic properties. However, resolving all root segments of a full-grown crop and the water potential gradients in the soil around them brings along a very high computational cost. For practical applications (e.g. crop yield predictions, irrigation and fertilizer management,...) one-dimensional soil water flow models, which describe the dynamics of soil water profiles by solving soil water balances over thin horizontal soil layers, or zero-dimensional models, which describe the dynamics of the water storage in the root zone, are used. To include root water uptake in the soil water balance, these models use relations between water uptake or water supply from the different depths in the soil profile on the one hand and soil water potentials, root properties, and transpiration demand on the other hand. These relations are semi-empirical and do not account for root hydraulic properties which make them unsuitable to assess the impact of root hydraulic properties on the water uptake function of the root system, i.e., they can, for instance, not be used to identify root ideotypes for water uptake. In this contribution we present an approach to derive these relations in a mechanistic way using a functional-structural root model.

Methods:

We start from the description of water flow in the three-dimensional root system, that resembles a network of leaky pipes (Doussan et al. 1998), and that can be solved to obtain the water flow from the soil towards and the xylem water potential in each root segment when the water potentials in the soil and in the root collar or the water flux in the root collar are known. Assuming that soil water potentials around all root segments in the same horizontal soil layer are equal, we can upscale the set of equations to a reduced set that relates the water uptake from each layer to the soil water potential and the collar water potential or collar flux. The coefficients of the equations can be calculated directly from the root segment hydraulic properties and their connectivity (Vanderborght et al. 2021). This approach assumes that the soil water potentials at the soil-root interface are equal to the bulk soil water potentials. To account for water potential losses by flow from the bulk soil to the soil-root interface, an additional rhizosphere resistance was included using an analytical solution of the axial-symmetric nonlinear soil water flow equation (Schröder et al. 2008, de Jong van Lier et al. 2008).

Results

The upscaled model can represent at a much lower computational cost the effect of both root and rhizosphere hydraulics on water supply functions and reproduce phenomena such as a root

water uptake compensation, root hydraulic redistribution and hydraulic lift. Under wet conditions, root hydraulic conductances are limiting whereas under drier conditions, rhizosphere hydraulic conductivity becomes limiting. As a consequence, supply functions depend on both the soil and the root hydraulic properties and become non-linear functions of soil water potential for drier soil conditions. The reduction in rhizosphere conductance when the soil dries out leads to an earlier reduction in transpiration during a drying period than in case rhizosphere conductance is not considered. The reduction of the rhizosphere conductance when the soil dries out makes that the root system does not dry out the soil to the wilting point and the bulk soil water potentials stay above the wilting point. During night when the root system re-equilibrates with the bulk soil water potentials, the simulated plant water potentials rise again far above the wilting point also during longer dry periods. This suggests that rhizosphere hydraulics may play an important role in the plant water status and how it can recover at night during dry periods.

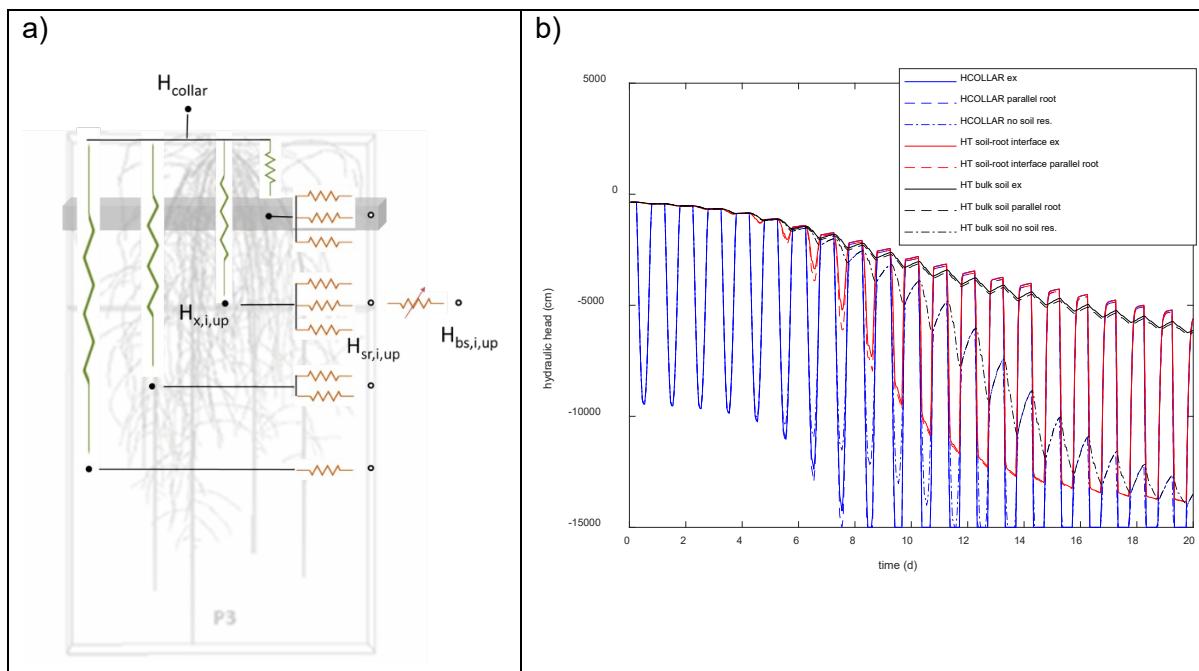


Figure 1: a) 3-D root system and its representation in a 1D soil water balance model, b) simulations during a dry down of collar water potentials (blue lines), water potentials at the soil root interface (red lines) and in the bulk soil (black lines). The model that does not consider rhizosphere conductance (dotted-dashed line) shows a later drop of the daytime collar water potentials to the wilting point but a stronger drop of collar water potentials at night, which match the bulk soil water potentials, compared to the model that considers the rhizosphere conductance.

Conclusions

The upscaling approach could be implemented straightforwardly in soil water flow models so that the effects of root and rhizosphere hydraulic properties can be represented in these models.

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Machine learning in studying sprouting patterns of *Platanus hispanica* under the influence of branch pruning

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Keywords: tree manipulation, TLS, tree QSM, deep learning, computational tree design

Introduction

Urban trees provide multiple ecosystem services (i.e., increasing biodiversity and thermal comfort) for humans' well-being. But their free growth in the context of densely built urban infrastructures can cause conflicts. Therefore, urban trees are commonly managed by humans: their crowns are partly removed if getting close to traffic lanes and power lines; overweight branches can be cut off to prevent root and branch failures; disordered shoots will be removed to keep pleasing aesthetic shapes. For such tree manipulations, pruning is the most common method. Cutting branches not only changes the appearance of the trees, but also affects their physiological processes through disturbing the balance of phytohormones which alters tree growth.

Therefore, in arboriculture, gardeners are trained to make pruning decisions for each individual branch (Clark and Matheny 2010). Generally, branches are sorted in strict hierarchy to reduce the weak tree forks; sub-branches should avoid over-competing the leading ones; damage needs to be restored with sprouting shoots. Sprouting of epicormic shoots can be influenced by pruning because it changes the light and stress regime (Meier, Saunders et al. 2012). These sprouts, which appear at uncertain positions after each prune, raise questions for best pruning solutions. Until now, such solutions only rely on tacit knowledge of experienced gardeners. Consequently, urban tree management remains a labor intensive and high-cost activity. Understanding tree sprouting patterns in relation to its topological geometry and pruning decisions is the first step for setting up a digital tree management agency.

Materials and Methods

Among trees at Bruns Nursery, Bad Zwischenahn (Germany), *Platanus hispanica* trees in a form of an umbrella were chosen as subjects for this study (see figure 1a). They are annually pruned between around mid of July and August at almost the same height. Standardized tree care and management as well as their abiotic environment in the Nursery rule out irrelevant variables for this study. In total, 191 pollarded such trees have been scanned in 2022 before and after the sprouting emerges with terrestrial LiDAR scanners (TLS) RIEGL VZ-400i. The acquired point cloud is then segmented into individual trees (figure 1b).

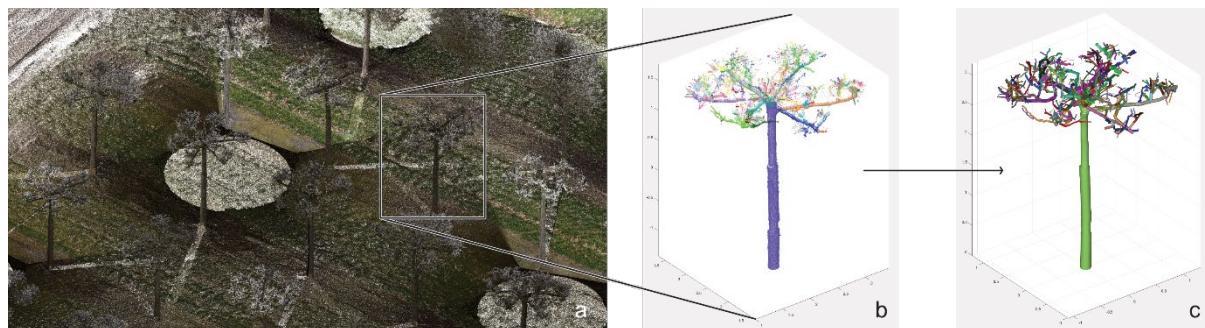


Figure 1: a) point cloud dataset of the *Platanus hispanica* trees at Bruns Nurseries; b) tree segmentation; c) its abstraction to a quantitative structure model.

quantitative structure models (QSMs) by cylinder fitting (Raumonen et al. 2013, see figure 1c). Several different approaches for this aim are listed in table 1. Their effect and robustness are being investigated.

Table 1: Methods for abstracting QSMs out of TLS point cloud of trees over the past decade

No.	Name	Year	Publication	Code
1	SkelTre	2010	Bucksch & Menenti. 2010. <i>The Visual Computer</i> , 26(10), 1283-1300.	n/a
2	PypeTree	2014	Delagrange & Rochon. 2014. <i>Sensors</i> , 14(3), 4271-4289.	Python
3	SimpleTree	2015	Hackenberg et al. 2015. <i>Forests</i> , 6(11), 4245-4294.	C++, Qt
4	3D forest	2017	Trochta et al. 2017. <i>PLoS one</i> , 12(5), e0176871.	C++
5	TreeQSM	2018	Lau et al. 2018. <i>Trees</i> , 32(5), 1219-1231.	MATLAB
6	Adtree	2019	Du et al. 2019. <i>Remote Sensing</i> , 11(18), 2074.	C++
7	AdQSM	2020	Fan et al. 2020. <i>Remote Sensing</i> , 12(18), 3089.	OpenGL

For each tree, abstracted topological and geometrical characters from Tree QSMs, pruning positions and sprouts will be structured in matrixes as shown in figure 2. Then, these matrixes for all trees will be divided into a training set and a validation set, feeding into different machine learning models (Choi 2020). Our hypothesis is that one of the machine learning models such as linear regression or artificial neural networks will be able to predict the sprout matrix in a meaningful accuracy. The risks lie in overfitting the model due to limited sample size and weak causality between pruning positions and sprout status.

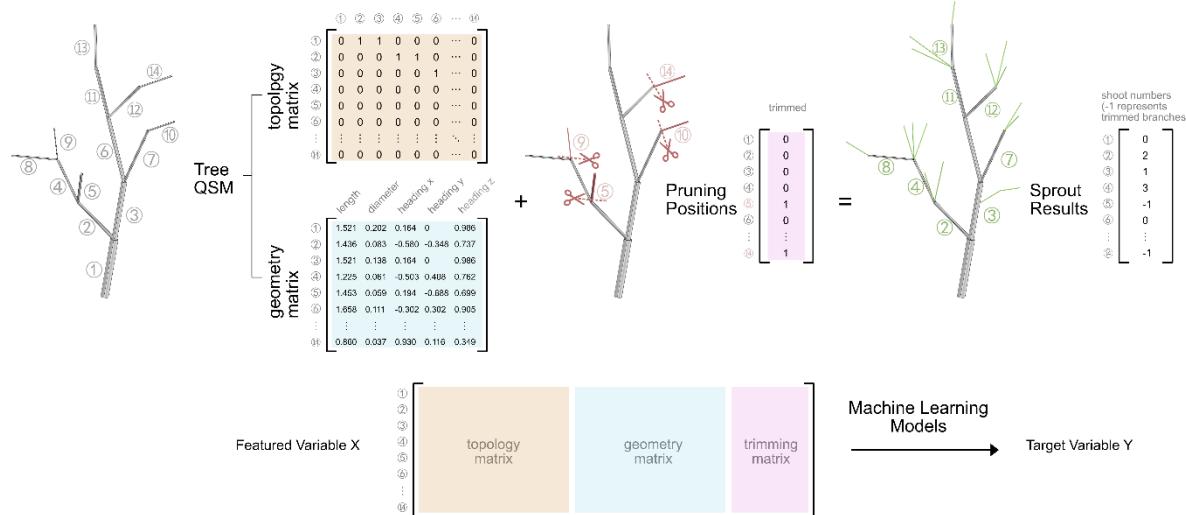


Figure 2: Machine Learning Models to forecast sprout with Tree QSM data and pruning positions

Limitations and Vision

Epicormic bud positions are not included in current datasets. They require higher detailed computer vision captions. This is a further step to improve the prediction accuracy. Overall, this study aims at quantitatively describing tacit knowledge to allow for artificial pruning decisions that are comparable to what an experienced gardener does. This study leads to a digital agent for tree management. In a vision, it will reduce the tree-caring cost and allow for more complex pruning regimes. Besides, branching geometry of urban trees can be more precisely managed for purposed design and use.

Acknowledgment

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Hybrid Mass-Spring L-System for modelling tree interactions with environment

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Keywords: tree growth, physics-based simulation, gravitropism, phototropism

Introduction

Tree model accuracy in digital twin cities is increasingly crucial for urban planning. Specifically, a tree model that considers the growth process and its responses to the environment may inform decision makers and provide recommendations on tree management and safety issues such as falling trees, obstructing branches, tree pruning and shades.

Existing L-System-based tree modelling techniques (Yi et al., 2018) (Stava et al., 2014) focus on implementing tree growth processes without accounting for the trees' continued mechanical responses to external forces and tropisms, after growth. Accounting for such responses will allow for more accurate tree models, which is important for urban tree planning. On the other hand, (Moulton et al., 2020) and (Hädrich et al., 2017) resolve this by modelling tree stems as inextensible elastic rods and particles respectively but neither integrates the domain knowledge of botanical growth processes such as branching patterns. (Jirasek et al., 2000) is similar to our work and they incorporate L-Systems while using equations involving moments to compute the rotation of the internodes. However this model does not account for the tree parts becoming stiffer and the possibility of branch breaking. Our model of incorporating L-Systems and the Mass-Spring system will allow us to keep track of nodal information while accounting for both biological growth processes and mechanical processes, thus it is more suitable for urban tree planning.

Methods

We generate our hybrid tree models based on species modelling work in (Gobeawan et al., 2021): stems are constructed by stacking and extending short cylindrical internodes over time according to L-System growth rules. Subsequently, mechanical responses are incorporated through a mass-spring system, where nodes and internodes are represented by point masses and connecting springs, consecutively. Springs connecting alternate point masses are also added for tree structure support. This is described in the following pseudocode.

for number of age timesteps:

tree grows for 1 unit of age by L-System production rules;

for number of substeps:

calculate forces acting on each node in mass-spring system;

calculate and update new position of each node;

To grow the tree until a target age, the system iterates for a number of age timesteps, each producing a new growth pair of internode and node at each active bud. Within an age timestep, for a number of substeps, forces on each node are calculated iteratively to update its position. Forces considered here include the tree's own weight and responses to environmental stimuli (phototropism and gravitropism), along with spring forces (elastic force and damping force) of the mass-spring system. To account for material changes from non-woody to woody branches, the spring constant for each branch varies with respect to its age.

Our model implementation uses L-Py (Boudon et al., 2012) and PlantGL for the L-Systems and its graphical representations. We implemented the mass-spring system (Baraff and

Witkin, 1999) using the implicit Euler (Mesit et al., 2007), gravitropism based on the sine law (Dumais, 2013), and phototropism by pulling stem tips towards the light source.

Results and Discussion

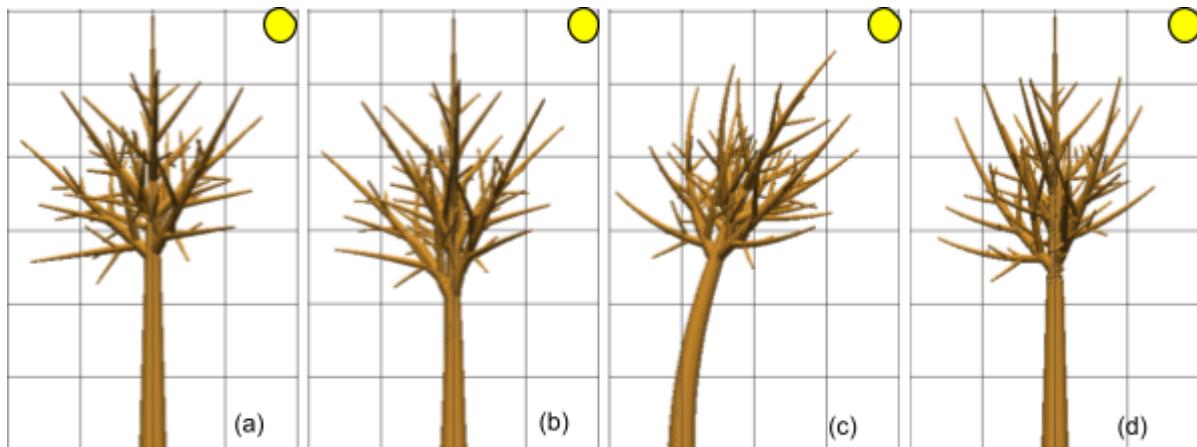


Figure 1. Simulated 25-year-old *Hopea odorata* tree considering: (a) no forces, (b) tree's weight ($g = 9.81 \text{ m s}^{-2}$), (c) response to phototropism (0.01N), (d) response to gravitropism (maximum 0.1N). The yellow dot represents a light source.

