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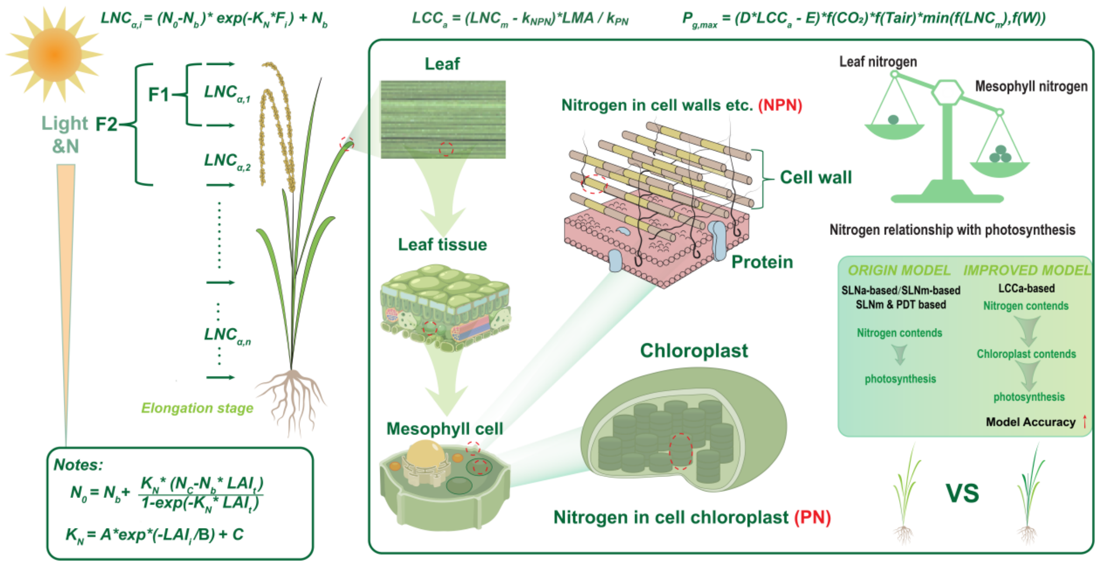
POSTER

SESSION 1 – SCIENTIFIC AND METHODOLOGICAL ADVANCES IN CROP MODELLING

Scientific and Methodological Advances in Crop Modelling

Bridging chlorophyll content and vertical nitrogen distribution for accurate canopy photosynthesis simulation

Accurate simulation of canopy photosynthesis is essential for predicting dry matter accumulation and crop yield. However, most current crop models overlook the effect of vertical distribution of leaf nitrogen and chlorophyll content on photosynthetic capacity at different canopy layers, resulting in greater uncertainties and weaker mechanistic explanation. Here, we developed a novel canopy photosynthesis model that establishes a bridge between chlorophyll content and photosynthetic nitrogen (PN, defned as total leaf nitrogen minus non- photosynthetic nitrogen) across different canopy heights, and then employs chlorophyll content as a reliable proxy forsimulating photosynthesis. The model was calibrated and validated using data from fve feld experi-ments under diverse treatments. Results indicate that leaves at higher canopy positions, receiving more light, contain higher nitrogen content and chlorophyll to support greater photosynthetic rates. The nitrogen extinction coeffcient (K_N), which characterizes the decline in available of leaf nitrogen, decreases exponentially with increasing LAI, varying among canopy depths, cultivars and growth stages. Chlorophyll shows a stronger cor-relation with photosynthesis compared to leaf nitrogen. By capturing these dynamics, the model enhances the accuracy of photosynthesis prediction by 60%, particularly correcting the overestimation of canopy photosyn-thesis and dry matter accumulation during post-fowering. These fndings advance the understanding and modelling of canopy-scale photosynthesis in crop models and provide insights for better integration with chlorophyll-related remote sensing data.



Functional–structural plant modelling as a tool for synthetic data generation for AI-driven applications

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Keywords: deep learning, depth camera, intercropping, phenotyping, point cloud

Introduction

Computer vision-based algorithms and sensing platforms are increasingly used in phenotyping research, enabling automated detection of pests and diseases and the quantification of physiological parameters such as leaf area index, biomass, and yield (Tanaka et al., 2024). However, these approaches are highly data hungry, and relying solely on ground-truth data for model training is costly. While data augmentation and self-supervised learning can improve robustness in object detection, generating biophysiologically meaningful synthetic data for quantitative predictions, such as physiological traits, remains challenging.

Three-dimensional (3D) sensing technologies including structured light, stereo, time-of-flight cameras, and LiDAR have become standard tools in plant phenotyping, offering richer canopy structural information than conventional 2D imaging (Akhtar et al., 2024). This provides opportunities for studying crop competitiveness and complementarity under complex conditions such as intercropping. However, 3D approaches demand even larger datasets, which increases the difficulty of applying advanced computer vision models at scale.

To address this challenge, recent studies have used process-based crop models as data generators for training machine learning algorithms, producing biophysiologically meaningful outputs across diverse environmental and management scenarios (Maestrini et al., 2022). Extending this concept, functional structural plant models (FSPMs) simulate 3D crop architecture and light interactions, offering the ability to render synthetic canopy data while retaining physiological realism (Baker et al., 2023).

This study evaluates the potential and limitations of FSPM-based synthetic data generation for AI-driven applications by comparing rendered canopy structures with 3D point cloud data collected from faba bean–oat intercropping systems using depth cameras.

Materials and Methods

A field trial was conducted in 2025 at Flakkebjerg, Aarhus University (55°32′ N, 11°39′ E). Faba bean (Vicia faba) and oat (Avena sativa) were intercropped and sown on 1 April 2025 at densities of 34 plants m^{-2} for faba bean and 90 plants m^{-2} for oat. Both species were sown within the same row at 25-cm spacing. Each plot measured 2.5 m × 8 m. Three-dimensional (3D) point cloud data were collected using a time-of-flight camera (Helios2 Ray, LUCID Vision Labs, Burnaby, Canada) with a spatial resolution of 0.3 MP (640 × 480 pixels). The camera was positioned approximately 0.8 m above the canopy, capturing a region of interest of at least 0.5 m × 0.5 m (covering two rows by 0.5 m). This sampling area was assumed to represent a single training unit for future deep learning applications.

Synthetic 3D canopy data were generated with the Virtual Plant Laboratory (VPL v0.0.6; Alejandro et al., 2025) implemented in Julia v1.10. Compared with other FSPM platforms (e.g., GroIMP, OpenAlea), VPL allows the complete modelling workflow (structure definition, simulation, visualization) within one language, benefiting from Julia's speed and flexibility. The simulation of legume–cereal intercropping systems was based on the publicly available script BASIC_CEREAL_LEGUME (https://git.wur.nl/david.kottelenberg/fspm_vpl_dk/-/tree/BASIC_CEREAL_LEGUME) with minor modifications to the initial spatial arrangement of the two crops. VPL originally outputs canopy structure as polygon meshes in ply format. To match the format of field data, these meshes were converted into point clouds using the Python library open3d, assuming the depth camera was positioned above the canopy as in the field experiment. Only visible points from the mesh surface were sampled to account for occlusion effects within the canopy. Finally, voxelization was applied to harmonize the spatial resolution of synthetic data with that of the Helios2 Ray camera.

Results and Discussion

Synthetic data from FSPM were visually compared with real 3D point cloud data collected by a depth camera. The FSPM successfully generated rendered 3D canopy structures as polygon meshes (Fig. 1a), which were subsequently converted into point cloud data (Fig. 1b). The distinction between broad legume leaves and narrow cereal leaves was clearly visible in the synthetic data. In contrast, the real point cloud data were affected by canopy occlusion (Fig. 1c), and occasional dead pixels appeared in the upper canopy layers (Fig. 1d), likely caused by strong solar illumination beyond the capacity of the depth camera. Moreover, the real 3D data captured smoother surface curvature of leaves, suggesting that the current FSPM outputs lack some textural realism.

Bridging the gap between synthetic and real data is therefore critical for enabling the effective use of FSPM-based data in AI applications. One approach is to calibrate FSPM parameters against field observations to better approximate realistic canopy geometry, particularly in cases where growth balance between legumes and cereals diverges from virtual representations. Another promising direction is the use of generative adversarial networks (Goodfellow et al., 2020) to enhance realism by producing synthetic point clouds that mimic field-acquired data.

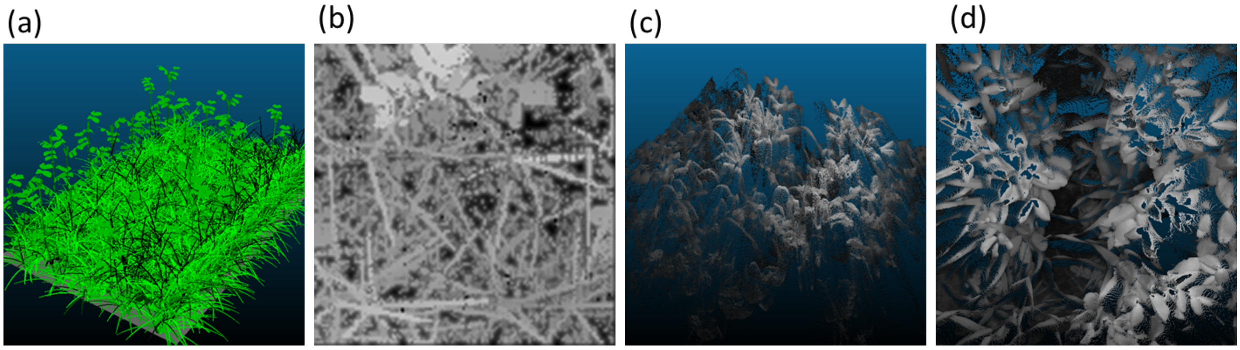

Figure 1. Examples of intercrop canopy data. Synthetic data generated by the functional–structural plant model (FSPM): (a) rendered 3D virtual intercrops and (b) corresponding synthetic point clouds. Real field data acquired with a depth camera: (c) raw point clouds from an oblique view and (d) raw point clouds from a top-down view. In subfigures (b–d), the color gradient from grey to black represents the distance from the sensor.