Fig. 1 shows several scenarios of a hybrid 25-year-old *Hopea odorata* model. For every age timestep which is set as $1/24$ of a year, the positions of all nodes were updated for 25 substeps of $8 \cdot 10^{-4}$ seconds. In Fig. 1(d) where the tree responds to all forces, its tips pull the stems towards a light source while its weight pulls them down, illustrating our model's response to environmental stimuli. However, our implementation requires small time steps for simulation stability. Inherently, our model requires relatively intensive computing resources to run long, accurate simulations.

Conclusion

We have developed a hybrid tree model involving species-specific L-System growth rules and mechanical responses to environmental factors such as gravity and light sources. The hybrid model shows typical reactions to these factors, given that realistic values were used for most parameters such as the spring constant. More work is required to investigate the different parameter values (e.g. magnitude of tropism forces). We have tested that our model can be used to investigate the strain acting on each node of the tree, and allow automatic branch breaking after the strain reaches a certain threshold. However, more work can be done to validate these models using data, and thereby make further improvements.

Acknowledgement

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Shoot based forest community model: Scots pine stand development under competition for light

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Keywords: forest growth, self-thinning, canopy development, *Pinus sylvestris* L.

Introduction

Ford and Sorrensen (1992) identify three principal interacting processes involved in the tree growth and stand development (Figure 1). First, resource capture as a response to the immediate environment and leading to tree growth. Second, allocation of growth to the development of 3D structure of the tree and third, modification of the immediate environment described as a 3D distribution of future resource flux. Stand dynamics result from the interplay of these processes and are primarily reflected in crown development. If a tree can lift its crown to a position that affords sufficient light in comparison to its neighbors then it can survive in the stand. Otherwise it will be suppressed and is liable to die.

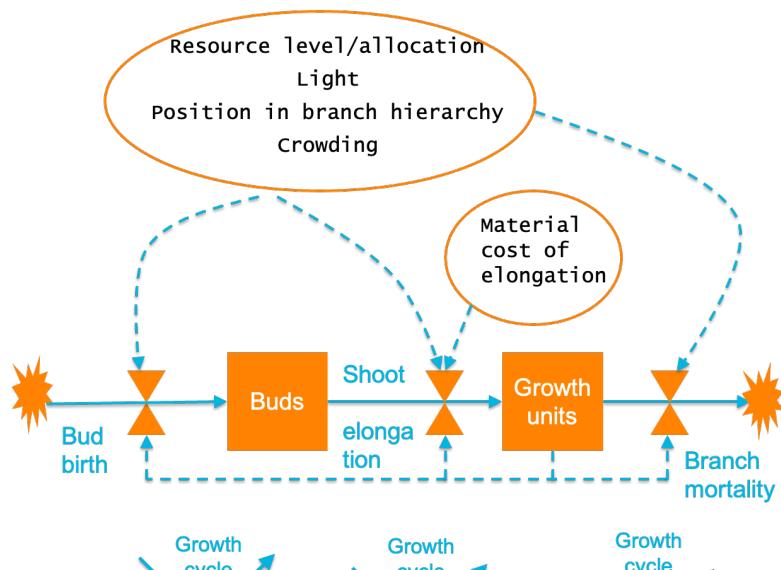


Figure 1. Processes in crown development

There has been a growing interest to understand the importance of 3D structure of forests based on individual trees because of the availability of terrestrial laser scanning devices which are able to collect required data promptly and economically (Saarinen et al., 2021). However, to our knowledge not many shoot-based models of forest (community) development exist today capable of simulating the long life span of forest trees. Such models could have the potential to study which shoot (internode) properties (local traits) are important for tree community dynamics — both in their biological meaning and also to reveal possibilities of simplified models.

Methods and Results

In previous articles (e.g. Sievänen et al., 2018) we have studied the performance of shoot-based tree model LIGNUM in a simplified spatial averaging manner: a tree surrounded by a homogeneous canopy space. We develop this approach and simulate a forest community consisting of individual trees interacting through light competition. We study an even-aged Scots pine (*Pinus sylvestris* L.) forest stand from seedling stage to maturity going through self-thinning. We observe that the model reproduces the general observed stand level growth patterns like self-thinning rule (e.g. Westoby, 1981), development of leaf area index and specific leaf area. We examine how different shoot-level traits contribute to stand level growth characteristics. We also test how different ways of allocation of growth resources, among others common pool for all crown or independent branches, affects stand dynamics (Ford, 2014).

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Could the theory “grow fast – die young” be applied to forest stands in Siberia?

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Keywords: rate-of-living theory, site index (bonitet), *Larix sibirica* Ledeb., tree annual increment

Bioclimatic statistic models of the forest productivity in Siberia (Tchebakova et al., 2016) demonstrate that site index (bonitet) increases in a warming climate if the tree species are still within its climatic ranges. Thus climate warming induces carbon sequestration by forests. The idea to create “Kyoto forests” in which enhanced tree growth captures greenhouse carbon dioxide from the atmosphere is based on this principle.

However, during recent years more publications appear in which there stated that forest productivity increase would cause quick mortality and the forest turns from a carbon sink into a carbon source (Buntgen et al., 2019; etc.). The authors explain their conclusions so called “rate-of-living theory” (Rubner, 1908). The paradox statement of this theory “grow fast – die young”) challenges many forestry measures and practices of reforestation and aforestation in a warming climate. Thus, in our epoch of striving toward low-carbon activities it is very urgent and actual to verify these statements of “rate-of-living theory” for Siberian forests which are a giant carbon reservoir with alternative trends of its carbon fluxes.

It is worth to mention that the conclusions of “rate-of-living theory” were drawn from dendrochronology/tree-ring data operating only tree ring width or basal area. While forest appraisal data (tree height, a number of trees per sq. unit, volume dynamics) are not used to conclude about carbon sequestration in trees drawn from only tree rings is not reliable in our opinion. ‘Rate of living theory’ (Speakman, 2005) suggests that as an organism reaches its maximal size so it approaches its life limit. In the last decade, an amount of publications has increased that testify the hypothesis “grow fast-die young” based on tree-ring data usually sampled in extreme alpine habitats of low site index (Buntgen et al., 2019). Conclusions drawn from those studies follow that the carbon sequestration of forests decreases as trees’ longevity shortens due to a greater growth rate and faster reaching a maximal size as climate warms. If this theory is correct then the idea of ‘Kyoto Forest’ makes no sense.

We focus on Siberian larch forests in the southern Siberian Mts and argue against those conclusions using inventory data (Shvidenko et al., 2008). For Siberian larch, initial rapid height growth slows down after the first 30-50 years and asymptotically approaches height limits characteristic of each site index. The site index curve family (Fig. 1) demonstrates how greatly individual tree heights differ depending on site index (bonitet). While the maximum larch age in Fig 1 is 280 years, there is ample historical evidence of *L. sibirica* thriving for 500-600 years or longer in productive (I-la bonitet) foothills throughout the southern Siberian mountains.

The hypothesis “grow fast- die young” was inferred from tree-ring data sampled in extreme alpine habitats. Such regression models are reliable and applicable only within the limits in which the models were constructed. In this study, data used for modeling were limited to widely spaced separate trees in extreme habitats at the alpine tree-line. It is inappropriate to apply inferences from separate trees to forest stands in more productive habitats of Siberian larch. The validity of the “grow fast – die young” hypothesis for forest stands could only be established based on data from forest stands. The results of this study, therefore, are not sufficient to conclude that the vast global forest stretching across its diverse ecological niches and habitats will have limited capacity to sequester carbon in a warming climate.

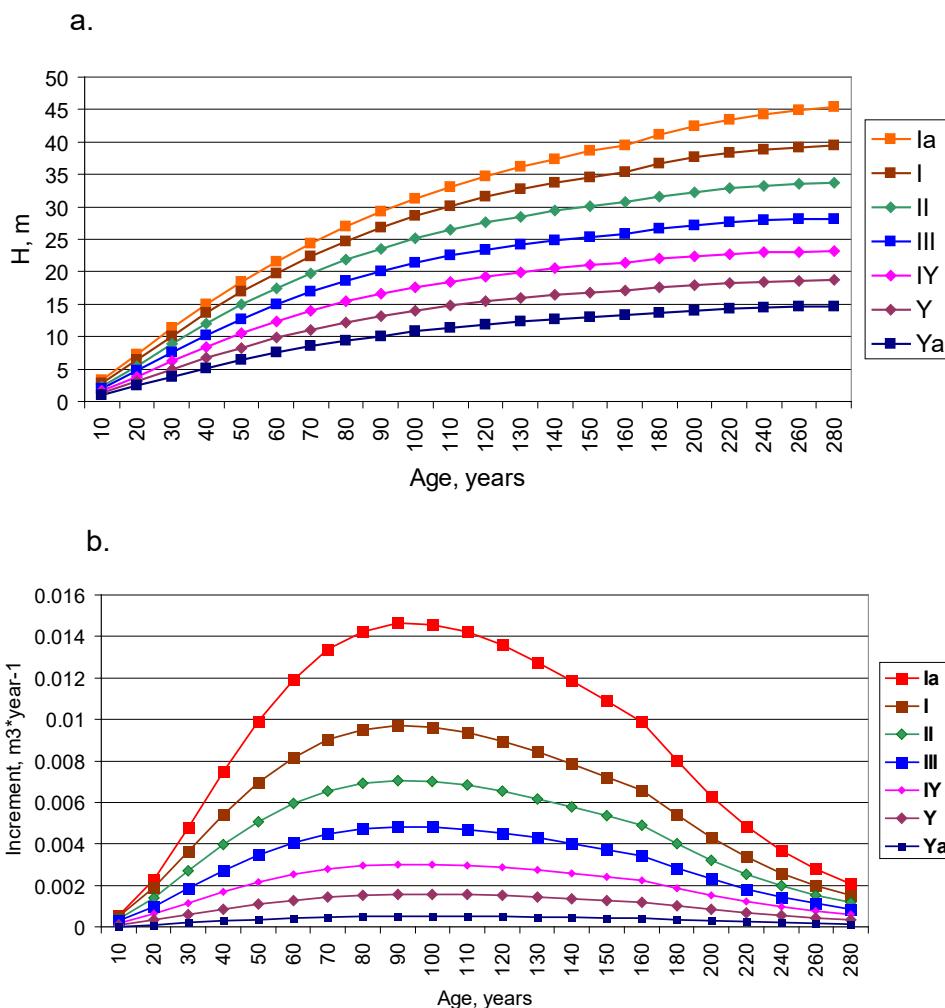


Figure 1: Growth trajectories for larch stands of the West Siberia southern mountains: a – average tree height (m); b – average tree annual increment. Bonitet ranges from Ia (high site index) to Ya (low site index).

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The GreedyGoat model: bringing new perspectives on woody plant-browser interactions by considering 3D plant architecture and its development

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Keywords: Plant architecture modelling, mammal browsing, spinescence, simulation.

Browsers eat plant leaves to survive. Plants need their leaves to survive. Both of these reigns have develop capacities to improve their survival chances. Plants protect their leaves by making them less tasty or accessible. Animals are able to adapt to plant poisons or structural protections. Focusing on mammalian browsers and woody plants, the ability of the animal to easily move from a part of the plant to another, the size of the bites, the sensitivity to woody or spiny obstacles and thus the potential protection of the branching structure of the plant are research topics that are raised. Anyway, from a mechanistic point of view, the way large mammalian herbivores impact woody plants remain poorly understood compared to other drivers such as drought, soil fertility, frost, fire, etc, and even compared to our understanding of herbaceous herbivory. Investigations of the role and importance of these factors are impaired by the fact that field observations and experiments are difficult, if possible at all.

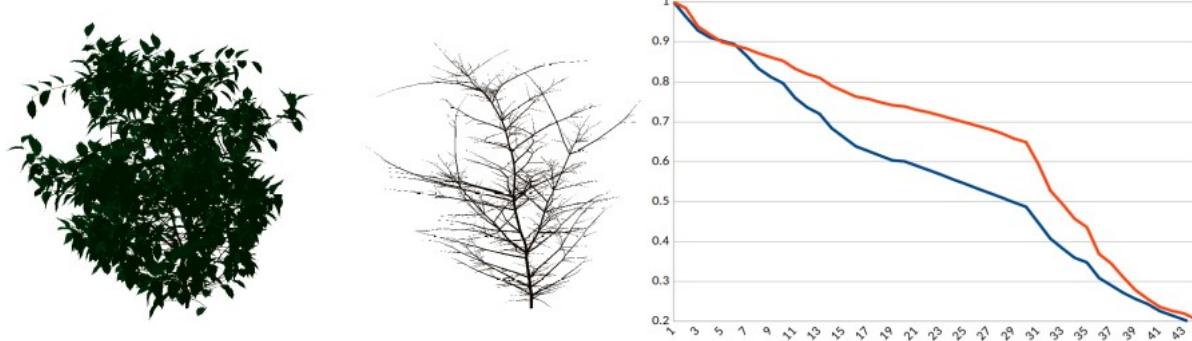
We propose GreedyGoat, a model that mimics a mammalian browsers behavior when attacking a woody plant. The model remains on browser capabilities facing the structure of this plant. This model will be coupled to the AmapSim model that dynamically grows plants (barczi 2008). AmapSim is able to accurately mimic plant growth with the correct number of branches, leaves and eventually spines.

The development of this model was motivated because we claim that plant architecture is a key trait that has been overlooked in the study of the interaction between browsers and woody plants, and that botanists and ecologists currently lack an appropriate model integrating this trait and allowing to (1) bring together our current knowledge, highlighting the gaps in our understanding and helping to derive new hypotheses to be tested *in silico* and *in natura*; (2) help estimating quantities that are difficult to record in the field, as for example the level of light interception of all leaves of a plant, or the number of leaves removed by a browser, or the cage protection effect on leaves surrounded by branches and needles; (3) make virtual experiments that would be difficult or even impossible to perform *in natura*, for example, exposing a sapling to browsing for 20 years, or simulating the browsing effect of an extinct herbivore; (4) understand the ecological and evolutionary conditions under which a plant or animal strategy is beneficial or detrimental to its fitness.

Thanks to GreedyGoat, a virtual browser is parametrized through its mouth size and max browsing height, its sensitivity to obstacles and its capacity to link up bites in a row before making a new try at an other place in the plant. GreedyGoat also allows to control the capability of the plant to resprout the buds that were browsed.

In this paper, we explain in details how GreedyGoat was built. We describe the set of parameters that are taken into account and the algorithms that are run. We also explain the

way how it is coupled to AmapSim and we illustrate the simulation of this coupled model through case study examples as shown in next figure. We finally discuss new avenues of research that could be considered thanks to the GreedyGoat model.



Test plant before and after browsing. light interception (red) and leaf surface (blue) loss along browsing (%)

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Radiation empirical crop model and real-time crop information adjustment for greenhouse leafy vegetables

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Keywords: crop model, greenhouse leafy vegetables, real-time crop information adjustment

Leafy green vegetables grown in subtropical regions such as Taiwan are susceptible to weather changes, making them difficult to store and leading to deterioration in quality over long periods of time. Therefore, developing a production plan based on demands would be one way to improve production efficiency and reduce the costs of leafy vegetables. The objective of this study was to develop a protocol for scheduling of leafy vegetable production using environmental data measured by IoT devices. The production schedule aimed to best satisfy both the delivery specifications (including plant length and fresh weight) and the expected delivery date of the order with some allowance of storage in the refrigerator. The crops of interest in this study included *Brassica chinensis* L. CV. Ching-Geeng, *Brassica rapa* L. ssp. *chinensis* Jusl. and *Ipomoea aquatica*. Firstly, the plant length and fresh weight of the above three leafy vegetables were estimated by the cumulative radiation exponential function. When there was a discrepancy between the model prediction and the natural growth, the crop growth simulation results were real-time corrected by modifying the model parameters according to the actual sampling results. The MSE of the original model was 245 and the MSE was reduced to 21 and 52 if corrected using sampling results took 19 and 27 days after planting. In conclusion, we believe the results of this study could provide farmers with the opportunity to update the actual growing conditions in the field to improve the efficiency of their agricultural operations.

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Simulations protocols to assess customized irrigation strategies on rice production under climate change in Taiwan

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Keywords: Climate Change, DSSAT, Rice Yield, Irrigation, Decision Support

Rice has been the major staple food crop in Taiwan in centuries. Due to the climate change, rice production in Taiwan had been suffered severe drought stress recently. In this study, we used the DSSAT crop model (Jones et al., 2003) together with R programs (R Core Team, 2022) to simulate the rice yield under three irrigation scenarios, including automatic irrigation, non-irrigation, and irrigation only on sensitive growth stages. We had performed simulations on grids of 5 by 5 km on arable lands with the corresponding soil and weather information and compared the amount of water required and the resulting risks of production losses under different scenarios. The result had shown that if only irrigating in sensitive growth stages in central Taiwan and eastern Taiwan, it might possibly save water consumption up to 76% without affecting the yield. This study had successfully incorporated detailed soil and weather information into simulations. Several R programs had knitted together with the DSSAT crop model to create flexibility to conduct customized simulations that better represent the actual irrigation operations. The protocols for simulations used in this study may inspire more ideas of crop model applications in response to different inquiries from the policy makers.

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CERES-Barley calibration for spring barley under German growth conditions

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Keywords: crop model, DSSAT, crop simulation model

Process-based crop simulation models (CSM) allow performing experiments *in silico*, investigating crop growth, development, and yield formation, for different genotypes under various management and environmental conditions, including future climatic conditions. Increasingly adverse weather conditions due to the ongoing climate change exert negative impacts on crop production and related food security. Predictive tools such as CSM can help to develop adaptation strategies considering the genotype (G) x environment (E) x management (M) interactions. Before applying a CSM for various research questions, it is important to calibrate it for the specific target genotypes and environment and evaluate its performance to be able to generate robust predictions. In this study, we calibrate and evaluate the crop model CERES-Barley embedded in DSSAT. We prepare the experimental input files based on a large dataset of federal and state variety trials from 1995 to 2019. We select four genotypes, namely Barke, Quench, Avalon, and RGT Planet, which were first tested in variety trials in 1993, 2003, 2009, and 2011, respectively, and hence represent breeding progress in spring barley in Germany over the past decades. The location x year-specific crop management data and the genotype-specific data on phenology, yield, and yield components are available for 45, 67, 89, and 114 site-years for Quench, Barke, Avalon, and RGT Planet, respectively. We use the time series estimator tool (TSE) for DSSAT to calibrate cultivar-specific coefficients. TSE estimates cultivar coefficients by minimizing the normalized root mean square error (nRMSE) between simulated and observed data. In addition to the empirical data from variety trials, we ran a field experiment at the Julius Kuehn Institute in Berlin for two consecutive years using the same four genotypes, growing them under good agricultural practice. We collected detailed growth data to complement the calibration dataset, including the development of leaf area index, biomass, leaf-stem-ratio, flag-leaf area, soil moisture, and others. After calibration and evaluation, the CSM CERES-Barley shows satisfactory model performance with regard to phenological development, growth parameters, and yield. The calibrated and evaluated model is available to conduct various CSM-based analyses, including the identification of optimal cultivar choice and crop management decisions for different target environments as well as climate change impact assessment. Being calibrated for four distinct spring barley genotypes commonly grown in Germany over the past three decades, we can comparatively analyze crop growth and yield formation of these genotypes for various growing regions over the past decades to help disentangle the effects of genetic and climatic changes on spring barley productivity.

Adapting the DSSAT-CERES model to simulate growth and production of cereal rye

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Keywords: process-based crop model, DSSAT-CERES, cereal rye, CERES-wheat

Rye (*Secale cereale L.*) is primarily grown as an annual winter crop throughout the temperate zones of the northern hemisphere. Due to its high resource use efficiency, rather low input requirements and high resistance to frost and drought, it has good potential to support more sustainable crop production in the face of future climate change and rising food demand (Båga et al., 2022; Kottmann et al., 2015).

Process-based dynamic crop simulation models (CSM) simulate crop growth, development, and yield under various soil, climate, and management conditions, making them essential tools in current agronomic research (Jones et al., 2017). A thoroughly developed and tested CSM to simulate rye growth, development and yield formation can help to assess the feasibility of rye production under various agro-climatic conditions. Only few rye simulation models have been developed to date, with limited applications and/or accessibility. We choose to adapt the widely applied CSM CERES-wheat as a starting point for the rye model development, as rye is similar to wheat in terms of its morphological and physiological properties. Furthermore, CERES-wheat is available in the Decision Support System for Agrotechnology Transfer (DSSAT), which is freely available and widely used in the crop modelling community (Hoogenboom et al., 2019).

We first calibrate the CERES-wheat model and building on that adapt the CERES-rye model. Therefore, we have established a large agronomic trial datasets of cultivar-specific data (rye cv. Palazzo and wheat cv. Winnetou) building on value for cultivation and use (VCU) trial data from the Federal Plant Variety Office and additional state variety trials of Saxony-Anhalt (SVT). The dataset covers all relevant wheat and rye-growing regions in Germany, allowing us to upscale the model calibration for those cultivars to the national scale. We supplemented VCU and SVT data with two additional in-season data sets, one from an N-regime trial conducted in Kiel, Northern Germany, from 2008 to 2010, and the other from the Julius Kuehn Institute in Braunschweig, Central Germany, from 2009 to 2010. Weather data for each experimental site were retrieved from the German weather service's climate data center (DWD), and soil data were derived from the European Soil Database (ESDB) v2.0, both data in 1km² grid scale (DWD, 2020; Panagos et al., 2012). For model adaptation and calibration, we randomly selected 75% of the trial dataset as calibration data and the rest 25% as validation dataset. We performed the model calibration using the time series estimator (TSE) tool for time-series calibration (Memic et al., 2021).

The calibration of the CSM CERES-wheat showed accuracy in simulating BBCH with an RMSE of 7 days, 2007.7 kg ha⁻¹ for above-ground biomass, 0.92 for leaf area index (LAI), 138.7 for tiller m⁻², 6769.4 for grain m⁻², 5.6 mg for unit seed weight, and 1611.7 kg ha⁻¹ for grain yield.

The CERES-rye model also showed satisfactory simulation accuracy regarding phenology, LAI, above-ground biomass, and tiller m^{-2} at harvest, unit grain weight, grain m^{-2} at harvest, and grain yield. Simulation-observation comparisons resulted in an RMSE of 3.3 days for emergence, 7.2 days for anthesis, and 7.3 days for harvest maturity date for the calibration dataset from the phenology part. From the growth and yield simulation, RMSE of 1.61 for LAI, 2468.7 kg ha^{-1} for biomass, 169.6 for tiller m^{-2} , 7708.0 for grain m^{-2} , 3.6 mg for unit grain weight, and 2182.7 kg ha^{-1} for grain yield.

CERES-rye is available to conduct various CSM-based analysis including the evaluation of crop management strategies, consideration in analysing crop rotations in DSSAT, and assessing rye's suitability for cultivation in different growing environments.

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Simulating phenology in perennial grasses using a morphogenetic model: L-GrassF

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Keywords: floral transition, grassland, temperature, photoperiod, individual-based model

Introduction

Predicting the reproductive phenology and in particular the heading date (HD, appearance of the spike) in perennial grasses is a major concern for farmers because it determines the quantity and quality of forage. This event exhibits a high genetic variability within species, reaching more than 30 days for European cultivars. To date, prediction methods of HD are empiric and do not address the consequences of reproductive phenology on grassland perenniability, *i.e.* the productivity of grassland over several years without resowing. Indeed, the reproduction of perennial grasses in grazed or harvested grasslands is mostly vegetative because spikes are removed before seed maturity. During the spring, some tillers become reproductive, produce a spike and finally die, while other tillers remain vegetative until the next season, depending on their ontogenic status. The tiller population is thus largely modified by phenology. The phenology of perennial grasses is controlled by the seasonal variations of temperature and photoperiod (Heide, 1994, Rouet, 2021). Predictions of climate change suggest significant changes in seasonal temperature pattern, which will create new combinations of temperature and photoperiod whose consequences on the floral induction of perennial grasses are unknown. Here, we present L-GrassF, a new FSPM simulating the genetic variability of the phenology of perennial ryegrass in order to better understand the perenniability of grasslands and better anticipate the effects of climate change.

Materials and method

L-GrassF extends the previous leaf growth model L-Grass (Verdenal et al., 2008) to the reproductive stages by integrating the interactions between vegetative growth and the processes of floral induction and reproductive organ development. The model is detailed in Rouet *et al.*, 2022 and is in open access on GitHub (<https://github.com/openalea-incubator/lgrass>). L-GrassF simulates the production of tillers in *Lolium perenne* as well as their growth according to self-organization rules between successive leaves. The model simulates floral induction, growth of reproductive organs and mortality for each individual tiller according to the environmental conditions to which they were exposed. The floral induction is modelled by two successive phases: the primary induction, controlled by temperature and the secondary induction, controlled by photoperiod. Leaf elongation, the rate of primordia production and their differentiation into leaves or spikelets are modulated by the state of floral induction. In the model, HD results from the interaction between floral induction and leaf morphogenesis.

The model was calibrated and validated on two independent datasets from the French Variety and Seed Study and Control Group (GEVES), which include the observations of HD for seven cultivars of *Lolium perenne* grown in six French locations between 2001 and 2017. The

calibration of the model was performed on the three most sensitive parameters identified by a sensitivity analysis. These parameters (Y_m^0 , kY_m^0 and $PPRM$). control leaf elongation during the vegetative phase, leaf elongation during the reproductive phase and the maximal daily rate of secondary induction. The calibration consisted in the identification of the set of parameters with the lowest RMSE between observed and simulated HD for each cultivar. Finally, the model was validated for HD predictions against the second independent dataset.

Results and discussion

For cultivars Bronsyn, Indiana, Lactal, Carillon and Escal, the model provided good overall estimates of HD (RMSE < 10 days) but the coefficients of determination were low. This could be explained by the narrow range of observed HD for these cultivars, especially for Carillon. For Milca, the elevated RMSE was partly explained by one environment for which the model clearly overestimated HD (Figure 1e). For Bargala, the RMSE was higher and the determination coefficient was very close to zero, meaning that the model was not able to give better prediction than the mean observed HD (Figure 1d). We did not find any clear explanation for the model's behavior in this situation which was not characterized by unusual environmental conditions. Considering all cultivars together (Figure 1h) highlighted an overall efficient prediction of HD (RMSE ~ 10 days) and a good representation of cultivar earliness ($R^2 = 0.48$). The functional-structural approach used in L-GrassF made it possible to account for the interactions between vegetative morphogenesis and floral induction of the apex as a function of the environment experienced by each individual tiller.

L-GrassF showed promising performances in predicting HD of *Lolium perenne* cultivars. The model is now intended to be used to study the determination of the proportion of reproductive tillers as well as the impact of future climatic conditions on perennial grass phenology.

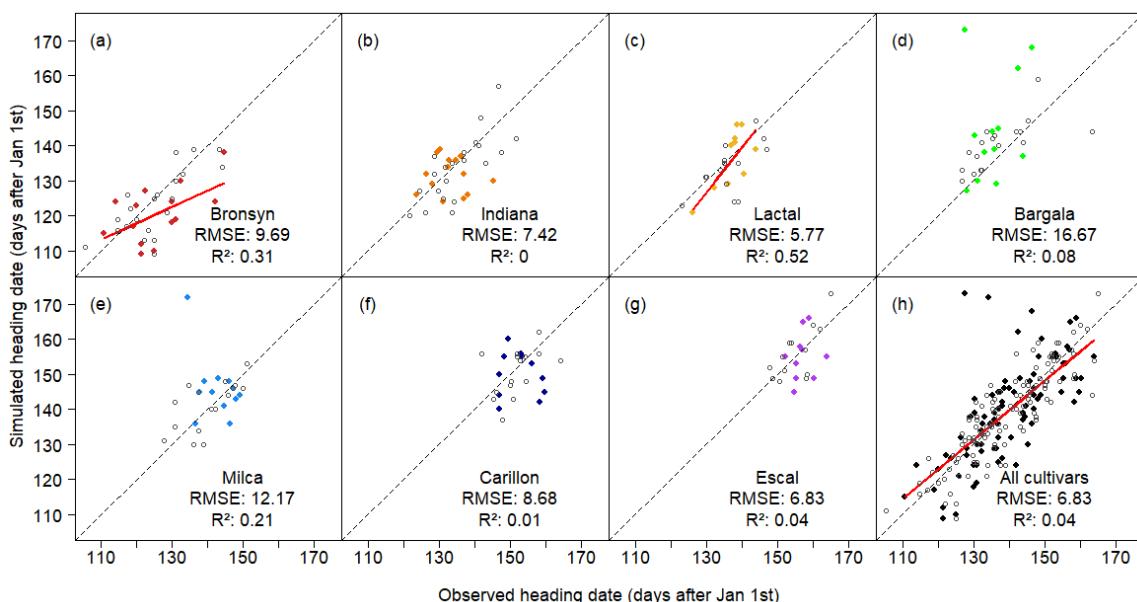


Figure 1: Comparison of observed and predicted values of heading date obtained with L-GrassF for seven cultivars.
 (a) Bronsyn, (b) Indiana, (c) Lactal, (d) Bargala, (e) Milca and (f) Carillon, (g) Escal. Grey and colored points represent the sub-datasets used for model calibration and validation, respectively. Reprinted from Rouet et al. (2022). *isP*, 4 (2), 1-17. Copyright © 2022, Oxford University Press

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Modelling weed suppression in intercropping systems

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Keywords: crop diversification, *in silico*, functional-structural plant modelling, plant plasticity

Introduction

In the past century, modern agriculture has focused mainly on increasing the yield in monoculture cropping systems. However, this has resulted in unsustainable cropping systems causing a variety of ecological issues, including soil degradation, biodiversity reduction, and increased weed infestations (Tilman, 2002). Yields are impacted severely by biotic stressors, of which weeds have the largest potential negative impact (Oerke, 2005). Herbicide use is associated with a variety of negative environmental and health effects. As a result, herbicide use is increasingly regulated by the European Union and its application is to be reduced severely in the future (European Commission, 2020). A diversification of cropping systems is frequently suggested to increase ecological sustainability and reduce weed infestations. Intercropping, a system where multiple crop types are cultivated on the same field, is one means to increase crop diversity. The benefits of intercropping depend on the specific intercrop system, and ecological benefits do not always align with monetary benefits. Additionally, there are technological barriers and associated costs, withholding the adoption of intercropping systems by farmers. More insight is needed into the effects of intercrop design on weed suppression and productivity of multi-species systems. Here, we aim to identify and quantify crop and plant traits that contribute to weed suppression in a cereal-legume intercrop system.

Materials and Methods

To understand the mechanism of enhanced weed suppression in intercrops, we investigated crop and plant traits that play a role in light competition through a combination of field experiments and functional-structural plant modelling (FSPM). We developed an FSPM in Julia using the Virtual Plant Laboratory (VPL) package (<http://virtualplantlab.com/>). VPL aids the construction of plants as individual graphs through dynamic updating of plant variables and the conditional rewriting of organ structures. Plant growth and development is based on simulated photosynthesis, respiration, and assimilate allocation, driven by light capture and temperature.

The weed suppressive ability of different cereal-legume intercrop combinations has been investigated through a field experiment using all possible combinations of wheat, rye, barley or triticale with pea, lupine, or faba bean, as well as all sole crops to compare. Measurements were taken for weed biomass, crop biomass, canopy cover, light interception, plant height, number of branches or tillers, legume branch length, tiller angle, and emergence.

Triticale (*x Triticosecale*) and faba bean (*Vicia faba*) were chosen as a case study in the FSPM and were subsequently modelled in detail through a reparameterization of architectural parameters of existing wheat and pea models already present in the FSPM. Parameter values for the plant models were obtained using data on plant development, growth, and architecture. The model includes plastic responses in traits like internode extension, tillering and branching, and tiller angle. Data from the field experiment was used to evaluate model performance. Furthermore, multiple virtual weed species were developed with different plant traits that characterize weeds. Weed traits that were used are seedling emergence time, plant height, biomass growth rate, and plant architecture. This way, the performance of the intercrop system was compared *in silico* against different weed types.

Results and Discussion

The FSP model provides detailed insight in the differences between the intercrop and sole crop systems in terms of biomass production, weed biomass, yield, and light competition factors like light capture. It enables detailed analysis of the contribution of the component species to light interception and canopy cover of a mixed system. Furthermore, the model allows us to quantify the influence of specific plant traits on the system's competition for light and by extension on its weed suppressive ability. This is achieved through the isolation of specific plant traits independent of other trait differences between intercrop and sole crop. Isolated traits include time of emergence, morphological traits (height and leaf size), and plasticity in internode extension, tiller angle, number of tillers and branches, and leaf mass area.