Conclusions

Although this study demonstrates the potential of generating synthetic data using FSPM, a substantial gap remains between synthetic and real 3D point cloud data. The impact of this gap on the accuracy and robustness of predicting crop physiological parameters, such as biomass and leaf area index, in intercrops will be examined in future work using deep learning models.

Acknowledgements

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Modelling potato quality: How drought and nitrogen stress influence tuber size and dry matter concentration

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Keywords: marketable tuber yield, WOFOST, data-driven modelling, climate change, fertiliser policy

Introduction

Potato is one of the most widely grown and most productive crops in the world. Its nutritional and economic value depend on yield quantity (tonnes ha^{-1}) and tuber quality (e.g., dry matter concentration and tuber size distribution). Climate change and legislations aimed at reducing nitrogen (N) pollution are expected to affect potato production (George et al., 2017; Martínez-Dalmau, 2021). Crop growth modelling plays an important role in identifying adaptations to these changing conditions, as it provides a means of simulating crop growth in a projected future climate or with amended management. Although potato crop growth models (CGMs) are useful for decision support by estimating potential and resource-limited yields (MacKerron and Haverkort, 2023), tuber quality simulations are currently insufficiently accurate. Tuber quality characteristics are affected by factors such as drought and N availability, and effects differ between cultivars (Aliche et al., 2019). The current, ongoing project aims to 1) run experiments to generate data on tuber quality as affected by drought and N availability and 2) develop a module to capture tuber quality development in the existing CGM World Food Studies (WOFOST).

Materials and Methods

In 2024 and 2025, large-scale field experiments were performed in two locations in the Netherlands to follow tuber yield and quality development over time. The experimental design included combinations of three irrigation levels, four N rate levels and 20 cultivars, which differed in maturity type (i.e., early to late). After tuber initiation, plots were harvested four (2024) or five (2025) times throughout the season. At each harvest moment, fresh yield and DM concentration of each sample were determined, as well as the size dimensions (i.e., diameter, length, width, height) of each individual tuber.

Modelling approach

Data acquired in the field experiments suggest that DM concentration and tuber size are affected by water and N availability throughout the season. These data will be used to develop a tuber quality module that simulates tuber size and tuber DM concentration. To this end, WOFOST will be used to simulate tuber growth which will be incorporated in the model structure of WOFOST (Figure 1). WOFOST simulates the potential and water- and nutrient-limited tuber DM yield based on weather and soil data. The tuber quality module will simulate tuber DM concentration and tuber number as affected by water and N availability. From tuber DM yield and DM concentration, the fresh matter (FM) yield can be calculated. From FM yield and tuber number, the average tuber size will be calculated and a size distribution will be applied to this fresh weight to derive the fresh marketable tuber yield.

The proposed tuber quality module will be developed with data-driven, empirical insights. It serves as a first step towards the development of a mechanistic tuber quality module. To evaluate and further improve the module, more detailed measurements will be done in following field trials in 2026 and 2027.

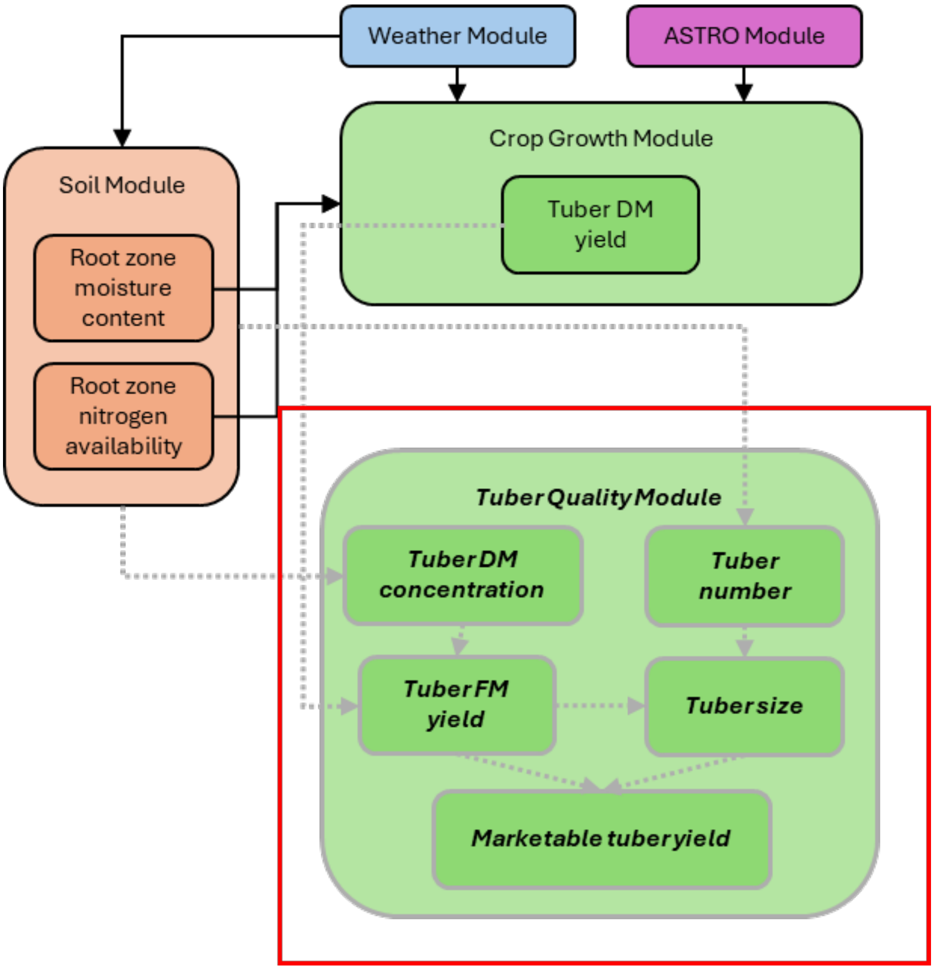

Figure 1: Overview of the modelling approach to simulate marketable yield from the output of the World Food Studies (WOFOST) model. The scheme is simplified and adapted from De Wit et al. (2019). The red box indicates the tuber quality module that is to be added to WOFOST. The grey, dotted arrows indicate the relations that are to be quantified from the acquired data.

Acknowledgements

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Statistical and crop growth model–based genomic prediction approaches for flowering time in raspberry

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Keywords: genotype-by-environment, climate-breeding, reaction-norms, process-based modeling

Introduction

Historically, plant breeders advanced crops through phenotype-based selection and pedigree-based best linear unbiased prediction (BLUP), but these methods rely on long breeding cycles, extensive phenotyping, and limited ability to capture Mendelian sampling or linkage disequilibrium. The decline in genotyping costs has shifted this balance, enabling genome-wide marker profiling at scale and creating an opportunity to accelerate breeding through genomic prediction (GP). Since its introduction, GP has allowed earlier and more accurate selection, with gBLUP becoming a widely adopted implementation that uses genomic rather than pedigree-derived relationships to improve predictive ability. While gBLUP has consistently outperformed pedigree-based prediction across many crops, it does not model genotype x environment interactions, thus limiting accuracy when genotypes are evaluated in new production conditions. Extensions such as multi-environment and reaction-norm models incorporate environmental covariates to capture genotype-specific plasticity yet remain fundamentally statistical and constrained by the information content of the data. To overcome these limits, mechanistic crop growth models (CGMs) explicitly represent physiological processes such as phenology and biomass partitioning, allowing in silico evaluation of genotype performance under diverse climatic and management scenarios. Integrating CGMs with GP (CGM-WGP) links marker effects to physiological parameters, embedding biological knowledge into prediction and enabling extrapolation to novel environments with improved interpretability (Technow et al., 2015; Messina et al., 2018, 2022). While ensemble of models is emerging as a method to improve predictive accuracy (Messina et al., 2025; Cooper et al., 2025), in this study, we first compare gBLUP, gBLUP with environmental covariates, and CGM-WGP prediction methodology to evaluate their predictive ability for flowering time in raspberry, with particular focus on the most challenging scenario: predicting new genotypes in new environments.

Materials and Methods

A multi-environment dataset from a private raspberry (*Rubus idaeus*) breeding program was used, consisting of 1,840 records for 453 genotypes evaluated across 19 environments (location × years) from 2021–2024. The trait of interest, flowering duration, was defined as the number of days from planting to first harvest minus 35 days, with genotypic means (BLUEs) estimated separately within environments. Given the highly unbalanced nature of the dataset, only genotypes with observations in at least 2 environments and complete metadata, including planting date and weather metadata, were retained. Genomic data consisted of genome-wide SNP markers. Daily weather data included mean, maximum and minimum air temperature, relative humidity, vapor pressure deficit, and photoperiod. Three genomic prediction approaches were evaluated: (i) baseline gBLUP, (ii) gBLUP with environmental covariates, and (iii) a linear crop CGM-WGP framework implemented with the Ensemble Smoother with Multiple Data Assimilation algorithm (ES-MDA). Predictive ability was assessed under four robust breeding-relevant cross-validation (CV) scenarios, where each scenario was implemented as 10 replicates of 5-fold cross-validation (CV2 - known genetics, known environments; CV1 – new genetics, known environment; CV0 – known genetics, new environments; CV00 – new genetics, new environments) using correlations between observed and predicted flowering time.