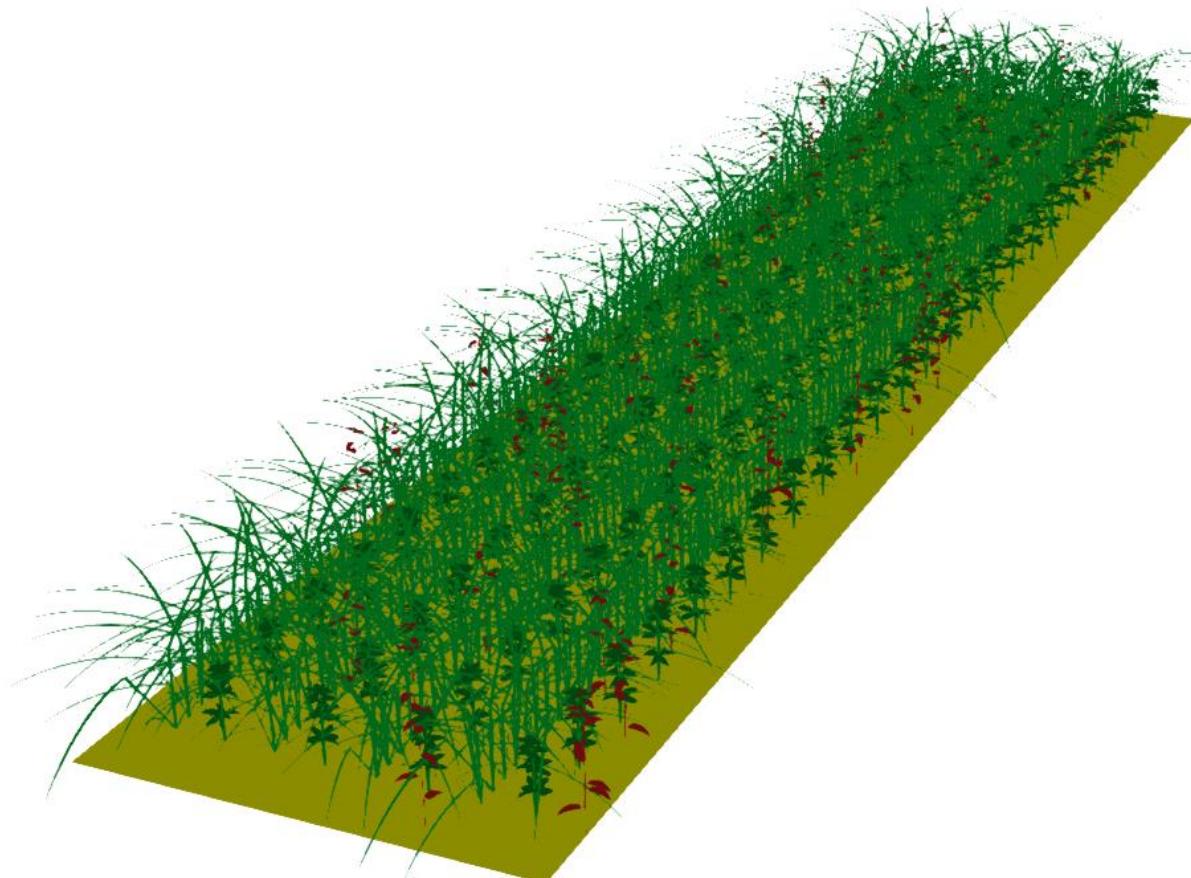


Figure 1. Example of an FSPM visual output of triticale – faba bean row intercropping with weeds at random locations (in red for emphasis).

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SIMBAL: A structural-functional plant model to simulate C and N dynamics and shoot-root architecture of winter oilseed rape associated with legumes

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Keywords: plant model, fababean, plant-plant interactions, FSPM for agroecology

Introduction

Species mixtures are of great interest to promote low-input agricultural practices while maintaining agricultural production. For example, winter oilseed rape sown with a frost sensitive legume reduces the use of nitrogen fertilizer and herbicide while maintaining yield at levels equivalent to pure cropping (Lorin et al., 2016). A disadvantage of such mixtures is that the legume might compete with the cash crop for resources and reduce yield. To optimize management of these mixtures, it is necessary to better understand the ecophysiological processes that drive the sharing of resources between plants (e.g. carbon and nitrogen). Mechanistic functional-structural modeling (FSM) is particularly suitable for such studies as it allows the analysis of the processes underlying plant-plant interactions and integrates both the architectural growth processes of the plant and its functioning (e.g. acquisition/allocation of resources) (Louarn and Song, 2020). For example, the model Virtual Grassland (Louarn et al., 2014) simulates competition for C, N and water between several herbaceous and legume species. However, no FSM for mixtures of annual crops with frost sensitive legume that considers the feedback of the carbon/nitrogen functioning in both shoots and roots has been developed so far. Such a modeling approach is shown in this study, with the aim of filling knowledge gaps on the role of carbon-nitrogen interactions in plastic responses of plants in mixtures, by taking the case study of winter oilseed rape sown with frost sensitive fababean at vegetative stage.

Conceptual framework of C and N fluxes

The model SIMBAL (SIMulated Brassica Associated with Legumes) is based on the ARNICA FSM developed for *Arabidopsis thaliana* (Richard-Molard et al., 2009). The model simulates shoot and root architecture of winter oilseed rape in which C and N fluxes determine the growth of each organ (leaf, internode, root segment). C is preferentially given to shoot and N to roots. As showed in Fig.1, the total internal N amount results from root uptake and remobilization from storage (1) and determine the increment of leaf and internode area (4). N in leaves is distributed along the light gradient within the plant, while N in internodes is distributed homogeneously (3). The total internal C quantity results from photosynthesis (6) and remobilization of C storage (9). Root growth results from the N available to roots (2) and the C available after satisfaction of shoot demand (7). C storage is filled if total internal C quantity is superior to C organ demands (calculated as the C quantity necessary to produce a unit of leaf, internode or root surface) (9). N storage is filled from leaf senescence (driven by a leaf lifespan) (5) and when N quantity for shoot is superior to N used for actual total photosynthetic area (8). When the crop is grown in association with fababean rather than in monoculture, the light availability to the plant is reduced and parameters value such as phyllochron are modified based on experiments.

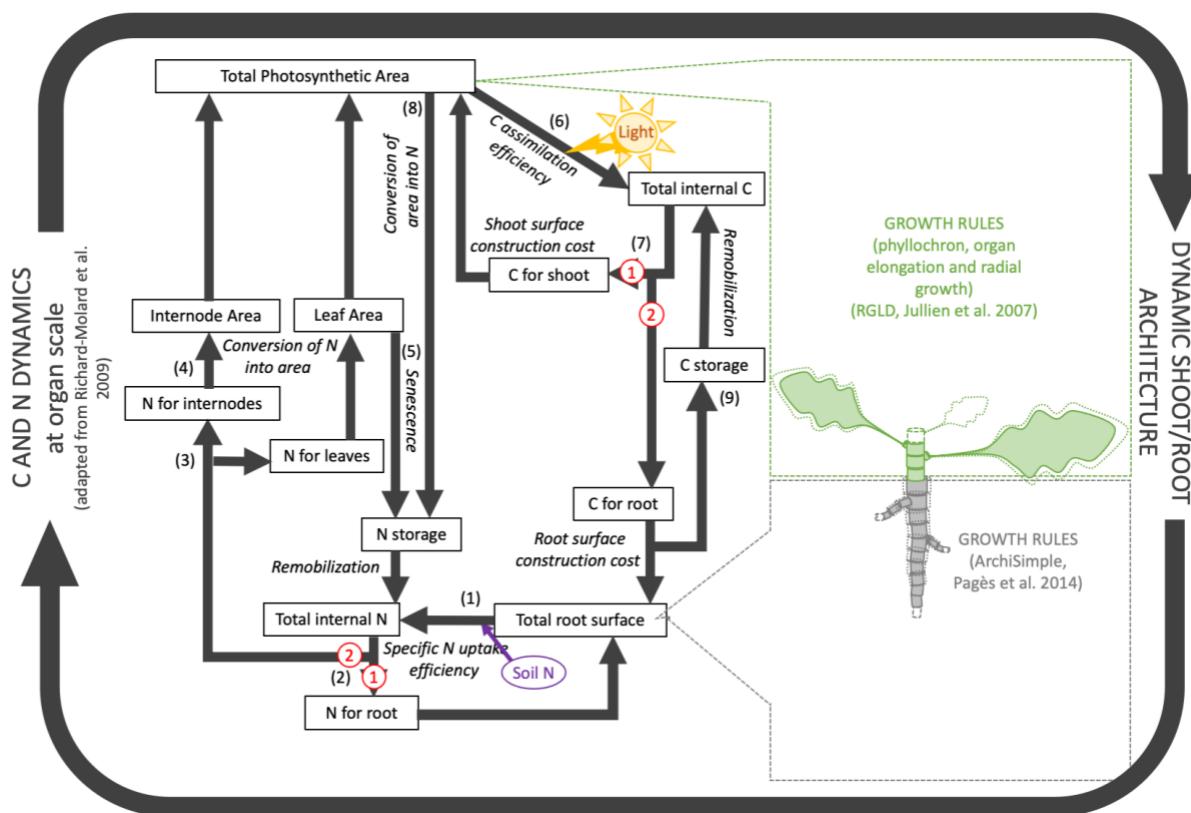


Fig.1: Conceptual framework of C and N dynamics and organ growth underlying the SIMBAL model

Towards a model of rapeseed and fababean mixture at the entire crop cycle

A first FSPM was built to study the N and C fluxes and organ growth within a whole plant of winter oilseed rape at the vegetative stage in OpenAlea (Pradal et al., 2008). This conceptual framework aims to be generic and adaptable to other species, in particular frost sensitive fababean. In the near future, we intend to develop the model upon the entire crop cycle of winter oilseed rape and to assess the effect of frost sensitive fababean on oilseed rape growth and CN functioning through direct (competition for light harvest and N uptake) and indirect (degradation of N-rich legume residues) effects.

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Searching for grapevine (*Vitis vinifera* L.) optimal stomatal traits using the HydroShoot functional-structural plant model

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Keywords: *in silico*, stomata, climate change, FSPM, viticulture

Introduction

Climate change is expected to increase water and heat stress in many wine regions (**Hannah et al., 2013**). Stomatal conductance plays a pivotal role in adapting viticulture to these adverse conditions (**Bartlett and Sinclair 2021**). We examined the maximum stomatal conductance (g_{\max}) and water potential at 50% stomatal closure ($g_s \Psi_{50}$) that optimize grapevine performance under the future conditions projected for economically important wine regions in California, using the functional-structural plant model (FSPM) HydroShoot (**Albasha et al., 2019**).

Materials and Methods

We ran HydroShoot on historical (1990 – 2010) and future (2079 – 2099) weather data to simulate the cumulative plant transpiration (ΣE , kg), net carbon gain (ΣA_{net} , kg), minimum shoot water potential (Ψ_{\min} , MPa) and maximum leaf temperature ($T_{L,\max}$, °C) of Vertical-Shoot-Position-trained vines. Simulated sites were the Oakville station (38.43N, 122.41W) in Napa Valley and the Fresno State station (36.82N, 119.74W) in San Joaquin Valley.

Historical data (source: <https://cimis.water.ca.gov/>) were averaged across years to produce a representative trajectory. Future data were compiled from four priority GCMs for California (CanESM2, CNRM-CM5, HadGEM2-ES, MIROC5, source: <https://cal-adapt.org/>) for the high emissions scenario (RCP 8.5). We focused post-véraison period (Jul 30 – Aug 30 for Oakville and Jul 11 – Aug 11 for Fresno) to capture the hottest, driest conditions. HydroShoot was parametrized with the 5th, 50th, and 95th percentile g_{\max} and $g_s \Psi_{50}$ values compiled from the literature for 21 winegrape cultivars ($g_{\max} = 148, 426$, and $531 \text{ mmol m}^{-2} \text{ s}^{-1}$ and $g_s \Psi_{50} = -1.54, -1.27$, and -0.85 MPa) with field-grown vines (**Bartlett and Sinclair 2021**). The three g_{\max} values with mean $g_s \Psi_{50}$ and vice versa were combined with all site and climate scenarios. Both sites were parameterized with the same soil type (clay loam), rooting depth (1.8 m), and irrigation schedule (weekly at 60% replacement). Other parameters and plant mockups were from **Albasha et al. (2019)**.

Results

Under historical conditions, shifting from mean to water-spending traits ($g_{\max} = 531 \text{ mmol m}^{-2} \text{ s}^{-1}$ or $g_s \Psi_{50} = -1.54 \text{ MPa}$) strongly increased ΣE by 12 – 17% and 11 – 14% at Oakville and Fresno, respectively, and reduced Ψ_{\min} by 10 – 15% and 11 – 18% but mildly increased ΣA_{net} and $T_{L,\max}$ at both sites by 2 – 3 % and 0 – 2%, respectively (Figure 1). Under future climate water-spending traits increased ΣE by 12 – 13% at Oakville and 8 – 10% at Fresno, reduced Ψ_{\min} by 10 – 15% and 7 – 14%, respectively, and caused small changes in ΣA_{net} by 2% and -1 to -4% and $T_{L,\max}$ by 0 – 3% at both sites.

Conversely, shifting from mean to water-saving stomata ($g_{\max} = 148 \text{ mmol m}^{-2} \text{ s}^{-1}$ or $g_s \Psi_{50} = -0.87 \text{ MPa}$) under historical conditions reduced ΣE by 20 – 41% at Oakville and 23 – 31% at Fresno, ΣA_{net} by 6 – 14% and 10 – 12%, increased Ψ_{\min} by 22 – 25% and 24%, respectively, and increased in $T_{L,\max}$ by 0 – 1% at both sites. Under future conditions, these traits reduced

ΣE by 22 – 35% at Oakville and 22 – 28% at Fresno, ΣA_{net} by 9 – 13% and 11 – 16%, and Ψ_{\min} by 20 – 23% and 22 - 23%, respectively, and mildly changed $T_{L,\max}$ by -1 – 2% at both sites.

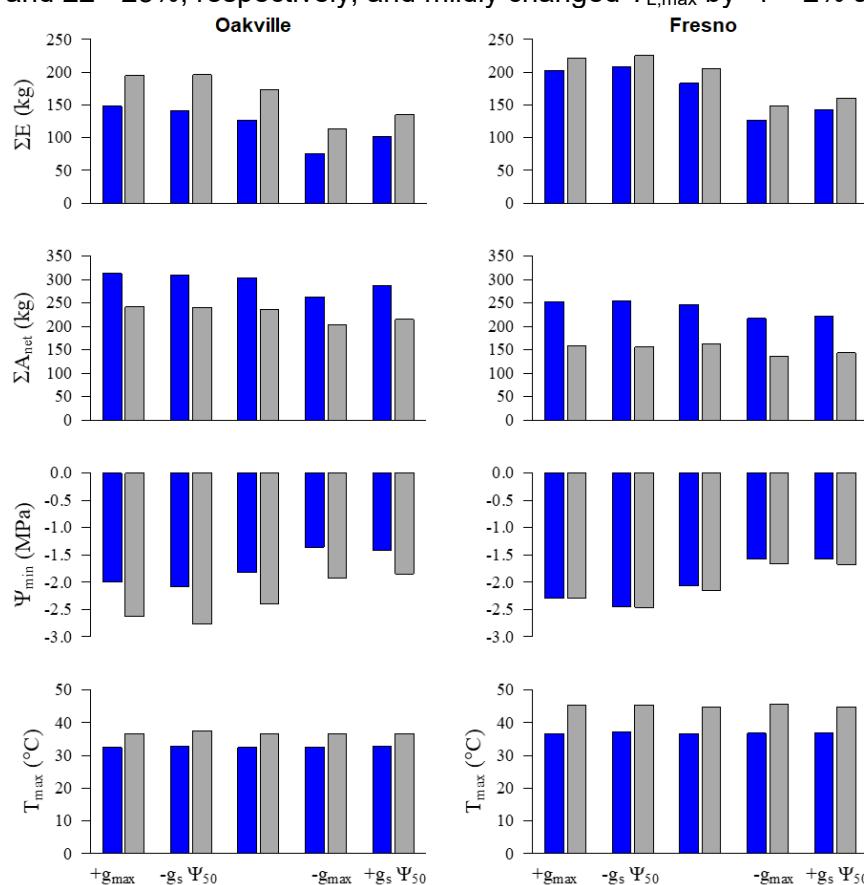


Figure 1. Predicted impacts of the maximum stomatal conductance (g_{\max}) and water potential threshold for 50% stomatal closure ($g_s \Psi_{50}$) on grapevine transpiration (ΣE), net carbon gain (ΣA_{net}), minimum shoot water potential (Ψ_{\min}) and maximum leaf temperature ($T_{L,\max}$). Blue and gray bars indicate historical and projected (RCP 8.5) climate scenarios, respectively. For each panel, middle, left and right bars indicate mean, water-spending and water-saving trait values, respectively.

Discussion and conclusions

Water-saving traits reduced transpiration and water stress (20 – 35%) with limited reduction on carbon gain (9 – 16%) compared to mean trait values under extreme warming. This suggests that selecting for water-saving stomata is a promising strategy to mitigate climate change effects on viticulture. However, such traits would reduce yield and quality if declines in carbon gain prevent the fruit from reaching target sugar concentrations. More work is thus needed to account for the tradeoff between water savings and carbon gain. Finally, these findings also suggest that FSPMs can aide in designing grapevine physiology for future conditions.

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Detecting plant tropism from LiDAR data

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Keywords: species modelling, tree bending, gravitropism, phototropism

1 Introduction

Understanding plant tropism is crucial in planning for a successful plant cultivation, although detecting plant tropism is commonly done on young, small plants in a controlled environment ((Coutand et al., 2019)). It is not trivial to measure tropism on mature street trees without elaborate setups or techniques. However, it will be very useful to capture the tropism information of mature street trees for environmental analysis and simulation purposes, e.g., root-soil condition, shading, tree pruning, etc..

With the abundance of urban LiDAR scan data in Singapore, measuring plant tropism of mature street trees from LiDAR data can be attained. We propose a methodology to measure plant tropism effects directly from LiDAR data without field observation work.

Most existing works to detect plant tropism from remote sensing data are image-based methods, with some limitations of observing tropism in higher-order branches as they are concealed by dense leaves and other objects. On the other hand, reconstructed tree skeleton from LiDAR data (Lim & al., 2020) will enable the derivation of an actual plant's tropisms information. Such tropism info, when fed into the species modelling module (Gobeawan & al., 2021) to instil tropism effect on the species models, will potentially give clues on the living condition of plants and their interactions or compatibility with the environment. Thus, in this abstract, we present our preliminary work for modeling accurate species model with tropism of real trees.

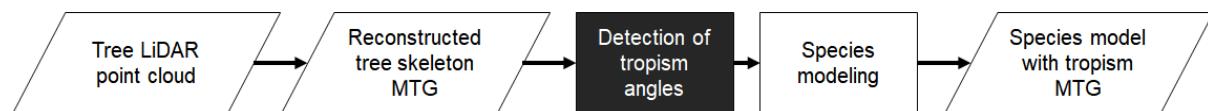


Figure 1: Workflow

2 Data and Methods

The workflow of plant tropism detection from LiDAR data is shown in Figure 1. A tropism angle, defined as an orientation difference between the tip of a branch with the base of the same branch, is detected from a tree skeleton (in MTG format) reconstructed from LiDAR point cloud (real tree data), and then fed into the species modelling module to generate a species model with tropism effect similar to that of real tree.

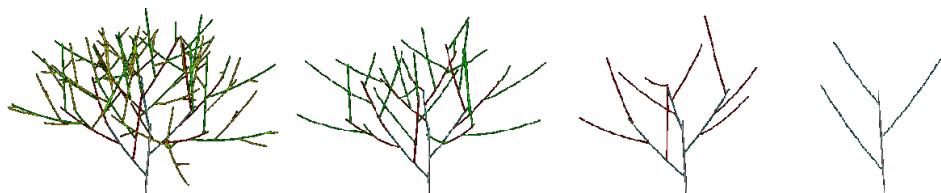


Figure 2: Branch grouping based on the branching order

To detect the tropism angles, the reconstructed tree skeleton is first parsed into groups of branches

with the same branching order (Figure 2). Subsequently, an average tropism angle for each branching order group is calculated. The average tropism angles are then applied uniformly to the branches of the species models with the same branching order.

3 Results and Discussion

We present a preliminary result of tropism effects applied on two individual species models (Figure 3), with various configuration of tropism angles at proximal and distal parts of the tree. By applying average tropism angles uniformly across the branch group of the same branching order, the tropism effect of the species model may not be highly similar to that of the actual tree. However, assuming the tropism angles across the same branching order group are similar to one another, the tropism effect will be transferred to the species model just fine.

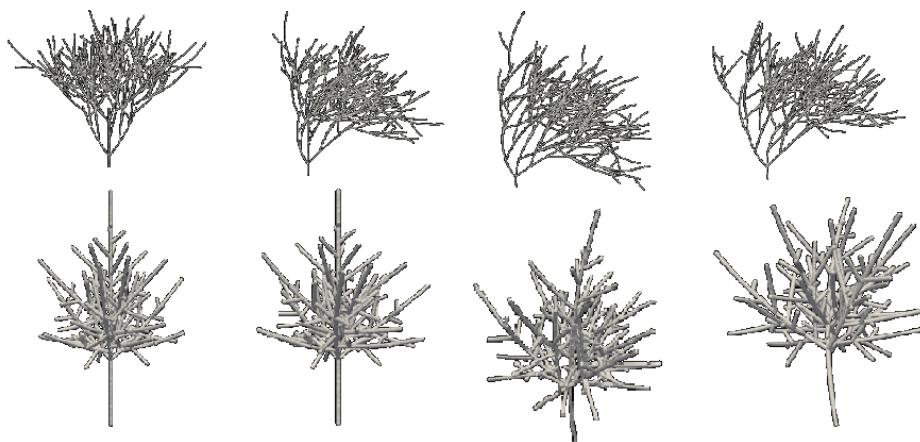


Figure 3: Row 1: *Samanea saman* – (proximal 0°, distal 0°), (proximal 0°, distal 60°), (proximal 30°, distal 0°), (proximal 30°, distal 60°), Row 2: *Hopea odorata* - (proximal 0°, distal 0°), (proximal 0°, distal 60°), (proximal 30°, distal 0°), (proximal 30°, distal 60°)

4 Conclusion

Tropism effect from real tree LiDAR data can be transferred to species models. This enables more realistic tropism effect on the species model. Work is ongoing to transfer all tropism angles from LiDAR data to the species models.

5 Acknowledgment

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Novel applications of functional structural ‘plant’ models in agricultural pathology, marine science, and theoretical ecology and evolution

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Keywords: coral, canola, *Sclerotinia*, root, foraging

Functional-structural plant models (FSPMs) have been used across a diverse range of fields and applications. Here we highlight three novel applications of functional structural ‘plant’ models in agriculture, marine science, evolution and ecology.

FSPMs have been used in conjunction with rain splash and wind dispersal models to simulate the spread of pathogens through a crop canopy (eg Streit et al., 2017). In this novel application, an FSPM was linked with a model of flower petal fall to simulate the spread of the fungal pathogen *Sclerotinia* within a canola crop (Figure 1). This pathogen often infects the petals first, but the severity of the disease and the impact on yield depends on infected flowers falling into branch axils, causing secondary infection within the stems and branches of the plants. This study tests the hypothesis that certain canola plant architectures may help manage *Sclerotinia* stem rot by reducing the probability of infected flowers falling into branch axils.

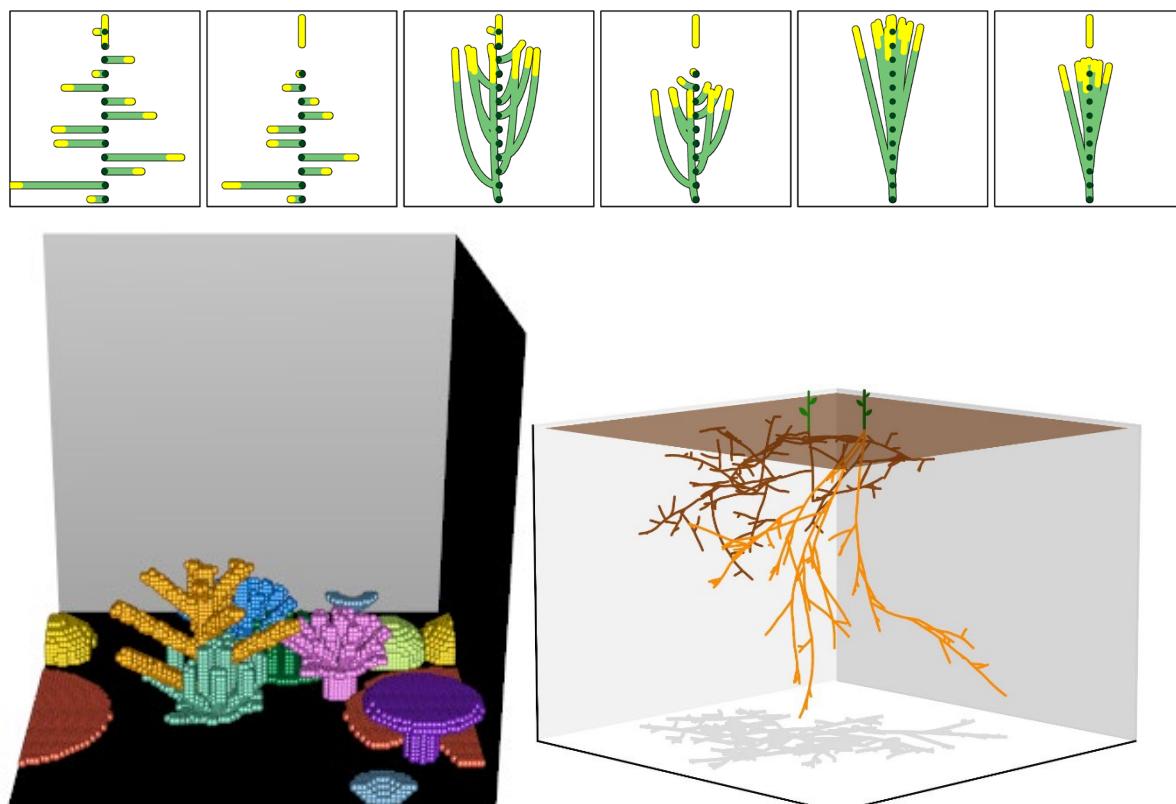


Figure 1: Three novel applications of functional structural ‘plant’ models in agricultural pathology (flower-fall disease transmission in canola: top), marine science (coral community dynamics: bottom left), and theoretical plant evolution and ecology (optimality and trade-offs of root foraging strategies in different conditions: bottom right).

Corals are not plants, but as sessile modular habitat-forming organisms, with modular growth patterns, that obtain the majority of their energy and nutrients from microscopic photosynthesising zooxanthellae that live within their tissues, they function more similarly to plants than to most other animals. We developed a novel functional-structural model of the growth and development of a coral community of diverse functional coral types, while accounting for structural trade-offs between competitiveness in capturing light and susceptibility to hydrodynamic disturbances (Figure 1). We used the model to explore and predict how changing disturbance regimes under climate change may affect the functional composition, diversity and architectural habitat complexity of coral communities (Cresswell et al., 2020; Cresswell et al., 2017). We are now using the model to investigate in more detail how structural habitat complexity metrics of relevance to coral reef fish communities will be affected by changing coral community composition.

Plants use their roots to forage for essential resources, including water and nutrients. We currently have limited understanding of how different root foraging strategies evolve in different environmental conditions, and how this evolution and the resulting foraging strategies are affected by intra- and inter-specific competition. To help address this, we use evolutionary functional-structural plant models that simulate how root foraging strategies in populations or communities of plants evolve over many generations in interaction with each other and their environments (Renton, 2013). These models were first used to look at rooting strategies to deal with extreme shallow soils (Renton and Poot, 2014). A more flexible and realistic version of the model was then used to look at the benefits of phenotypic plasticity in root foraging strategies. The model has now been further updated to represent communities of interacting plants, in order to investigate how root foraging strategies evolve with and without competition, and to what extent strategies optimised for certain competitive conditions may be sub-optimal in different conditions, and how the processes of evolution may navigate among such trade-offs (Figure 1)

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The relative seedling emergence time of individuals matters in belowground competition for resources

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Keywords: soil exploration, root interactions, competition, plant research

Introduction

A great number of models have been developed for the simulation of plant-plant competition for resources (light, water, nutrients) in plant science and ecology disciplines (e.g. Renton and Chauhan, 2017, Faverjon, et al., 2019). Most of these studies implicitly consider uniform seed/seedling size across populations. In reality, however, plants in a population could develop variation in seedling size due to the difference in emergence time, seed size and initial growth rates (Benjamin, 1990). This seedling size variation may have substantial consequences on subsequent plant-plant interaction and subsequent growth. The initial seedling size advantage of a plant may result in competitive asymmetry in the plant community and thereafter result in a stronger differences between individual plants. Roots are normally the first organs that initiate from seeds and are essential for anchorage of the plant and acquisition of soil resources (water, nutrients) to ensure shoot growth later on. Understanding the effect of size variation on competitive interactions and how this in turns is influenced by root traits needs more quantitative research. Functional-structural plant (FSP) models are excellent tools to analyze the competition between plants for resources, but in order to accurately represent the plant system under study, ignoring initial variation between plants may be an oversimplification.

The purpose of this study is to show and quantify the importance of the variation in seedling emergence time and growth rate and the subsequent development of the plant community, when individual plants are simulated. There are several research domains within which it is worth to take the variance in emergence time into account when an FSP model is applied. For example, in grasslands, the possible different emergence time of species seeds may play a role in the size dependent competition, where larger plants have an advantage under size asymmetric competition (Stoll and Bergius 2005). In agricultural weed suppression practices, relative time of emergence of crops and weeds is crucial for weed suppression and crop productivity (Baumann et al., 2002; Evers and Bastiaans 2016). In intercropping, the emergence time can differ between species even when sown simultaneously, which potentially leads to asymmetrical competition and under-yielding of the dominated species.

To quantify the relevance of taking variance in seedling emergence time in a population into consideration in FSP modelling studies (in that case, the “arrival” time of a virtual plant) on below-ground resource competition, a pot experiment on crop mixtures was carried out. Parameters from this study will be used in FSPM to further study the effects of seedling emergence on plant growth.

Materials and Methods

The pot experiment (20cm diameter, 72 cm depth) was performed for faba bean - wheat mixtures. The wheat was planted 14 days before or after the faba bean in the same pot. A treatment with only faba bean (without wheat) served as control. Aluminum separators were used between species to minimize the aboveground interactions. Plant aboveground and belowground biomass, shoot N content and root vertical distribution were determined.

Results, Discussion and future work

The relative early emergence time of wheat compared to bean can alter the N availability in the soil through niche pre-emption. Shoot biomass and N content of faba bean was strongly suppressed when wheat had relatively early emergence time. For belowground, faba bean was not sensitive to this competition at early vegetative stages (27 days after sowing), however, as the size difference of both species became larger, the early sown wheat constrained bean root biomass allocation and proliferating depth. This competition was eased by the relative later sowing time of wheat.

This study indicates that, for the multi-disciplinary fields of plant modelling, especially on the individual plant levels, even a 14-day earlier seedling emergence resulted in a great belowground competitive advantage in the plant community. This arrival time advantage will most likely be considerably larger, if aboveground competition is also taken into consideration. Thus, the variation in time of seedling emergence should not be neglected in FSP modelling studies.

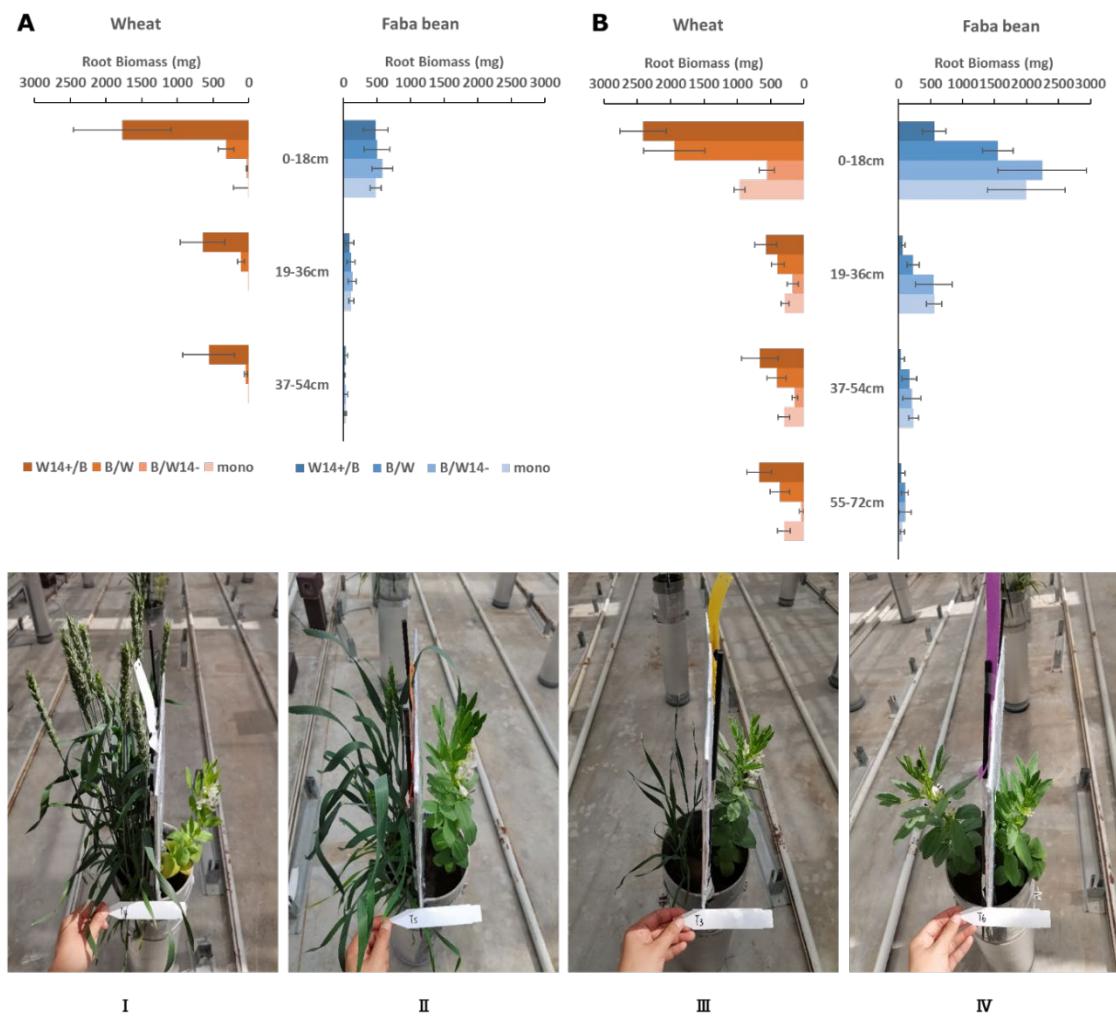


Figure 1 Upper panel: Root vertical distribution of faba bean and wheat, when wheat was sown in different times. A) root biomass at 27 days after sowing. B) root biomass at 49 days after sowing. Values are means \pm s.e. ($n = 5$). Lower panel: Treatments when faba bean was focal plant: (I) wheat was sown 14 days earlier than faba bean. (II) wheat was sown together with faba bean. (III) wheat was sown 14 days later than faba bean. (IV) faba bean pure stand (control).