Results and Discussion

In CV2, the predictive ability of gBLUP models was exceptionally high (0.920–0.929), while the predicitve ability of CGM-WGP was lower (0.844), a decrease of 8.26%. In CV1, accuracies remained high for gBLUP apporaches (0.903–0.909) but lower for CGM-WGP (0.832), showing that statistical approaches excel when both genotypes and environments are represented in the training set. In CV0, however, gBLUP predicitve ability dropped substantially (0.527–0.546), whereas the CGM-WGP approach achieved an accuracy of 0.703, a 31% increase relative to the baseline gBLUP model. The clearest separation emerged in CV00, where gBLUP models predictive ability fell to 0.295–0.350 while CGM-WGP reached a median predictive ability of 0.577, more than doubling predictive ability of any gBLUP-based approaches (+65% gain). These results demonstrate a consistent pattern: gBLUP excels in interpolation (CV2, CV1) but loses power as novelty of the prediction scenario increases (CV0, CV00). By contrast, CGM-WGP maintains accuracy in the face of novel genetics and environments, leveraging physiological information to extrapolate beyond the observed data. The particularly strong CV00 performance emphasizes its breeding relevance, since predicting new genotypes in untested environments is the central challenge in forward-looking selection. Overall, these findings highlight the promise of physiology-based models as a pathway toward more reliable genomic prediction under climate change and expanding target populations of environments. Future research should focus on optimizing the model collective within the diversity theorem framework to maximize prediction accuracy (Messina et al., 2025).

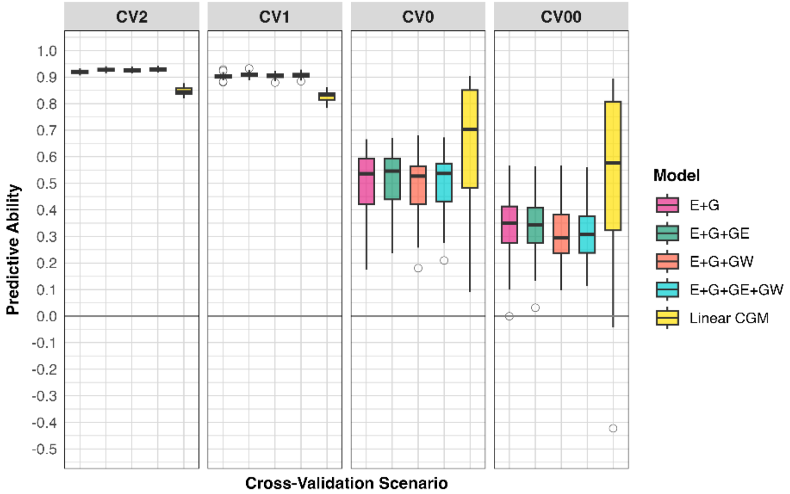

Figure 1. Predictive ability of five genomic prediction model types across 50 cross-validation analyses. Predictions were evaluated under four breeding scenarios: CV2 – known genotypes, known environments; CV1 – new genotypes, known environments; CV0 – known genotypes, new environments; and CV00 – new genotypes, new environments. Boxes show the interquartile range (25th–75th percentile), with the median indicated by the central line. Whiskers extend to ±1.5 × IQR, and points denote correlations outside this range (outliers).

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Synthetic data augmentation for enhanced in-season crop phenology prediction

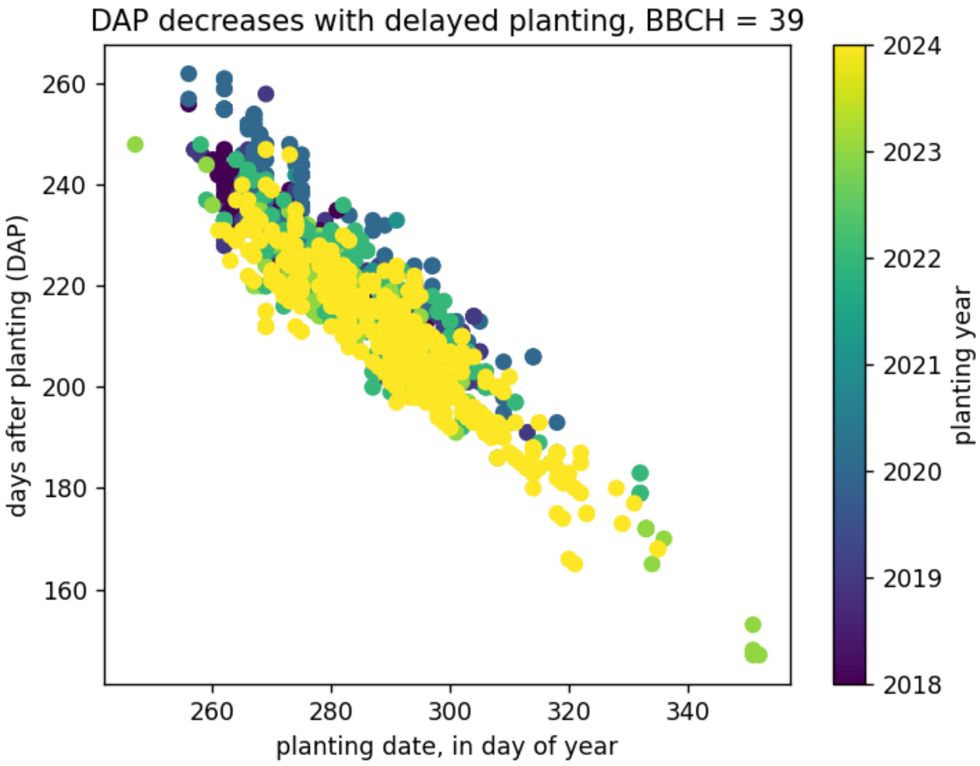
Keywords: Phenology, Modeling, Machine Learning, Statistical Analysis, Data Augmentation

Accurate crop phenology modeling plays a vital role in modern agriculture by enabling farmers to manage risks and optimize productivity. Since 2021, BASF's Digital Farming business unit has adopted machine learning (ML) techniques to enhance the scalability and efficiency of phenology model deployment. However, ML models require large volumes of high-quality data, and data gaps—often caused by inconsistent sampling and environmental biases—pose significant challenges to model robustness.

This paper introduces a novel data augmentation strategy to synthetically generate phenology data for German winter wheat, addressing data gaps caused by shifts in planting windows. We analyzed historical phenology records to identify key features, revealing a strong correlation between planting dates (expressed as day-of-year) and the number of days after planting (DAP) required to reach specific growth stages. To account for interannual weather variability, we performed cluster analysis to identify historical seasons with winter conditions similar to those of the 2024–2025 season. The 2020–2021 season emerged as the most comparable and was used to build linear regression models predicting DAPs for each growth stage based on planting date.

Using these models, we generated synthetic phenology data to fill gaps caused by the late planting in the 2024–2025 season—an environmental condition underrepresented in the existing training data. Incorporating this augmented dataset into the training pipeline significantly improved in-season prediction accuracy. The enhanced model achieved a 10% increase in 5-day-error accuracy, demonstrating the effectiveness of synthetic data in bridging phenological data gaps and improving model performance.

Figure 1: Days required to reach the same growth stage decrease with delayed planting. This plot also demonstrates accelerated crop development of 2024/2025 season due to late planting and unique wintertime weather conditions.



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vLeaf@DSSAT: Integrating Two-Leaf Sun–Shade Photosynthesis and Energy Balance into CERES-Maize

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Keywords: Photosynthesis, Transpiration, Leaf energy balance, Stomatal Conductance, DSSAT

Introduction

The global population is expected to exceed 9 billion by 2050, requiring a 60–100% increase in food production (FAO, 2021; Long, 2025). Agronomic advances to meet rising food demand have already increased agricultural water use, while freshwater resources remain stagnant and, in many cases, are declining (Rodell et al., 2018). Therefore, future yield gains must be pursued in parallel with improvements in crop water-use efficiency (WUE). A recent modelling study for C4 maize leaves showed that reducing stomatal conductance (g_s) in C4 leaves can improve WUE without compromising photosynthesis (Srivastava et al., 2024). However, the analyses remain limited to the leaf scale and do not capture the implications on canopy growth and yield since plant-scale processes are required to resolve these interactions. Yet, current crop models offer only partial solutions: CROPGRO includes stomatal regulation but is restricted to C3 legume crops, and CERES-Maize lacks a biochemical photosynthesis module. While an APSIM modelling framework by Wu et al. 2019 allows modelling for both C3 and C4 crops along with a biochemical photosynthesis module, it lacks consideration of leaf energy balance (assumes leaf temperature (T_{leaf}) = air temperature (T_{air})). This omission is critical because g_s reduction lowers transpiration and increases T_{leaf}, altering enzyme kinetics, canopy energy balance, and potentially crop growth (Srivastava et al., 2024). To address this gap, we present a new cross-scale framework that couples the DSSAT CERES-Maize model with vLeaf, a process-based leaf model. Within this framework, a two-leaf (sunlit–shaded) representation of the canopy is implemented, capturing canopy scale fluxes with reasonable accuracy and enabling two-way interactions between DSSAT and vLeaf. This integration allows biochemical processes simulated at the leaf scale, such as including photosynthesis, stomatal conductance, boundary layer conductance, and energy balance, to dynamically influence crop growth and development, while the crop state simulated in DSSAT constrains diurnal leaf-level processes.