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Calibration of *Cucumis sativus* L. Functional-Structural Plant Model architecture with high throughput phenotyping data

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Keywords: digitization, *in silico*, genotype, 3D point cloud, parameterization

Both labor costs and the demand for fresh food products are rising. High value, high wire indeterminate crops such as *Cucumis sativus* L. require intensive cultivation and harvesting practices which has led to increased interest in automation of such practices (Kootstra et al., 2021; Bac and van Henten, 2014). The unique canopy structure of these crops creates a delicate balance of interactions between the architecture of the plant and light interception. In addition, many genotypes are used for commercial production, which differ in plant and canopy structure. Three-dimensional models, and specifically Functional Structural Plant Models (FSPM) are particularly useful tools for depicting the impacts of plant architecture on physiological processes and vice versa. However useful for traditional research, they contain numerous parameters and are constrained to one specific genotype used during the initial calibration experiment. The calibration and validation of these models is a labor intensive and time-consuming process. We will be exploring the possibility of using young cucumber plant data collected via high throughput phenotyping techniques to inform the structure of an FSPM. Thereby speeding up the process and allowing for the collection of data at a higher resolution than reasonably feasible with manual measurements. A greenhouse trial will be conducted at the Netherlands Plant Eco-phenotyping Centre (NPEC) where the plant architecture of two genotypes of *Cucumis sativus* L. will be captured in the form of three-dimensional point clouds. These 3D data sets will then be integrated into an existing dynamic FSPM of cucumber, Y-Cucumber, (Pao et al., 2021) using the software GroIMP (Growth-grammar-related Interactive Modelling Platform). A global sensitivity analysis will be conducted with the intention to determine the most impactful structural parameters on efficiency of light interception for further investigation (Perez et al., 2018, Chen et al., 2014). We aim to explore whether there is potential for decreasing the constraints associated with architectural parameterization of models for more diverse and generalized applications via high throughput phenotyping of young cucumber plants.

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Quantifying differences in architecture and source-sink relations between hybrid potato plants from two propagules using an FSP Model

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Keywords: hybrid potato, lateral branching, source-sink relations

Introduction

Seed or ware potatoes of newly developed diploid hybrid potato (*Solanum tuberosum* L.) can be produced from two different types of starting material: true botanical seeds or seed tubers. There are differences in plant development and architecture between plants grown from these two propagules (Lindhout et al., 2011; Kacheyo et al., 2021). Main differences in plant architecture relate to the number, size and the spatial distribution of stems, leaves and flowers on the main axis and aboveground lateral branches, as well as the stolons (modified lateral branches that grow belowground) and tubers (swollen stolons) (Struik and Wiersema, 1999; Kacheyo et al., 2021).

The plant architecture results from source-sink relations that regulate plant growth and development. Aboveground, the leaves intercept light and photosynthesize, producing assimilates to maintain their own growth and/or produce new organs (e.g., lateral branches). Leaf area development affects the light distribution within the canopy, while the light profile, in turn, influences the development of leafy branches and therefore has a feedback effect on the leaf area distribution. Particularly, stolons compete with the aboveground branches for assimilates and store biomass in tubers. In essence, the whole potato plant comprises a constellation of different types of stem segments. The number, size and 3D distribution of these stem segments determine the plant architecture. Dynamic interactions between source and sink branches interplay with their architecture, which ultimately determines the growth and development of the whole plant, including tuber production.

Genetic, physiological and environmental factors can influence plant processes and lead to differences in their architecture (Vos et al., 2010). Even when grown in the same environment, genetically identical potato plants grown from different propagules produce different plant architectures, both above- and below-ground. For example, true-seed-grown plants produce more lateral branches, longer branches and higher order of branching but less tuber dry matter, compared with seed-tuber-grown plants. This raises the question how their architectural differences develop and to which extent above-ground development affects below-ground development and production.

Materials and methods

Lateral branching behaviour of plants grown from two propagules were studied. Using FSP modelling, dynamics of contribution of source branches to photosynthesis and assimilates partitioning to sink branches within the whole plant can be quantified.

A combination of experimental and modelling approaches was implemented. A greenhouse pot experiment was conducted to obtain parameter values for model input. Plants of the same genotype were grown from two propagule types. The number and size of individual leaves, stems and tubers as well as their location on the plant and their orientation to the plant main stem were recorded from planting to senescence. Parameters such as appearance rate, expansion rate and duration, and final size of each organ were derived. Photosynthetic parameters of representative leaves were determined based on measured light response

curves, including maximum leaf photosynthetic rate (A_{\max}), dark respiration rate (R_d) and quantum yield (Φ). Biomass of individual branches (above- and below-ground) was determined at tuber initiation, tuber bulking and senescence.

Preliminary results

Comparisons of architectural differences between plants grown from two propagules are shown in Figure 1. Compared with seed-tuber-grown plants, the true-seed-grown plants had shorter main stem and plant height, while there were more lateral branches both above- and below-ground (leafy branches, stolons and tubers). Moreover, the order of branching was higher for true-seed-grown plants. For instance, much less fourth order branches were observed in seed-tuber-grown plants than in true-seed-grown plants (data not shown).



B	True-seed-grown plants	Seed-tuber-grown plants
Main stem length (cm)	30.4 a	45.8 b
Plant height (topmost leaf to soil level) (cm)	64.8 a	71.8 a
Main stem leaf number	15.9 a	17.7 b
Branch number (1 st order)	11.5 a	10.6 b
Proportion of 1 st order branch number of all potential branching sites on main stem	0.70 b	0.61 a
Stolon number	12.8 a	10.5 a
Tuber number	33.3 a	21.0 a

Figure 1: A) An illustration of architectural differences between true-seed-grown plant (left) and seed-tuber-grown plant (right), both above- and below-ground. B) A quantification of differences in architectural traits of plants grown from two propagules. Values are means (n=8) on a per plant basis, measured at 10 weeks after planting. Means followed by different letters in a row are significantly different at $p < 0.05$.

Future work

We are developing an FSP potato model based on the data obtained from the experiment and literature. The model is expected to simulate the development of plant architecture and plant growth. Photosynthetic contribution of individual leaves, individual above-ground branches, as well as the biomass partitioning in different organs can be estimated at different developmental stages. Ultimately, this simulation model can be a useful tool to gain more insights into how the dynamics of lateral branching contribute to tuber production.

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Assessing architectural ideotype of dwarf tomato plants for improved carbon assimilation in vertical farming

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Keywords: FSPM, canopy architecture, light absorption, vertical farm, global sensitivity analysis

The vertical farming industry has taken an interest in dwarf plants of tomato (*Solanum Lycopersicum*). The architectural phenotype of dwarf tomato cultivars used so far could be optimized for vertical farms. A plant in a vertical farm is exposed to a different light spectrum than sunlight and, as it grows vertically, to an increasing light intensity as a result of its proximity to the light source. Changes in architectural traits, such as leaf shape and leaf angle, have been demonstrated to affect light absorption and carbon assimilation in a variety of crops, including high wire tomatoes. Therefore, it should be possible to increase biomass accumulation and yield by optimizing dwarf tomato plant architecture. The aim of this study is to identify one or more architectural ideotypes of dwarf tomato plants that improve carbon assimilation in vertical farming. Functional Structural Plant Models (FSPM) are valuable for demonstrating how plant architecture affects eco-physiological processes such as light absorption and carbon assimilation at the canopy level. An existing FSPM for juvenile high-wire tomatoes in greenhouse is adapted and calibrated to simulate dwarf tomatoes in a vertical farm. We examine the use of 3D scanning technologies to quantify the architectural characteristics of *in vivo* dwarf tomato plants to calibrate *in silico* the current FSPM tomato model. We evaluate and validate the accuracy of the FSPM light simulation by comparing it to *in vivo* measurements. A Global Sensitivity Analysis is performed to evaluate and rank the impact of the different architectural trait combinations on the performance of the simulated architectures. Based on simulation results, one or more ideotypes that maximize canopy carbon assimilation of the simulated dwarf tomato plants in vertical farming can be identified.

A descriptive spring wheat FSPM to elucidate the interaction between light phylloclimate and leaf nitrogen dynamics in a controlled environment

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Keywords: SPAD, light distribution, *Triticum aestivum* L.

As the first manned missions to Mars are approaching, the growing of green plants in extraterrestrial life support systems is put forward as a way of feeding the crew. Spring wheat (*Triticum aestivum* L.) has great potential because of its efficiency in converting energy into a high grain yield, and its importance in the human diet. Cultivation of wheat in an optimized controlled environment required for space travel is still largely unexplored due to the relatively high input costs compared to field cultivation. Controlled environment cultivation of wheat is therefore still faced with some early stage challenges such as finding a balance between yield, quality, and optimal use of space and time. The latter may include the shortening of plant height, so more cultivation layers may be used, as well as shortening the growth cycle, by manipulating the day-night cycles with assimilation light. Elucidating these balances requires thorough understanding of the complex interactions between plant growth and functioning with its environment. Even under controlled conditions, the environmental conditions effectively perceived by the plant, also called the phylloclimate (Chelle, 2015), can be rather heterogeneous, partly due to more drastic light extinction patterns compared to natural lighting. This results in significantly different plant growth and functioning compared to field conditions and, thus, differences in optimal growing conditions.

Functional-structural plant models (FSPMs) are well suited to investigate such interactions in closed growing systems as they allow a virtual recreation of reality. In this study, reconstruction of observed plant growth with calibration of the light conditions in such a 3D model, allowed evaluation of difficult to measure dynamics such as individual leaf light absorption and shading, which affect important plant dynamics such as leaf nitrogen (N) translocation. N translocation is an important dynamic in wheat growth whereby older leaves remobilize stored N to supply newly developing plant organs and eventually also the grains, impacting both yield and grain quality. A SPAD sensor was used to measure leaf chlorophyll content as a non-destructive proxy of leaf N content to capture time-series data in growth chamber experiments with different light regimes and nutrient solution concentrations. The empirical relationship between these SPAD values and actual N content was also quantified. The time-series data revealed different dynamics of leaf N content over the different leaf ranks and treatments. This presents an important step towards a better understanding of N translocation in wheat grown under a controlled environment. This is essential, as leaf N affects leaf light absorption and photosynthetic capacity, as well as plant grain yield and quality. Thus, this relationship is required for the construction of a predictive model, which can be used to optimize the growing conditions for controlled environment cultivation of wheat, in the future.

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***digital* TOMATO – a student project**

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Keywords: functional-structural plant model, cucumber, light, canopy architecture, *in-silico* experiments

The project “*digital* TOMATO” by Hanna Bau and Matthew Suomi was part of the module “Modeling complex plant systems”, lecturer Katrin Kahlen, in the *Horticultural Science Program* at Geisenheim University, Germany. The project spanned six weeks and results were presented in the summer semester of 2022.

The goals of this project were to produce a simplified working model of a tomato plant grown under ideal greenhouse conditions and to demonstrate the effects of shading interactions among multiple plants in a plant canopy. A secondary virtual experiment was also conducted to demonstrate the general approach of crop optimization. Previous studies producing 3D models of tomato plants have been oriented towards finding and optimizing parameter values for relevant plant organs in order to increase outcomes such as light interception, dry matter production, or rate of photosynthesis. In this project, we compared the proposed parameter values of various studies found in literature (e.g. Chen et al. 2014, Najla et al. 2008).

The workflow for model development is shown in Fig. 1 (top). We modified a simple purely descriptive cucumber model into a tomato model. Main steps were developing a proper leaf shape model of tomato and coupling of the model with the light modeling program *QuasiMC*. The plant model is written in *lpgf* and simulations run on *L-Studio* (algorithmicbotany.org). A virtual canopy consisted of five plants. To verify whether the virtual plant model behaved realistically in comparison to real plants, four hypotheses were tested:

- H1: The middle plant will intercept less light due to shading by the surrounding plants.
- H2: The middle plant will produce less biomass due to shading by the surrounding plants.
- H3: The lower leaf ranks will produce more dry weight than the upper ranks.
- H4: The middle plant will grow higher due to induced stem elongation.

Simulation output was collected and graphically plotted. Values produced by this working model do not correspond to real-world units, but serve to show ratios of differences.

The tomato model created in this project behaved as predicted and successfully demonstrated various effects of shading on plant growth (exemplarily shown in Fig. 1 bottom). These effects can be seen both within individual plants – different leaf ranks produced varying amounts of dry matter, according to their exposition to the light source – as well as between plants. Additionally, although not presented here, the model was able to identify alternative morphotypes which would, under the selected parameters, produce even more dry matter (see also Sarlikioti et al. 2011, Zhang et al., 2022).

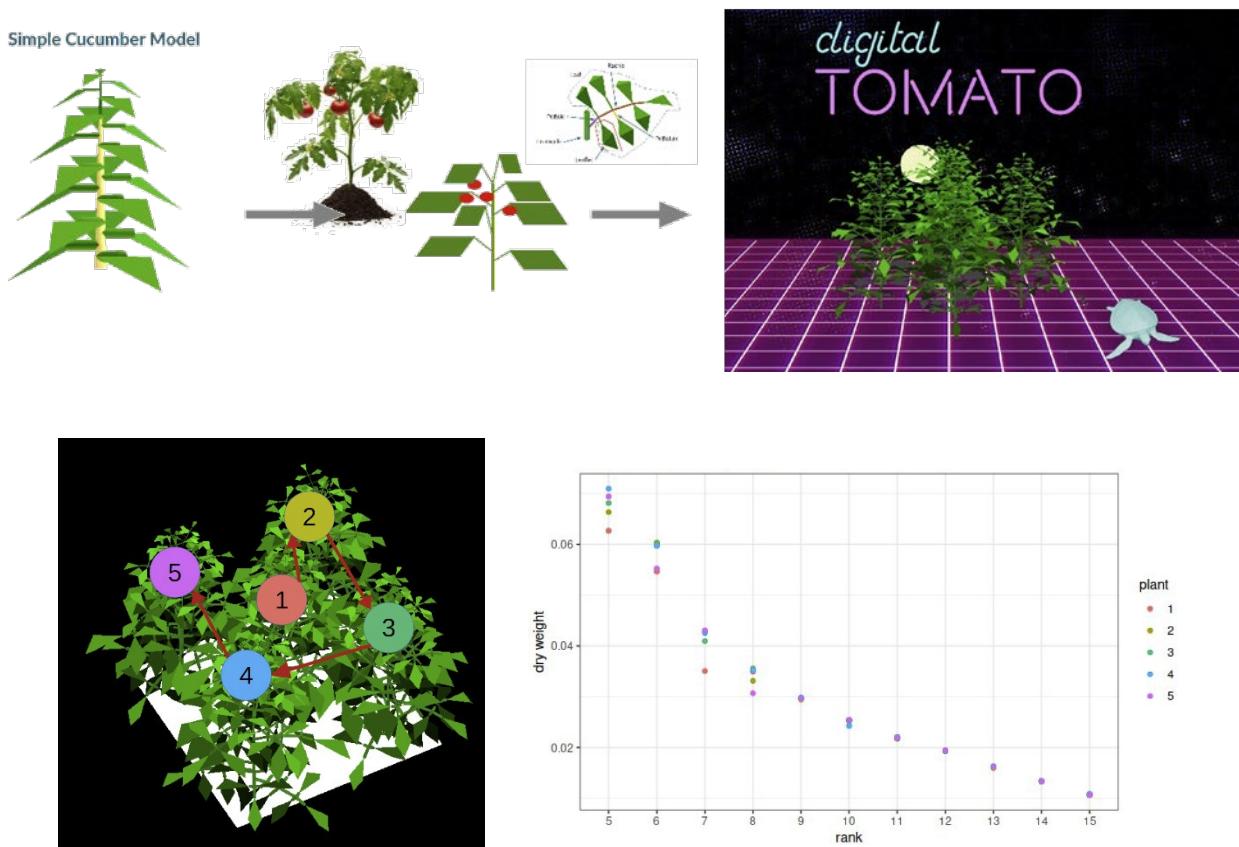


Figure 1: Workflow for model development and analysis: A simple cucumber model was modified into a tomato model with advanced leaf shape model (top), virtual canopy showing the numeration of five plants, and dry weight per leaf rank and plant on day 19 of the simulation (bottom).

Concluding remarks and outlook

This project offers a small glimpse of what is currently possible in the field of plant modelling. Whereas our model incorporated the dimension of time and the external factor of light availability, more complex models already in use today take temperature, water availability, nutrient availability, and atmospheric conditions into consideration (e.g. Pao et al. 2021). The complexity of current plant models is therefore limited only by the availability of suitable data. However, whether the time and computational effort of incorporating further parameters is warranted for a specific use case must be decided on an individual basis.

In the future, especially in light of rising production costs and the growing need for stable and resource-efficient systems of cultivation, we expect FSPMs to gain even more relevance in the planning and optimization of horticultural and agricultural production.

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Architectural plasticity in response to plant density increases canopy light interception

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Keywords: workshop, virtual plant, *in silico*, plant research

With rising population levels and increased pressure on our agricultural system due to climate change a key challenge is increasing crop productivity. Recent agricultural practice in winter wheat (*Triticum aestivum*) uses high planting density to increase yield potential per ground area but also enhances intra-genotypic competition, which can cause yield penalty.