Materials and Methods

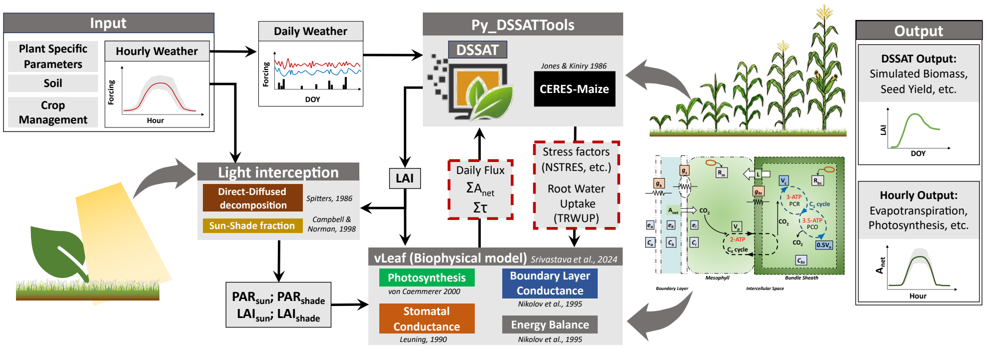

Figure 1. Coupling DSSAT CERES-Maize with vLeaf to integrate leaf-scale gas exchange and energy balance with crop growth.

We use an open-access Python library, pyDSSATTools, to run a modified DSSAT (v4.8) executable that integrates the DSSAT crop growth model with the vLeaf (Figure 1). In addition to incorporating vLeaf outputs into DSSAT simulations, the framework also stores them in a separate output file, allowing deeper insights into crop-scale feedbacks. CERES-Maize (Jones & Kiniry, 1986) simulated crop state variables in DSSAT, including leaf area index (LAI), soil water, nitrogen status, and phenology. The vLeaf module then computes hourly assimilation and transpiration rates for sunlit and shaded leaf area based on their respective absorbed radiation (Spitters, 1986; Campbell and Norman, 1998). The leaf model vLeaf (Srivastava et al., 2024) incorporates four coupled submodels: (i) a biochemical model of C4 photosynthesis (von Caemmerer, 2000), (ii) a modified Ball–Berry stomatal conductance model (Leuning, 1990), (iii) a leaf boundary-layer conductance model (Nikolov et al., 1995), and (iv) an energy balance solver for steady-state T_{leaf} (Nikolov et al., 1995). The two-way coupling works by having vLeaf simulate the potential diurnal carbon uptake and transpiration for sunlit and shaded leaves, with DSSAT root water uptake constraining the transpiration demand. vLeaf is then rerun with this water stress, updating leaf energy balance, T_{leaf}, g_s, and net assimilation (A_{net}), which is passed back to DSSAT to compute biomass accumulation and update plant status for the next day.

Results and Discussion

Simulations were conducted to evaluate the consequences of neglecting leaf energy balance under contrasting temperature conditions. Simulations under cooler (–3 °C) and warmer (+3 °C) environmental conditions, relative to the US Midwest, revealed substantial seasonal differences in carbon gain and water use predicted by the vLeaf model. Omitting energy balance ($T_{\text{leaf}} = T_{\text{air}}$) results in the cumulative carbon gain being underestimated by 10% in cooler conditions and 1% in warmer conditions. However, a much greater effect is observed on crop water usage. Cooler environments show a 29% underestimation in water demand, while warmer conditions show a 6% overestimation of transpiration water demand. Such biases have important implications for seasonal predictions and testing the WUE gains in hybrid crops. For instance, an underestimation of water use may mask the severity of drought stress or the true costs of water-saving strategies, and an underestimation of yield may misguide breeding or management decisions aimed at improving crop performance. This is particularly critical when evaluating climate-resilient strategies such as stomatal manipulation, where reduced g_s improves WUE at the leaf scale but simultaneously increases T_{leaf}, which can alter physical canopy processes and plant biochemical processes. Neglecting this feedback could lead to misleading conclusions about the benefits of trait-based crop improvement. By explicitly resolving energy balance, the framework will capture both direct and indirect effects of any physiological modification, providing a more reliable basis for assessing WUE and yield outcomes under diverse environmental conditions.

Conclusions

The DSSAT–vLeaf framework highlights the importance of explicitly representing leaf energy balance in cross-scale crop modeling. Neglecting this process introduces significant errors in carbon gain and water use. Integrating energy balance provides a more reliable foundation for evaluating WUE and yield-improving strategies.

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Measuring root hydraulic conductance in olive trees

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Keywords : sap flow, leaf water potential, microtensiometer

Introduction

Root hydraulic conductance (Lp) relates water flow with the decrease in water potential from the soil to the leaf. Stomatal conductance models based on water potential are essential parts of models of the soil-plant-atmosphere continuum (SPAC) (Garcia-Tejera et al., 2017). Recent advances in the measurement of tree water potential using microtensiometers (Pagay et al. 2014) allowed quantifying the diurnal evolution of root conductance in young olive trees (Villalobos et al., 2025).

Here, we report root hydraulic conductance data in irrigated adult olive trees in Cordoba (Spain) obtained with measurements of sap flow and sapwood water potential.

Materials and Methods

The experiment was performed in a drip-irrigated olive orchard at the Instituto de Agricultura Sostenible of Cordoba (Spain) during 2024. Sap flow was measured with the Compensated Heat Pulse- Average Gradient (CHP-AG) method (Testi et al. 2009). Sapwood water potential was determined with microtensiometers (FloraPulse Co., Davis, CA, USA). Measurements were performed in 5 trees, though here we will only present data from a single tree of cultivar “Picual”.

Results and Discussion

The time course of sap flow, sapwood water potential at the trunk base, and calculated resistance were similar to those shown in Fig. 1 for a tree of cultivar “Picual” for two dates - spring and full summer - with clear sky. Some patterns are common for the two curves: maximum sap flow peaks during 2-3 hours after noon, minimum water potential occurs later than that, hydraulic conductance is maximum in the early morning and decreases during the daytime, being very low at night. This day/night difference was also found by Villalobos et al. (2025) with young trees. In May, we find a lower sap flow, higher potential and higher hydraulic conductance. The decrease in conductance in summer is the result of irrigation not meeting the water requirement, which is also shown by the lower pre-dawn water potential (Fig. 1).

Conclusions

Hydraulic conductance varied during the daytime and was very low at night. Daytime values of conductance decreased during the summer.

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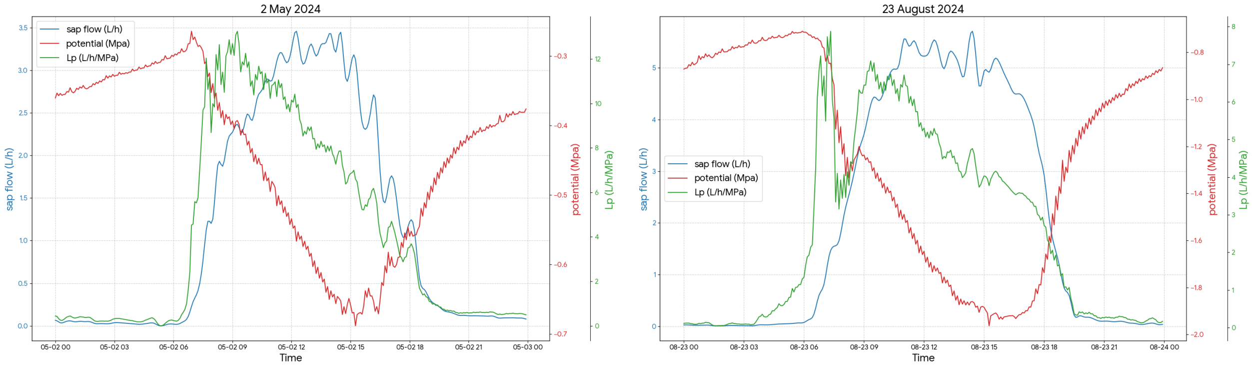

Figure 1. Time course of sap flow, sapwood water potential and hydraulic conductance of an olive tree cv. “Picual” on 2 May (left)and 28 August (right) 2024.