To understand the balance between yield potential and penalty under high planting density, we phenotyped 200 winter wheat genotypes and their plasticity in response to three planting densities (30, 89 and 270 plant m⁻², Fig. 1A) using high-throughput phenotyping platform PHENOARCH (INRAE, Montpellier, Fig. 1B). The image data (Fig. 1C) and ground truth measurements allowed to quantify dynamic changes of 10 categories of functional and architectural traits during four weeks experimental period: 1) plant height and plant elongation rate, 2) tiller number and tiller development rate, 3) total leaf area and leaf expansion rate, 4) fresh and dry biomass 5) absolute and relative growth rate of biomass, 6) canopy leaf area distribution, 7) canopy leaf angle distribution, 8) canopy light interception, 9) light extinction coefficient and 10) degree of self-shading.

Interestingly, the development of leaf area was fastest under intermediate density, suggesting competition-driven plasticity in biomass allocation and/or in leaf mass per area. Genome-wide association study showed that genomic regions on the D6 and B6 chromosomes associated with these traits. Biomass and tiller number per plant decreased with increasing density and the degree of this plasticity differed largely between genotypes. High correlation between plasticity of biomass and tillering suggests that biomass of genotypes maintaining tiller development under high density was least affected by planting density, probably by increasing light interception per plant. To prove this, we conducted *in silico* experiments simulating the effects of architectural plasticity (Fig. 2) in response to density on light interception at individual and canopy levels. This was achieved by coupling the 3D plant architecture models obtained from the experiment with a light model. Interestingly, increasing density without architectural adaptation of individual plant reduces canopy light interception in the most studied genotypes. This indicates that architectural plasticity in response to high planting density is not purely a "selfish" behavior, but also beneficial to canopy light interception and therefore productivity.

Our results highlight how non-invasive phenotyping in combination with 3D modelling can reveal the important functions of phenotypic plasticity on canopy productivity.

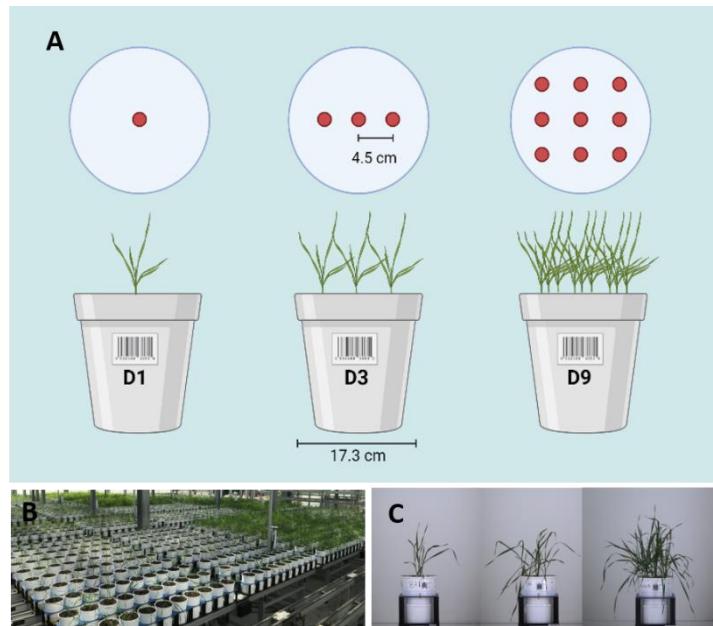


Figure 1: (A) Set up of three different planting density; (B) In total, 2400 pots were imaged; (C) example of the plant image in D3 treatments.

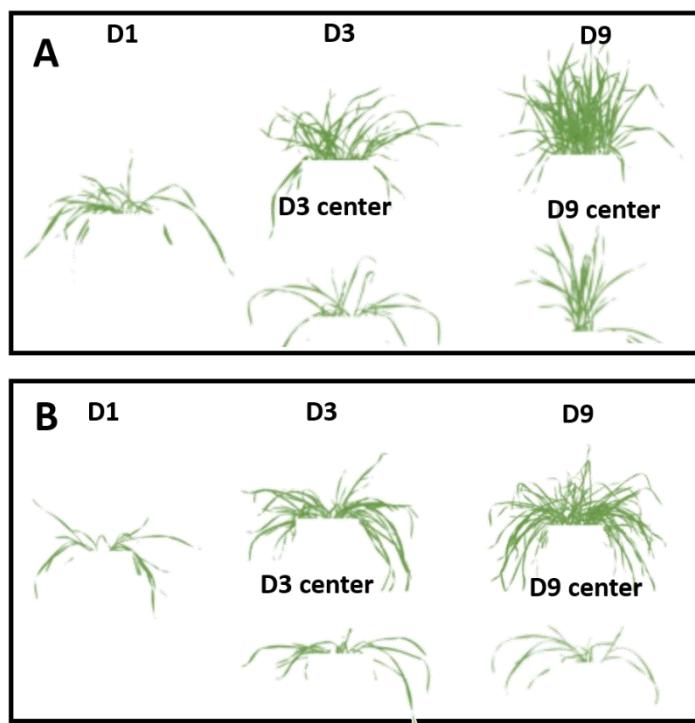


Figure 2: Two-dimensional projection of a architectural plastic (A) and a non-plastic (B) genotype in response to the planting density.

Digital Tomato Crop: what complexity is required for optimal functionality of the virtual tomato model?

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Keywords: virtual tomato plant, tomato FSPM, photosynthesis, optical properties, NPEC

Wageningen University & Research is building a digital twin of a greenhouse crop called the "Virtual Tomato Crop" (VTC), based on the concepts of functional-structural plant (FSP) modelling. The digital twin of the greenhouse crop-climate environment must provide a reasonable simulation accuracy and must perform at a functional speed in order to be used as a real-time cultivation feedback tool.

In this study, we explored how model complexity impacts model performance in terms of both speed and simulation precision. We particularly focused on two key crop growth processes: absorption and photosynthesis. Complexity was defined by considering either one uniform or two canopy layers with specific photosynthetic and optical properties. Furthermore, we evaluated multiple photosynthesis modules, from a simpler Thornley model (Thornley, 1998) to the widely used FvCB model (Farquhar, von Caemmerer & Berry, 1980).

The VTC experiment was conducted at NPEC (Netherlands Plant Eco-phenotyping Centre). NPEC is a joint initiative of Wageningen University & Research and Utrecht University and facilitates high-throughput phenotyping and high-resolution data from plants above and below ground (NPEC, 2022). A greenhouse experiment was set up including three tomato varieties (Brioso, Merlice, Moneymaker). The measurements were used to parametrize the FSP model.

Our simulations of the virtual tomato crop show that increasing complexity of leaf optical and photosynthetic parameters has a substantial effect on the VTC model predictions, and increased complexity of crop growth properties should seriously be considered for FSP model simulations.



Figure 1: Tomato crop in NPEC

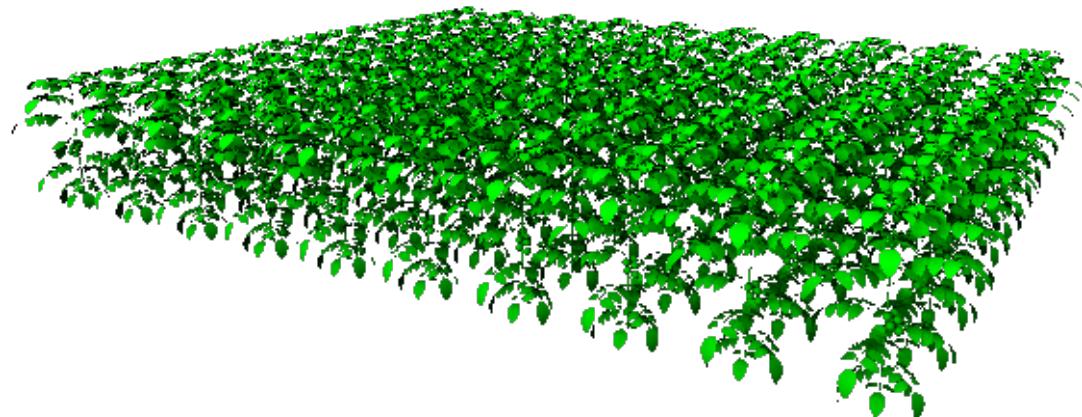


Figure 2: Virtual tomato crop

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Knowledge-based learning for plant phenotyping

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Keywords: tree modelling, species profile, machine learning

1 Introduction

Plant phenotyping, an effort to assess plant physiology traits such as growth, architecture or profile, and quantitative measurements, has been on a rising trend for its importance in understanding functioning and cultivation of plants for sustainable agriculture. The trend is mainly supported by emerging technologies in imaging and sensing (Li et al., 2014), and then, artificial intelligence (Ubbens & Stavness, 2017).

Correspondingly, we attempt to automate the recognition of plant architecture from remote sensing LiDAR (laser imaging, detection, and ranging) data based on our related works in species modeling (Gobeawan et al., 2021) and recognition (Chattoraj et al., 2022).

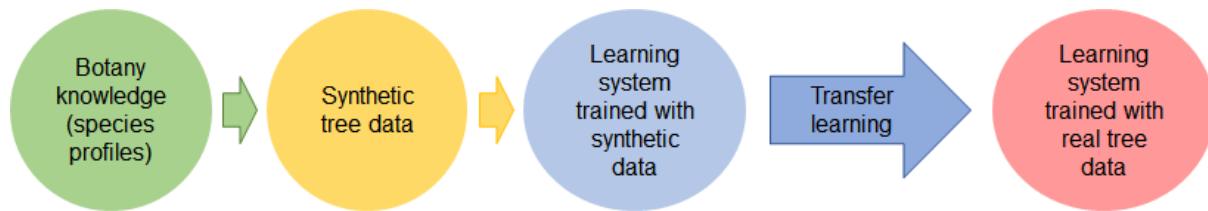


Figure 1: Knowledge-based learning of tree species profiles

2 Data and Methods

To recognise profiles or plant architecture aspects of LiDAR tree data, we develop a knowledge-based learning methodology (Figure 1) which learns the profiles of synthetic species model data, adjusts the learning from real tree data, and then uses this refined learning system to recognise the profiles of other real tree data (Chattoraj et al., 2022). The knowledge-based learning has an advantage of training on ideal data instead of noisy, limited LiDAR real tree data.

Our methodology leverages species modelling work (Gobeawan et al., 2021) to synthesise a large number of noise-free tree species data for training the machine. The synthesis data are generated based on the botany knowledge which allows a controlled learning to focus on each profile parameter.

3 Results and Discussion

We present preliminary results of the knowledge-based learning for recognising four species profile parameters in (Chattoraj et al., 2022): phyllotaxis type (alternate/opposite/n-whorled), phyllotaxis divergence angle (steps within 0-360 degrees), branching mode (monopodial/sympodial), and branching delay (0 to n years). For training the learning system, 1000 labeled, synthetic species models and 38 real tree models (leave-one-out for testing) are used, with effectively 38 real tree models for testing.

There is a total of 11 species in the whole datasets. Each dataset corresponds to a unique species profile configuration on a list of comprehensive profile parameters (Gobeawan et al., 2021). The current preliminary results correspond to just learning four parameters. The test results are summarised in Table 1 which shows potentially higher accuracy of our proposed knowledge-based learning method over a generic machine learning model to recognise species profile parameters.

Table 1: Knowledge-based learning accuracy for recognising four tree profile parameters on real trees

Experiment	Phyllotaxis type	Divergence angle	Branching mode	Branching delay
Machine learning	0.763	0.711	0.737	0.632
Knowledge-based machine learning	0.842	0.734	0.789	0.658

Profile parameters with clear categorical values such as the parameter *phyllotaxis type* are suitable for learning by classification. However, profiling parameters of different natures often involves some simplifications or assumptions of the parameter values. For example, the value ranges of parameters *divergence angle* and *branching delay* are continuous and non-discrete, while the values of parameters *branching mode* and *branching delay* may vary over time for different tree parts. However, those profile parameters are regarded as discrete variables in our knowledge-based learning.

As a work-in-progress, our knowledge-based learning system will progress to recognise a comprehensive range of profile parameters as listed in (Gobeawan et al., 2021).

4 Conclusion

We have developed a knowledge-based learning to recognise species profiles or tree architecture aspects of an individual tree. Such learning system may fully automate plant phenotyping which will be useful for horticulture and sustainable agriculture.

5 Acknowledgment

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Ontological plant representation for dynamical simulations

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Keywords: Ontology, UML, Conceptual Modelling, OBCM, FSPM

Functional Structural Plant Modeling (FSPM) is a discipline studying how single plants as well as vegetal tissues, populations and communities can be simulated together with their spatial configuration accounting for interaction with exogenous and endogenous factors. Such a detailed representation of plants and processes can be fruitfully used for teaching purposes of botany and growing techniques, as well as in Precision Agriculture. FSPM attracted researchers from several disciplines, including mathematics, computer science, botany, agriculture and forestry.

In some of these disciplines, to increase communication of methodological approaches and scientific results within and across different branches, ontologies have been developed, which consist of a shared conceptualization of a domain of interest (Gruber-1993) given by terms, annotations and relationships with a semantic meaning.

Two different kind of ontology may be easily identified, Domain Ontologies (DO and Foundational ontologies (FO).

A DO consists of large annotated dictionary of terms and relations, collected in a multi-hierarchical framework. They are coded as OWL (Ontology Web Language) and RDF (Resource Description Framework), both based on XML (Extensible Markup Language). Most of ontologies are collected at [Obolibrary \(2022\)](#) and querable from Ontobee (2022). Several of them are already dedicated to plants, as Plant Ontology (PO). They include definitions of terms useful to simulate a plant and its components including 'WholePlant', 'Shoot', 'Stem', 'Internode', 'Leaf', 'Bud' which inherit feature from abstract classes as 'multi-tissue plant structure', 'plant organ', 'shoot sysstem' or 'phyllome'. Entities defined in some ontologies are easily found in other ones, and enriched of details (e.g. branch angle can be found in TO-Trait Ontology).

FOs are used to add semantical constraints to Conceptual Modeling Language as the Unified Modeling Language (UML-2017). They are used for an Ontology-driven Model Design (ODCM) and a popular one is UFO (Guizzardi-2015) which lead to an extension of UML (OntoUML-2022) that defines those constraints among entities to be used in modelling. As an example, in UFO a distinction is made between 'sortal' and 'non-sortal' objects, the former endowable to some 'identity' (e.g.'bud') not the second (e.g.'tissue'). It also considers the concept of 'rigidity', as in 'vegetative-bud' which is mandatorily a child of a general 'bud', not required on type of entities identified as 'roles' or 'phases'.

OntoUML also define structural typologies used to feature objects structure (incl.'Part-whole','Component_of','Containment','Member_of','SubCollection_of','SubQuantity_of'). To support dynamical features entities as 'participates' are useful to relate objects to to 'events'. Semantic contents include concepts as 'situation' (state of affairs) that may change after the occurrence of an 'event' or 'disposition' (meant as power, ability, capacity, etc) related to 'causal explainability' of the occurrence of a given event or the 'triggering' of a 'transition'

(suitable of a probabilistic approach), all concepts used in simulations, included those of biological entities.

As much as UML, basically designed to use Object Oriented programming languages, UFO supports the pattern- and the component-based approaches, which can be used to interpret many DO entities aimed at representing dynamical aspects as 'development stage' (in PPO-Plant Pheno Ontology), deriving from an ancestor class 'occurrent' together with 'process'.

In figure 1 an example of entities with relations derived from several DOs is given, represented within a conceptual diagram using symbols from OntoUML and Onto-PML.

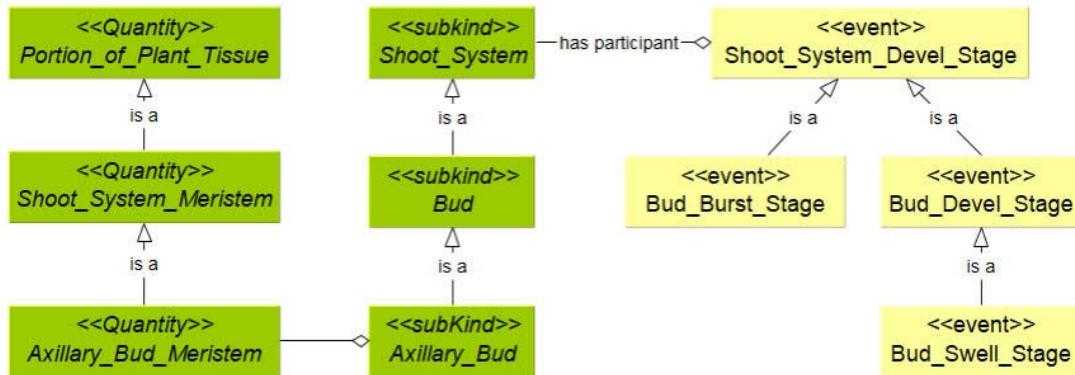


Figure 1 Conceptual model using OntoUML and OntoPML collecting some entities form PO and PPO aimed at describe a bud development

In conclusion, the present study describe how the knowledge collected in available ontologies can be practically used to formulate conceptual models using scientifically assessed languages. In particular here we give the former directions for the design of the backbone of an automated OBCM tool which can useful to identify the features required for a consistent scale-independent simulation of plant and its components.

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GrapeInSilico: a modelling framework for building grapevine FSPMs

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Keywords: grapevine, software, architecture, leaf gas exchange, carbon allocation.

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 GrapeInSilico 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.