Acknowledgements

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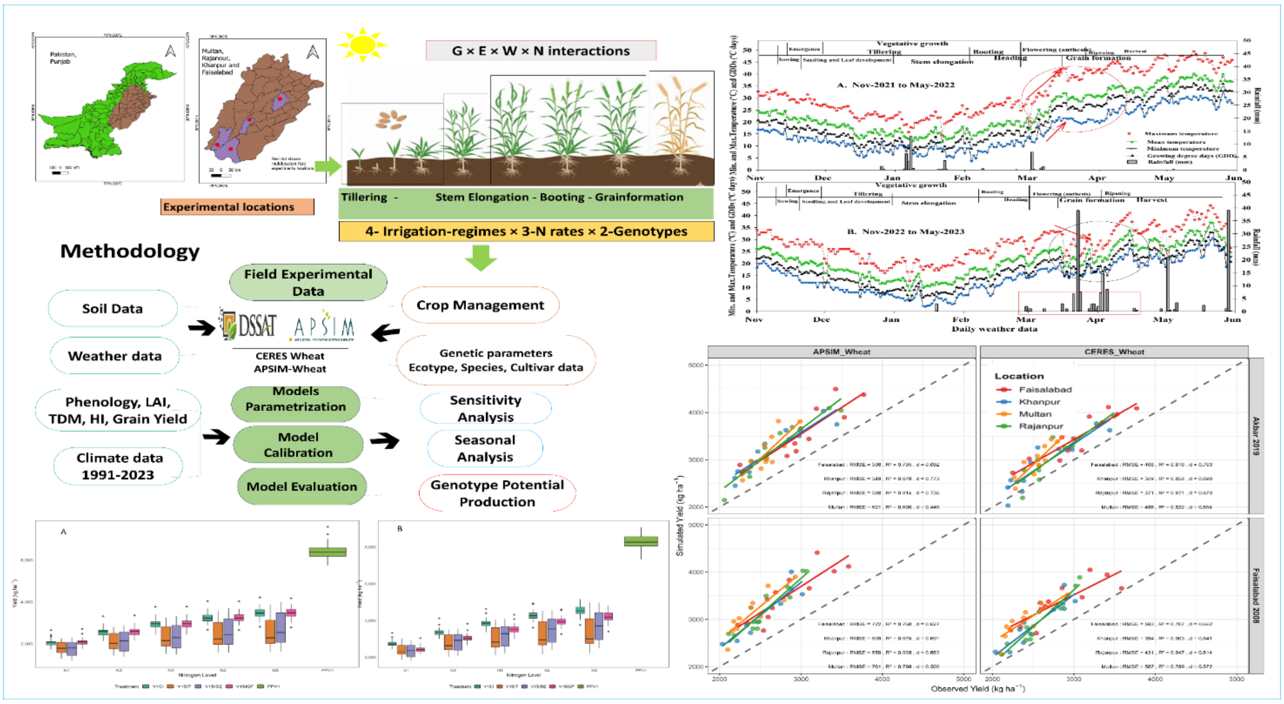
Graphical Abstract



Testing a new POM–MAOM module in the ARMOSA process-based crop model across contrasting soil textures

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Keywords: soil organic matter fractions; crop modelling; ARMOSA; POM; MAOM.

Introduction

The explicit representation of soil organic matter (SOM) fractions in crop models is essential to capture their contrasting stability, turnover rates, and sensitivity to management and soil texture. Traditional three-pool SOM structures provide only a simplified representation and do not explicitly separate particulate organic matter (POM), linked to short-term residue turnover, from mineral-associated organic matter (MAOM), which represents long-term stabilization. This distinction is particularly relevant when assessing management effects, since tillage, residue retention, and soil texture strongly modulate the balance between POM and MAOM. Therefore, testing a mechanistic POM–MAOM module provides an opportunity to improve the process-based representation of SOM dynamics and their links with crop performance.

Materials and Methods

We extended the process-based crop model ARMOSA (Perego et al., 2013) with a new module simulating POM and MAOM according to the Microbial Efficiency-Matrix Stabilization (MEMS) framework. The module links residue decomposition, microbial turnover, and stabilization/desorption processes. The evaluation used long-term data from two sites in northern Italy with contrasting textures: Landriano (silty loam) and Piacenza (silty clay). At Landriano, three management systems were compared (conventional tillage, semi-conservative, and no-till), while Piacenza included two (conventional and no-till). The Landriano trial, started in 2023, follows a biennial silage rotation of maize, winter barley, and soybean, with cover crops under no-till. The Piacenza trial, established in 2013, adopts a four-year rotation of double maize, wheat, and soybean, also with cover crops under no-till. Observed SOC fractions were used to evaluate model performance for POM and MAOM, while ancillary crop variables (LAI, aboveground biomass, yield) were simulated to ensure consistency of the crop–soil system. For independent testing, calibration used conventional and no-till in Landriano and two thirds of the years in Piacenza; validation used the semi-conservative system in Landriano and the remaining years in Piacenza. Calibration followed a stepwise approach, combining automatic optimization with trial-and-error refinements, starting from soil water and crop variables and extending to soil mineral N and SOC fractions.

Results and Discussion

Results showed that the model reproduced the main temporal patterns of both SOM fractions and crop growth, with the best performance at Landriano (Figure 1). Model–data comparison at Landriano showed variable agreement across fractions, with high d-index values for MIC (0.62–0.98) and SOCtot (0.71–0.88), moderate agreement for MAOM (0.61–0.66), and lower performance for POM and DOC (0.44–0.49 and 0.44–0.82, respectively). The weaker agreement for

POM and DOC reflects their intrinsically higher spatial and temporal variability, which makes these fractions more difficult to capture consistently in both field measurements and simulations. These findings demonstrate the capacity of the new ARMOSA module to capture management and texture effects on SOM fraction dynamics while maintaining robust performance on crop variables, thus strengthening confidence in its process-based representation.

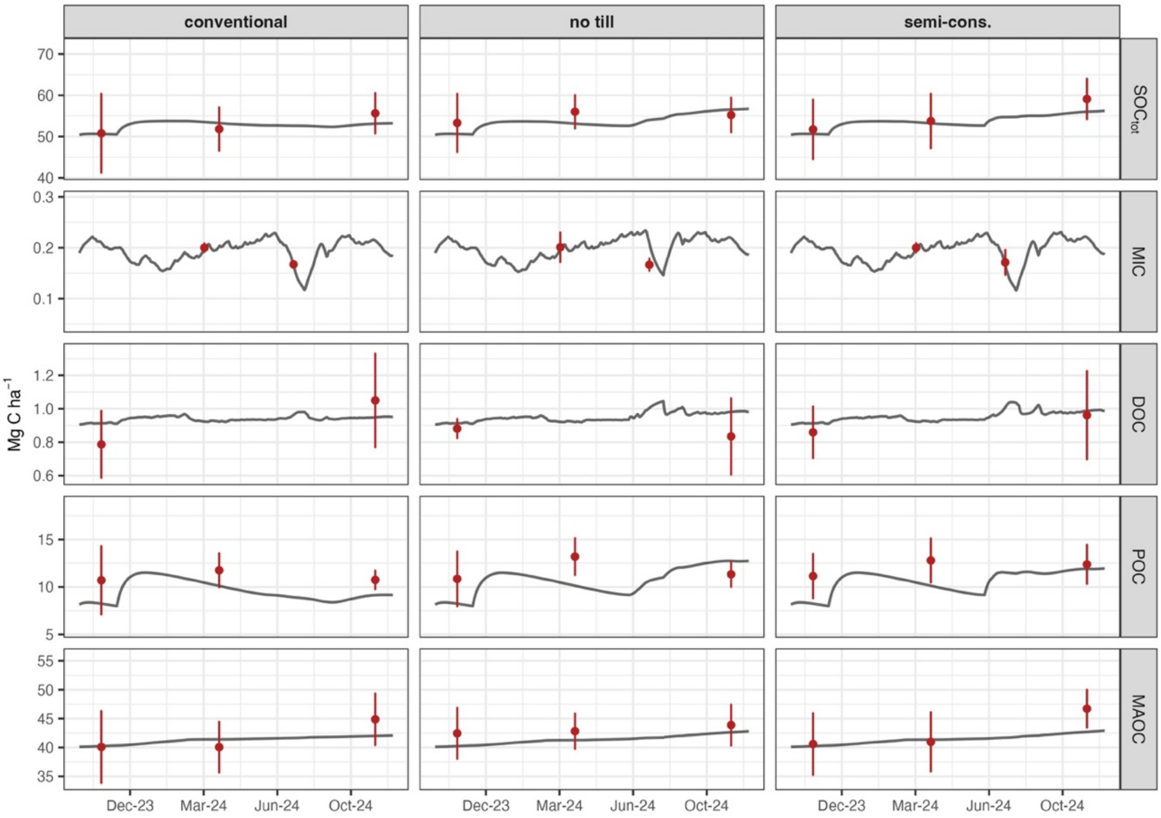

Figure 1. SOC pools of the soil layer 0 to 30 cm in calibration (conventional and no till) and validation (semi-conservative) datasets of the Landriano site

Table 1. Fitting indices for SOC and SOC pools in calibration (conventional and no till) and validation (semi-conservative) datasets of the Landriano site

"component"	"group"	"RRMSE"	"d"
"SOC[tot]"	"calibration"	3.84	0.71
"SOC[tot]"	"validation"	3.51	0.88
"MIC"	"calibration"	11.59	0.62
"MIC"	"validation"	2.05	0.98
"DOC"	"calibration"	12.44	0.44
"DOC"	"validation"	4.63	0.82
"POC"	"calibration"	19.41	0.44
"POC"	"validation"	18.94	0.49
"MAOC"	"calibration"	4.21	0.61
"MAOC"	"validation"	5.45	0.66

Conclusions

The explicit representation of POM and MAOM in crop models represents a step forward compared to traditional three-pool SOM structures, providing a more mechanistic understanding of SOM stabilization processes and their responses to management and soil texture.

Acknowledgements

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Assessing the adaptation of kidney bean to Southern Germany using the DSSAT CROPGRO-Drybean model

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Keywords: crop modelling, *Phaseolus vulgaris*, calibration

Introduction

Dry beans (*Phaseolus vulgaris* L.) are the second most important food legume worldwide, after soybeans, contributing significantly to human diets due to their high protein content (Takeoka et al., 1997). Despite this global importance, dry beans remain a relatively new crop in Germany, where legumes account for only 1.8% of arable land. In 2021, the average per capita bean consumption was 2.2 kg, with kidney beans being the most consumed type in the country. The gap between consumption and domestic production reflects Germany's strong dependence on imported protein crops, with roughly one-quarter of its feed protein being imported (BLE, 2020). Expanding bean cultivation in Germany is therefore strategically crucial for reducing reliance on imports, enhancing local food and plant-based protein security, while contributing to climate mitigation goals. However, bean cultivation has not been widely tested under German conditions, and no official genotype recommendations exist. Process-based crop models such as DSSAT CROPGRO-Drybean provide valuable tools for evaluating genotype×environment×management interactions. Originally developed and validated in tropical and subtropical regions (Hoogenboom et al., 1994; Melo et al., 2011), CROPGRO-Drybean has been successfully calibrated for diverse environments, yet its application in temperate Europe remains limited. Simulating kidney bean growth under Southern German conditions offers an opportunity to assess adaptation potential and generate insights for management strategies that support sustainable crop diversification. Due to the comparatively limited research investment in minor crops such as kidney bean, conducting extensive multi-site and multi-year field trials often proves unfeasible. Crop models are effective tools for testing a wide range of hypothetical scenarios and management options, thereby obviating the need for costly and time-consuming field experiments. The objective of this study was to calibrate and test the CROPGRO-Drybean model for kidney bean under Southern German conditions.

Materials and Methods

The DSSAT CROPGRO-Drybean model (version 4.8.5; Hoogenboom et al., 2024) was used in this study. The experimental site was Ihinger Hof research station of the University of Hohenheim, Southern Germany (48°44′ N, 8°55′ E, 475 m a.s.l.). Two kidney bean cultivars, Red Kidney and Canadian Wonder, supplied by MyLocalFarm Company (Germany), were grown in a field experiment sown on 16 May 2025. The experiment included measurements of phenological development stages, biomass accumulation, and final grain yield. These observations formed the basis for estimating cultivar- and ecotype-specific genetic coefficients required by CROPGRO-Drybean. Soil profile characteristics were determined from site-specific analyses, and crop management information was derived from experimental records. Together with daily weather data collected at the station, these parameters were used as model inputs. As a starting point for calibration, the DSSAT default cultivar Canadian Wonder (IB0014) was used. The calibration process involved iterative adjustment of ecotype followed by cultivar coefficients to achieve good agreement between simulated and observed data for key traits, including flowering, first pod day, and physiological maturity (phenology-related coefficients), in-season biomass, and final yield (growth-related coefficients).

Results and Discussion

The calibrated DSSAT CROPGRO-Drybean model showed overall good agreement between simulated and observed values for both kidney bean cultivars (Table 1) under Southern German conditions, based on one year of data. Simulated anthesis dates (ADAT) were within 2–10 days of observed values, with a slight tendency to underestimate anthesis for Canadian Wonder. The first pod (PD1T) and physiological maturity date (MDAT) were closely matched between simulations and observations, indicating that the model successfully represents early reproductive development. Grain yield was reasonably predicted, with Red Kidney showing a simulated yield slightly higher than the observed yield. At the same time, Canadian Wonder was slightly overestimated by the model, suggesting that further calibration may be required to account for cultivar-specific responses under local conditions.

Table 1. Comparison of simulated (Sim.) and observed (Obs.) phenological dates and grain yield for two kidney bean cultivars grown at Ihinger Hof, Southern Germany, in 2025. ADAT = anthesis date; PD1T = first pod date; MDAT = physiological maturity date. Yield is expressed in kg DM ha^{-1}.

Cultivar	**ADAT**		**PD1T**		**MDAT**		**Grain Yield**	
	Sim.	**Obs.**	**Sim.**	**Obs.**	**Sim.**	**Obs.**	**Sim.**	**Obs.**
Canadian Wonder	46	56	55	65	96	102	1385	926
Red Kidney	46	48	55	58	96	101	1344	1296

Simulated leaf area index closely matched observed values, with peak achieved around 45–85 days after sowing (DAS) for both cultivars (Fig. 1a). For leaf weight, the model accurately reproduced the growth trajectories of both cultivars, with rapid biomass accumulation beginning around 30 DAS and peaking near 85 DAS (Fig. 1b). The slightly lower d-statistic for these two traits may reflect greater variability in canopy development. Nonetheless, both cultivars showed similar growth patterns, suggesting shared responses to environmental conditions. Thousand-grain weight simulations were highly accurate, with the model capturing the timing and magnitude of grain filling and maturity (Fig. 1c). The high d-statistics demonstrate reliable model performance in simulating final yield outcomes.

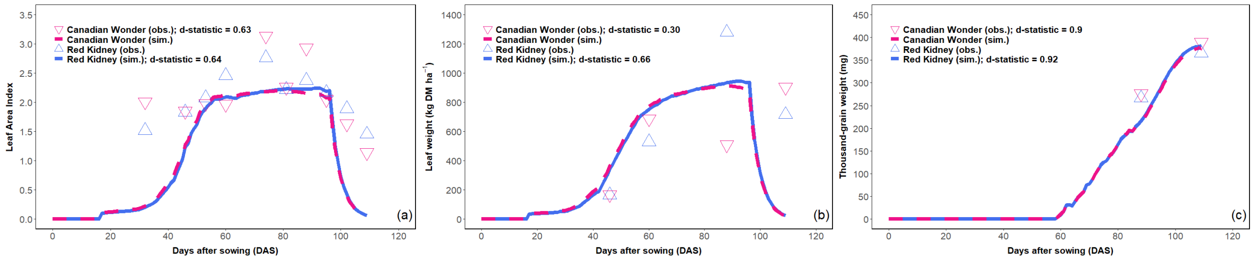

Figure 1. Simulated (sim.) and observed (obs.) growth dynamics of two kidney bean cultivars, grown at the Ihinger Hof research station, Germany, and modeled using DSSAT CROPGRO-Drybean (v4.8.5). Panels show: (a) Leaf area index, (b) leaf weight, and (c) thousand-grain weight over days after sowing (DAS). Model calibration was based on field measurements taken during the 2025 growing season. Final d-statistics are reported for each cultivar and trait, indicating model fit.

Conclusions

Preliminary results of CROPGRO-Drybean for the Canadian Wonder and Red Kidney cultivars based on one year of data underscore the model’s ability to simulate growth and yield dynamics of kidney beans under Central European conditions. Key phenological events and patterns of biomass accumulation and partitioning were consistent with field observations, apart from stem and pod. Additional data will be used for further testing of the model with respect to the weather-related seasonality factor. Overall, these results demonstrate that the model provides a reliable baseline for simulating kidney bean growth in Germany and could potentially be used to optimize management strategies in future studies.

Acknowledgements

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Effect of Nitrogen Concentration in Olive Leaves on Tree Photosynthesis

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Key words: Fertilization, *Olea europaea* L., OliveCan.

Introduction

Nitrogen (N) deficiency leads to a marked reduction in the photosynthetic capacity of crops since Rubisco and the light-harvesting proteins involved in photosynthesis account for 60% of the N content in leaves (Sadras et al., 2024).

Díaz-Espejo et al. (2006) modeled photosynthesis in olive leaves under drought conditions. The results showed that the reduction in photosynthesis capacity was strongly related to the decrease in N content per unit leaf area, rather than to other factors such as water deficit.

Materials and Methods

N concentrations were measured in an experimental olive orchard under ample water and fertilizer supply including different olive varieties (‘Picual’, ‘Arbequina’, ‘Hojiblanca’, ‘Arbosana’, ‘Cornicabra’, ‘Empeltre’, ‘Frantoio’ and ‘Cobrançosa’). The resulting values were used to estimate maximum carboxylation activity of Rubisco under saturating conditions of CO_2 and ribulose biphosphate ($V_{c,max}$) and the maximum electron transport rate without light limitations (J_{max}) with the equations proposed by Díaz-Espejo et al. (2006).These two parameters are included in the photosynthesis-stomatal conductance submodel used in *OliveCan* (López-Bernal et al., 2018), a process-based model of olive orchards. Assuming no genotype effects on the remaining parameters of the photosynthesis-conductance submodel, a simulation experiment was performed to evaluate the effects of cultivar variability in $V_{c,max}$ and J_{max} on the simulated seasonal estimates of gross photosynthesis for a hedgerow olive orchard.

Results and Discussion

N concentration in olive leaves ranged from 3.61 g N m^{-2} (‘Cornicabra’) to 4.54 g N m^{-2} (‘Arbequina’), with statistical differences between cultivars. Such values resulted in extreme values of $V_{c,max}$ and J_{max} of 83.7-95.0 µmol m^{-2} s^{-1} and 137-168 µmol m^{-2} s^{-1}, respectively. Simulation results showed average seasonal estimates of gross photosynthesis ranging from 4322 ± 487 g glucose equivalents m^{-2} y^{-1} (‘Cobrançosa’) to 4174 ± 414 g glucose equivalents m^{-2} y^{-1} (‘Arbequina’) (Table 1). This implies that the measured differences in N_a between cultivars led to 3% variations in seasonal gross photosynthesis. Although the results of this exploratory analysis must be taken with caution, they highlight that future studies should explore in greater detail the effect of N availability on photosynthetic parameters and the interaction between cultivars and N availability in olive trees.