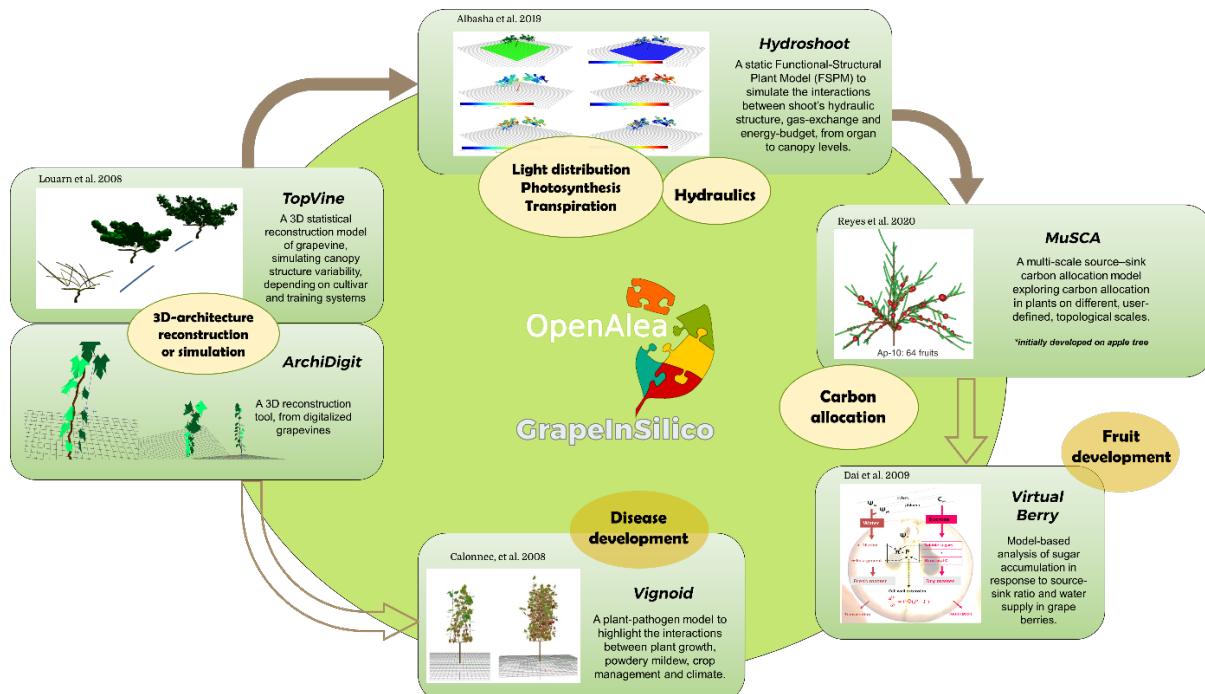


Figure 1: The GrapelnSilico framework allows to integrate a variety of processes coming from various models from the OpenAlea platform. The above figure illustrates the main coupling pipelines of its models, aimed at gaining a better understanding of the interactions among the simulated ecophysiological 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 GrapelnSilico, 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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Evaluation of nutrient, chlorophyll, and photosynthetic levels of tomato leaves using chlorophyll fluorescence imaging

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Keywords: chlorophyll fluorescence, abiotic stress, tomato, leaf condition

Tomato (*Solanum lycopersicum* L.) growth are influenced by physiological processes related to whole-plant carbon and chlorophyll, and nutrient conditions (Kalaji, et al., 2014). In order to enhance the understanding of photosynthesis, chlorophyll, and nutrient conditions in the tomato fruit, it is crucial to evaluate the link between plant growth and leaf health condition. True leaf of every plant for the analysis of chlorophyll fluorescence parameters, SPAD, chlorophyll and proline content, and other physiology phytochemicals were measured. The difference between chlorophyll content and chlorophyll fluorescence parameters for each true leaf was characterized and the results of correlation between chlorophyll fluorescence parameters, SPAD, chlorophyll and proline content, and other physiology phytochemicals value were used to evaluate the photosynthetic activity more objectively. The chlorophyll fluorescence parameters were related with in the Quantum yield of PSII and Quantum yield of non-regulated energy dissipation and while the leaves were cultivated under the general cultivation conditions. These results showed that Fv/Fm, Y(NO), NPQ, and Rfd can be used for the detection of nutrient condition in tomato plant using chlorophyll fluorescence imaging.

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The Virtual Plant Laboratory: developing, simulating, and visualizing functional-structural plant models in the Julia programming language

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Keywords: software, 3D visualization, graph rewriting

The Virtual Plant Laboratory (VPL) is a new free software (free as in “free beer” and “free speech”, MIT licensed) that facilitates the development, simulation, and visualization of functional-structural plant (FSP) models within the Julia programming language (Bezanson et al. 2017). Julia is a dynamic programming language with strong support for interactive scripting but capable of achieving the same performance as traditional statically compiled languages, such as C++ or Fortran.

VPL is implemented 100% in Julia, and it leverages all the functionality that is already available for the Julia language. For example, VPL relies on existing Julia packages for data import, export, and visualization. Similarly, VPL code can be executed in any context where Julia code runs, including Jupyter notebooks, a headless server or a conventional IDE on a laptop. Furthermore, it is easy to create interface code in R or Python that allow users to execute models built in VPL without having to learn Julia.

VPL is a single Julia package that provides the basic data structures and algorithms for developing, simulating and visualizing FSP models alongside with abundant documentation on how to use it. Internally, VPL is composed of four modules that implement the different functionality. These modules are:

Core module: A graph rewriting module that uses a simple algebra to define graphs and a procedural approach (rather than a grammar) for context and environment-dependent relational graph rewriting rules and queries. This module builds heavily on the experience developed at our lab by using GroIMP (Kniemeyer et al., 2007). VPL also incorporates additional features that are beneficial to the type of models it is intended to support. For example, it can assign a different graph to each plant in the model and these graphs can be rewritten and queried in parallel. This leads to improvements in run time as multiple cores can be leveraged and individual graphs remain smaller.

Geometry module: An implementation of procedural geometry generation via “turtle graphics” based on triangular meshes. VPL can export 3D scenes to external mesh file formats (e.g., STL, OBJ or PLY) as well as import them. That way the user can create complex 3D geometry in an external software of their choice and use them within their FSP model. VPL also provides methods to generate 3D meshes from common geometry primitives, so expertise in meshing is not needed unless a complex geometry is required (e.g., serrated or lobed leaf blades).

Rendering module: An interactive 3D visualization of any 3D scene generated by VPL using both native (OpenGL) and web based (WebGL) backends. The latter is recommended when the results of simulations are going to be displayed on a Jupyter notebook. This module relies on Makie as backend, a 3D engine built in Julia (Danisch and Krumbiegel, 2021).

Ray tracing: A multithreaded Monte Carlo ray tracer that supports multiple optical materials and radiation sources and arbitrary number of wavelengths. It is possible to construct multiple ray tracing objects and use them in the same model. This is useful when wavelengths have

very different optical properties (e.g., red, and far red) or when the radiation sources differ per wavelength (e.g., solar, and thermal radiation).

In addition to the VPL package, a series of satellite packages (forming the *VPLverse*) are being developed to support eco-physiological FSP modelling of field crops, with an emphasis on above-ground processes and plant-plant interaction. Currently, the *VPLverse* includes the following:

- **Sky** is a package that generates radiation sources approximating the distribution of solar radiation in the sky (according to the CIE standards) as well as other variables related to solar geometry, daylength, etc. This allows the user to easily generate all the radiation sources required for simulating field crops.
- **Ecophys** is a package that provides data structures and functions to simulate different ecophysiological processes, with an emphasis on short-term and long-term responses to above-ground environment (e.g., photosynthesis, transpiration, energy balance, phenology).
- **Generic Crop Interaction Model (GCIM)** is an FSP model that can simulate a wide range of crops by modifying spatial patterns and supporting multiple crop species. GCIM is built with VPL and other packages in the *VPLverse* and serves as a first example of how VPL can be used to develop non-trivial models.

Future plans for VPL include a greater emphasis on the interface of plants and the physical environment above- and below-ground, including support to efficiently simulate canopy microclimate, water and nutrient transport in soil. For more information on VPL visit virtualplantlab.com.

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Making the FSPM platform GroIMP better accessible for non-modelers

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Introduction

GroIMP (Growth-grammar related Interactive Modeling Platform) is a software project based on L-Systems and rule-based graph rewriting (Kniemeyer, 2008). It comes with a long list of components, 3D modeling tools, light simulators, several interfaces to other projects, etc. (GroIMP-Repository, 2022). This still growing set of components, however, leads to a problem many scientific software projects face at some point: it is no longer easy to use GroIMP, especially in the frame of larger scientific projects.

For modelers this is not really a problem since the size of the projects grows together with their experience in using the software. However, when a large model is used as a single component of a project designed by a team, there might be team members, who only need the results of a simulation without knowing how GroIMP exactly works.

One suitable solution would be to let users work with simpler interfaces, which then interact with GroIMP: the user would only send a set of configurations and receive a set of results. Approaches to achieve this objective will be discussed below.

Approaches

In the following three levels of a new approach will be discussed. These levels were originally designed and implemented as a part of a digital twin project of a semi closed greenhouse, a model considered to be quite large.

Headless mode:

The basic level is to run GroIMP headless, i.e. without any visual output. This has been a core function of GroIMP all along (Henke, 2013), but there are still things to prepare by the user, since a “normal” result would include some visual output based on interface interaction.

Firstly, a configuration file must be created to pass commands, parameters and environmental variables to the simulation. Additional files like tables can be referenced in this file.

To write the results to csv files, GroIMP’s own Java-based programming language XL is used. This last step completes the base level workflow shown in a simplified form in the first part of *figure 1*.

R-Markdown

The R programming language is a popular option for statistical analysis and visualization, and with the Rmarkdown library comes the possibility to create PDF reports (rmarkdown, 2022). Combined with the GroIMP headless mode one can automatically create PDF reports based on different scenarios, especially since R can execute system commands and therefore could run GroIMP as a sub process.

This leads to a workflow (part 2 of *figure 1*) starting with R executing GroIMP, GroIMP creating csv files, R reading these files and creating a PDF report.

CI/CD Pipeline

Though the Rmarkdown approach is already quite close to the original goal, it still requires several software packages to be installed. To avoid this and also to outsource the computational workload, it is possible to run the same approach on a server, in a deployment pipeline with all packages installed in a Docker image (gitlab, 2022).

Using for instance a Gitlab server, this results in the workflow (part 3 of *figure 1.*) of pushing a new configuration, waiting and then downloading the artifacts including the csv files and the pdf report, therefore the only required tool is a web browser.

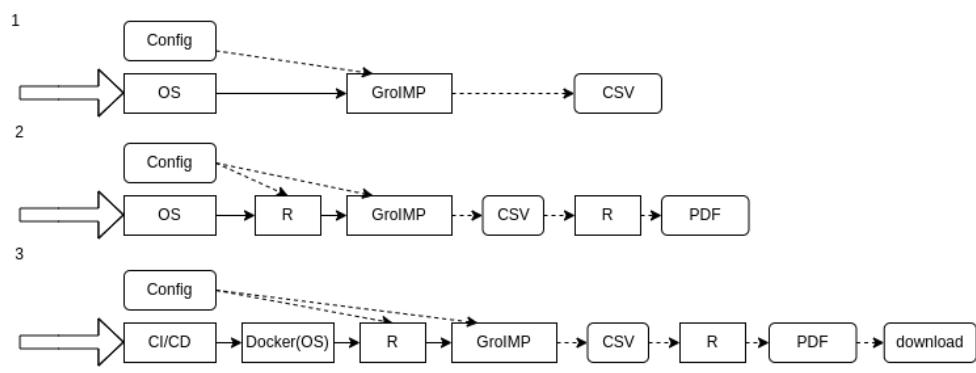


Figure 1: Three different levels of automated workflow using the GroIMP platform

Results and Discussion

In the digital twin project; the first results show that the workflow itself can be simplified to the level that was aimed at in the concept. In that model it is possible to set the number and positions of sensors and plants in Excel sheets and the run time and environmental conditions in the configuration file. All three levels of the approach work as expected and create suitable results.

Moreover, as a positive side effect, the simulation speed increases due to the absence of a visual component consuming computing power.

However, for the local versions, the installation and the setup of the different components is quite advanced and error prone. Furthermore, the model must be designed or customized for this kind of usage.

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Conveying the Effects of Climate Change - Interfacing *Virtual Riesling* with an interactive *R shiny* application

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Introduction

Climate change is a major challenge for viticulture. For example, heat waves and severe drought periods are threats to grapevine production. To proactively address such challenges of climate change, research uses complex models, among other things. An example of such a model is the functional-structural plant model *Virtual Riesling* (Schmidt et al., 2019), which can simulate the architecture of vines as a function of temperature and represent it at vineyard level. As part of the *WinUM 2.0* project (DBU), we want to use this model approach to also convey the consequences of climate change to students. To this end, we want to develop a graphical user interface (GUI) that is as simple, interactive and intuitive as possible for the use of model and simulation software in schools.

Software Setup and Workflow

The implementation of an interactive and intuitively useable GUI was realized by combining three main software components. First, a modified version of the modelling platform *GroIMP* (v1.5; Kniemeyer, 2008) has been compiled to enable compatibility with the model code described by Schmidt et al. (2019). The second required software component, the functional-structural model *Virtual Riesling*, simulates grapevine growth in rows based on daily temperature data. The third component is the *R* environment (v4.2.1; R Core Team, 2022) and all appropriate dependencies needed to run the new GUI based on the *R* package *shiny* (v1.7.2; Chang et al., 2022).

In order to transfer selected model parameters from the new GUI to *GroIMP* or to hand back simulation results to the *shiny* application simple read and write operations have been implemented. To start simulations in *GroIMP* with the new GUI, *R* passes a console command to the operating system. The input parameters are saved with the help of a text file and read in by *GroIMP* when the simulation is started. The simulation output is stored in the folder structure of the computer as image files and table documents. In addition, the output of *GroIMP* is read in, processed and displayed by the *shiny* application.

Graphical User Interface

The GUI of the *shiny* application is divided into an input and an output area. With the help of the input area, simulation scenarios can be selected and started using historical weather data. Additionally, global settings such as number of plants per row and duration of simulation can be set. Furthermore, advanced settings have been implemented to enable additional features as well as corresponding conditional application widgets (e.g. light model or set seed). The output area of the GUI displays the simulation results of two simulation scenarios to facilitate comparisons. This is done by interactive graphical representations of the virtual vineyard architecture in 2d and 3d. In addition, the comparison of characteristics like leaf area, light uptake and plant height are also shown using interactive graphs based on the *R* package *plotly* (v4.10.0; Sievert, 2020). Canopy development can be displayed at any time step within

the simulation period (day of year) using sliders or played as an animation. In order to convey changes in plant development caused by varying temperatures, dynamic event markers like bud burst of main and side shoots have been implemented.

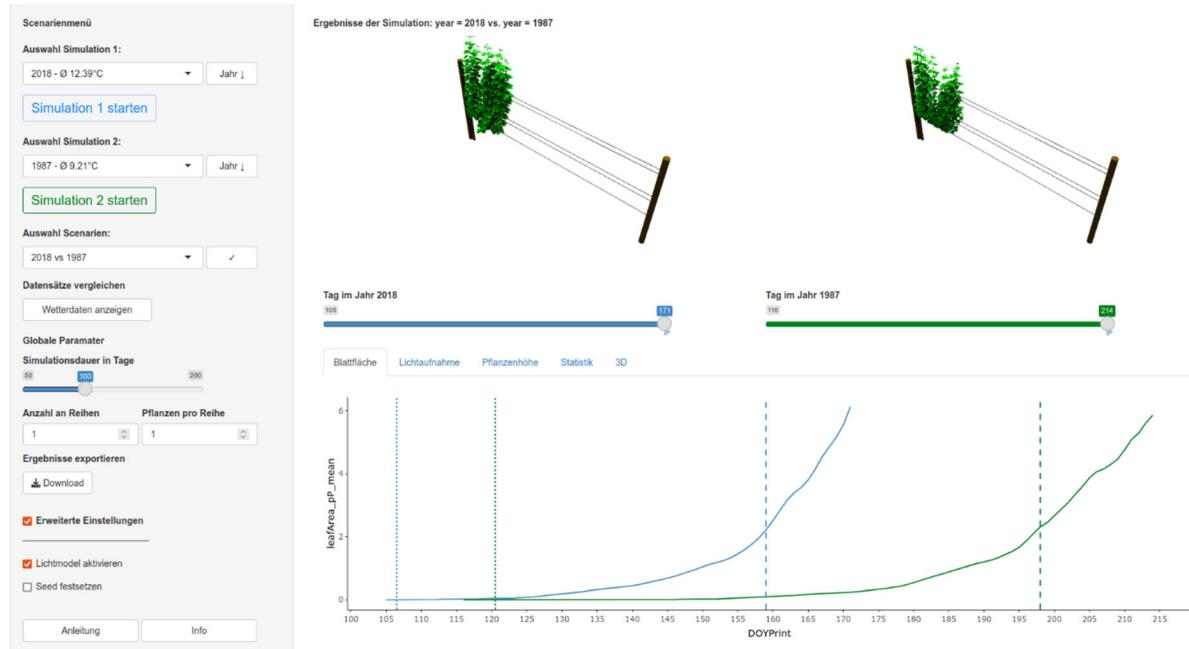


Figure 1: New interactive *shiny* application interfacing *Virtual Riesling* model.

At FSPM2023, we will demonstrate the functionality of the newly developed GUI. In addition, the current state of the GUI will be tested in teaching units at upper secondary schools. Based on feedback and evaluations this GUI will be revised.

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