Table 1. Annual gross photosynthesis simulated with the OliveCan model using $V_{c,max}$ and J_{max} values derived for each cultivar from leaf N concentrations

	‘Arbequina’	‘Arbosana’	‘Cobrançosa’	‘Cornicabra’	‘Empeltre’	‘Frantoio’	‘Hojiblanca’	‘Picual’
YEAR	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$	g m^{-2} $year^{-1}$

Average	4174	4232	4322	4222	4319	4282	4297	4296
Std. Dev.	414	466	487	466	486	479	482	481

Conclusions

Differences in leaf N concentration were found among the studied varieties. According to the simulations, photosynthesis rates could differ among cultivars by up to 3% due to the variability in leaf N concentration alone.

Acknowledgements

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Linking soil water status to canopy development: a mechanistic chickpea model for semi-arid systems

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Keywords: fraction of transpirable soil water, leaf area index, drought stress response

Introduction

Semi-arid croplands are expanding, and drying trends are intensifying, increasing the frequency and severity of water stress during critical stages of crop development (Huang et al., 2016). Many process-based crop models underperform in these environments. By simplifying stress interactions, canopy dynamics, and field heterogeneity, they underestimate drought-induced yield losses and generate uncertain predictions in water-limited systems (Webber et al., 2025). For broader use beyond research calibration, models must remain transparent, parsimonious, and operationally deployable. Building on the framework of Soltani and Sinclair (2011), we developed a mechanistic chickpea model tailored for semi-arid systems. Its core innovation is a two-threshold soil-water modifier that regulates leaf area development: above an upper threshold expansion proceeds, between thresholds it is progressively constrained, and below a lower threshold expansion ceases with drought-induced senescence. This physiologically interpretable mechanism links soil water status to canopy growth, radiation capture, and yield formation. The model is released as open-source code, ensuring reproducibility, extensibility, and operational use, in line with principles outlined by Wallach et al. (2018).

Materials and Methods

Model calibration was conducted using data from field experiments carried out in a semi-arid region of southern Israel (31.333° N, 34.664° E) during 2019–2021. The trials were arranged as randomized complete block designs with six replicates. All plots received sprinkler irrigation during the vegetative phase, followed by differential drip irrigation ranging from 0 to 140% of weekly reference evapotranspiration (ET_o). Physiological data (phenology, leaf area index, above-ground biomass, and grain yield) were used to parameterize phenological thresholds, leaf area parameters, the two-threshold soil-water modifier, radiation use efficiency, and maximum harvest index. For validation, the model was applied to 21 commercial chickpea fields cultivated between 2022 and 2025 in the same semi-arid region, using field-specific information on sowing, harvest, irrigation, and yield to test model robustness across contrasting water regimes. Model performance was evaluated using four statistical indicators: the coefficient of determination (R^2) which measures the proportion of observed yield variance explained by the model; the Root Mean Square Error (RMSE, $t\ ha^{-1}$), which quantifies the average magnitude of prediction error; the normalized RMSE (nRMSE, %), which expresses RMSE relative to the observed mean yield to allow comparison across datasets; and bias ($t\ ha^{-1}$), which indicates systematic over- or underestimation by the model.

Results and Discussion

Calibration on experimental plots (2019–2021) produced R^2 = 0.68 and nRMSE = 22.3% for grain yield, while validation on 21 commercial fields (2022–2025) reached R^2 = 0.78 and nRMSE = 18.7% (Figure 1). These consistent results across experimental and farmer-managed conditions highlight the robustness of the model, with performance comparable to benchmarks reported by Soltani and Sinclair (2011). Yield variation was primarily explained by the two-threshold LAI modifier, underscoring canopy development as the dominant driver of water-stress responses. The model effectively differentiated yield under rainfed and deficit irrigation, but its discriminating power declined once irrigation exceeded 100% of weekly ET$_o$, a limitation also evident in high-yield commercial fields.

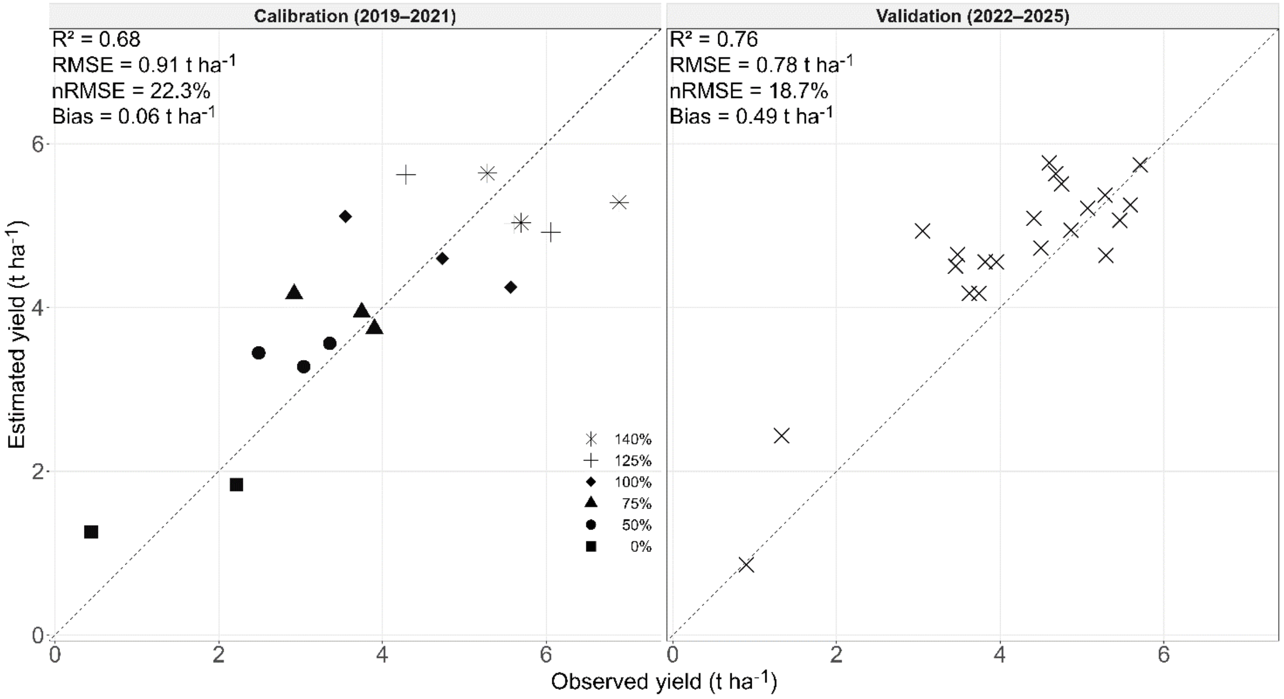

Figure 1. Simulated vs. observed chickpea yield for calibration (left, 2019–2021) and validation (right, 2022–2025). Calibration points are grouped by weekly irrigation as a percentage of reference evapotranspiration (ET$_o$, 0, 50, 75, 100, 125, 140%), averaged across blocks, giving 17 treatment-year combinations (five levels in 2019; six in 2020; six in 2021). Validation includes 21 commercial chickpea fields, each represented as an individual point. The dashed line indicates the 1:1 reference. Performance metrics (R², RMSE [t ha^{-1}], nRMSE [%], bias [t ha^{-1}]) are reported per panel.

Conclusions

This study shows that yield variability in semi-arid chickpea systems can be captured by a simple, physiologically based canopy modifier linking soil water status to leaf area development. By targeting a key driver of yield formation, the model demonstrated robust performance across both experimental trials and commercial fields. Its open-source R implementation ensures transparency, reproducibility, and adaptability, supporting use in research as well as operational decision-making under water-limited conditions. More broadly, the results highlight the value of parsimonious mechanistic approaches for advancing crop modeling and strengthening the resilience of semi-arid agriculture**.**

Acknowledgements

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A mobile application for estimating biophysical quantities to improve crop model parameterization

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Keywords: leaf area index; stomatal conductance; extinction coefficient; plant nitrogen content; nitrogen nutrition index.

Introduction

The reliability of crop models is often threatened by problems dealing with the robustness of parameterizations. Ideally, model parameters should only reflect morphological and physiological characteristics of specific genotypes. However, in most cases, the parameterization is hindered by unfavorable relationships between the number of observations and the number of parameters to be calibrated. This may lead to include, in parameter values, site-specific factors (e.g., weather conditions) which can compromise the model capability to simulate growth and development under conditions different from those explored during the calibration.

Good practices suggest running sensitivity analysis, measuring as many parameters as possible and calibrating only a number of parameters (for which measurements are unavailable) which should be *small* compared to the number of observations (possibly on different state variables) available to estimate the objective function. However, these guidelines are far from being regularly adopted, also because of the time needed to collect measurements, and of cost and usability of available instruments.

This study aims at presenting a mobile application designed to enable an efficient and rapid collection of quantitative data on both parameters and rate/state variables relevant for crop model parameterization. In the current version, the app estimates leaf area index (LAI), extinction coefficient for solar radiation (k), plant nitrogen content (PNC), nitrogen nutrition index (NNI), and stomatal conductance (g_s).

Scientific background

The method for LAI makes use of the device accelerometer to capture live-preview camera frames at 57.5° zenith angle while the user is rotating the device along its main axis. Frames are then automatically segmented to identify the percentage of “sky pixels”, i.e., the gap fraction, which is converted into LAI values using the light transmittance model described by Baret et al. (2010). PNC is estimated from leaf greenness, in turn quantified according to Karcher and Richardson (2003). A dedicated reference panel is used during image acquisition to flatten spectral reflectance, thus normalizing the settings of the device exposure meter. PNC is used – together with critical N concentration (Ncrit) (derived from LAI according to Confalonieri et al. (2011)) – to estimate NNI, as the PNC to Ncrit ratio. The application enables 3D scanning of leaf surfaces using the device accelerometer and magnetometer. The resulting leaf angle distribution is used (i) to derive k as a function of the parameter χ of the Campbell’s ellipsoidal distribution, and (ii) to estimate g_s from changes in leaf architecture (Paleari et al., 2024; Rusconi et al., 2025).

The mobile app

The mobile app (Fig. 1), currently available for Android devices, is designed for data collection in field experiments, with a user-friendly interface, an integrated user guide and the possibility to tag and store data. Measurements referring to the different quantities are georeferenced using the device GPS, and data can be exported in both text and shapefile formats for further analysis and processing.

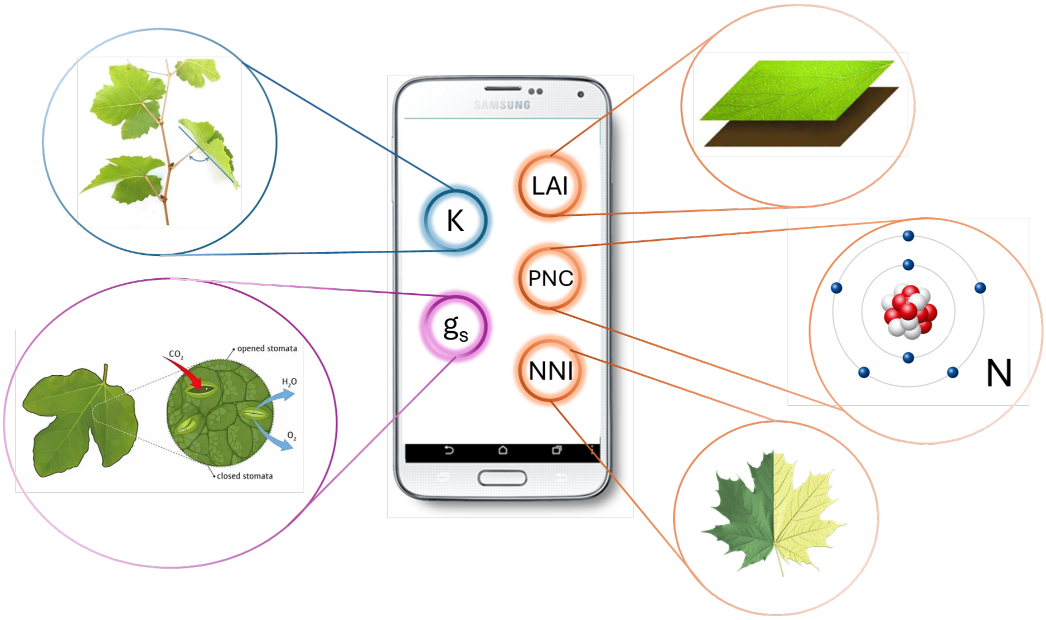

Figure 1. The mobile application scheme illustrating parameters (blue), rate (purple) and state (orange) variables of interest for model parameterization.

Conclusions

The proposed mobile application provides an innovative, low-cost, and portable solution for in-field data collection of key crop parameters and rate/state variables, thus enhancing the robustness of model parameterizations and supporting more reliable applications of crop models across different contexts.

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Machine learning surrogate for coupled leaf gas-exchange model

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Keywords: FvCB; leaf gas-exchange; Cropbox; surrogate modeling; XGBoost

Introduction

The Farquhar–von Caemmerer–Berry (FvCB) model describes leaf photosynthesis by defining key biochemical parameters that determine carbon assimilation limited by Rubisco activity, electron transport, or triose phosphate utilization. Cropbox is a Julia-based declarative framework for developing process-based crop models (Yun & Kim, 2023). Using this framework, we implemented a coupled leaf gas-exchange model commonly used in crop models (Yun et al., 2020). While the framework facilitates optimization and integration of physiological sub-models, strong feedback among coupled components still leads to high computational costs under high-resolution input features.

To address this, we developed a machine learning (ML) surrogate trained on Cropbox outputs to reproduce the coupled model's accuracy with greatly improved efficiency. Previous canopy-scale studies have used hybrid models combining FvCB parameters with artificial neural networks (ANNs) for generalization (Kaneko et al., 2022). Other recent studies have applied ML approaches such as Random Forest, XGBoost, and ANNs to address re-parameterization challenges of semi-empirical stomatal conductance models (Gaur & Drewry, 2024). In contrast, our study emulates the complex leaf gas-exchange system implemented in Cropbox. As illustrated in Figure 1, our ML surrogate reproduces its outputs by incorporating both environmental variables and model parameters that can be freely adjusted.

Materials and Methods

Environmental variables and FvCB parameters (Vc_{max}, J_{max}, R_d) were uniformly sampled via Latin Hypercube Sampling (LHS) and used as inputs to generate reference data. The environmental range was constructed to encompass extreme climate conditions derived from multi-decadal meteorological records across various regions of Korea.

Simulated assimilation components (A_c, A_j, A_p, A_{gross}, R_d) from the leaf gas-exchange model were used as targets to train multiple machine learning regressors, including Random Forest, Extra Trees, HistGradientBoosting, Gradient Boosting, and XGBoost. Comparative analysis was conducted to assess the accuracy and computational efficiency of the ML surrogate relative to the original Cropbox simulation.

Results and Discussion

Among tested algorithms, XGBoost yielded the best agreement with the original model for A_{gross} (RMSE = 0.34, MAE = 0.21, R^2 = 0.996). Processing 20,000 samples with the trained surrogate was over 50 times faster than the original Cropbox simulation while maintaining comparable accuracy. Direct prediction of gross assimilation (A_{gross}) by ML also surpassed the indirect minimum (A_c, A_j, A_p) method, confirming that the surrogate captured integrated physiological constraints within the coupled gas-exchange system.

Conclusions

The proposed XGBoost surrogate model accurately emulates the coupled FvCB–stomatal conductance system implemented in Cropbox while reducing computation time by more than 98%. Existing process-based crop models suffer from computational inefficiency because the strong feedback among coupled components requires iterative numerical optimization during the coupling process. By contrast, our surrogate model based on machine learning effectively alleviated these computational limitations. Future work will focus on extending Cropbox with a functionality that can automatically generate and substitute surrogates for computationally intensive modules during runtime.

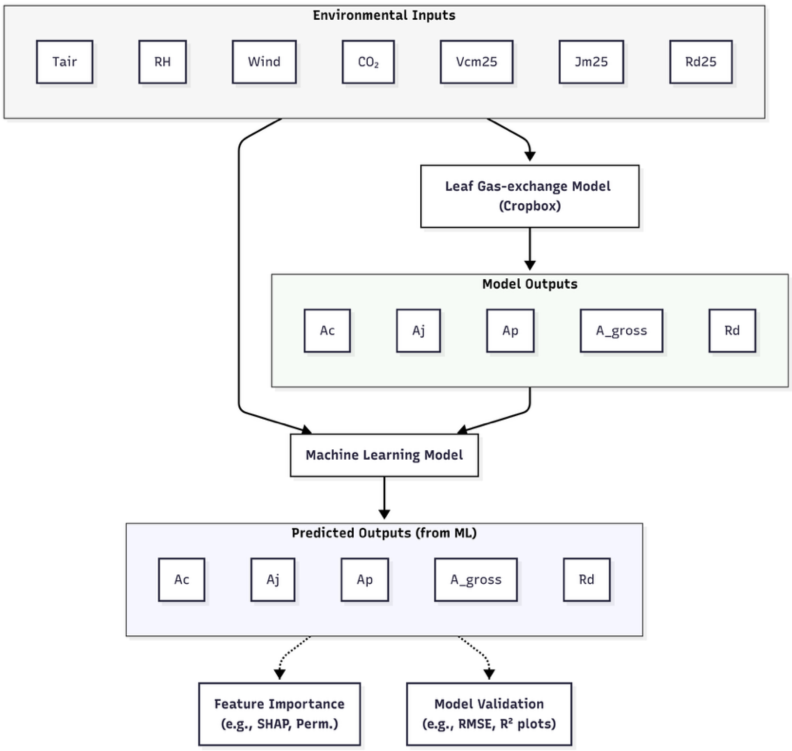

Figure 1. Schematic Diagram of the Proposed Hybrid Modeling Approach

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Groundwater should be considered in crop risk assessment

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Keywords: water table, drought, waterlogging, crop model, model improvement

Introduction

Extreme weather events such as drought and flooding are becoming more frequent and intense, causing devastating impacts on agricultural productivity, farmer livelihoods, and food security. Recent studies suggest that shallow groundwater influences the severity of drought and waterlogging stresses on crop yields (Deines et al., 2024). Capillary rise from shallow groundwater provides additional water for root uptake, plant transpiration, and soil evaporation, thereby mitigating drought stress. On the other hand, very shallow water tables can lead to excess soil water around root zone, intensifying waterlogging stress. A global analysis estimates that water table depth lies within or near the root zone in 22–32% of terrestrial land area, highlighting the need to improve our understanding and modelling of the shallow groundwater impacts on aboveground productivity (Fan et al., 2013). However, groundwater impacts on vegetation are often neglected in risk assessment studies using process-based models, which may result in systematic biases in simulated drought and waterlogging stresses (Ukkola et al., 2016). Here, we present field- and nation-scale evidence demonstrating that incorporating groundwater effects enhances the skill of a process-based crop model to simulate water balance and crop growth.

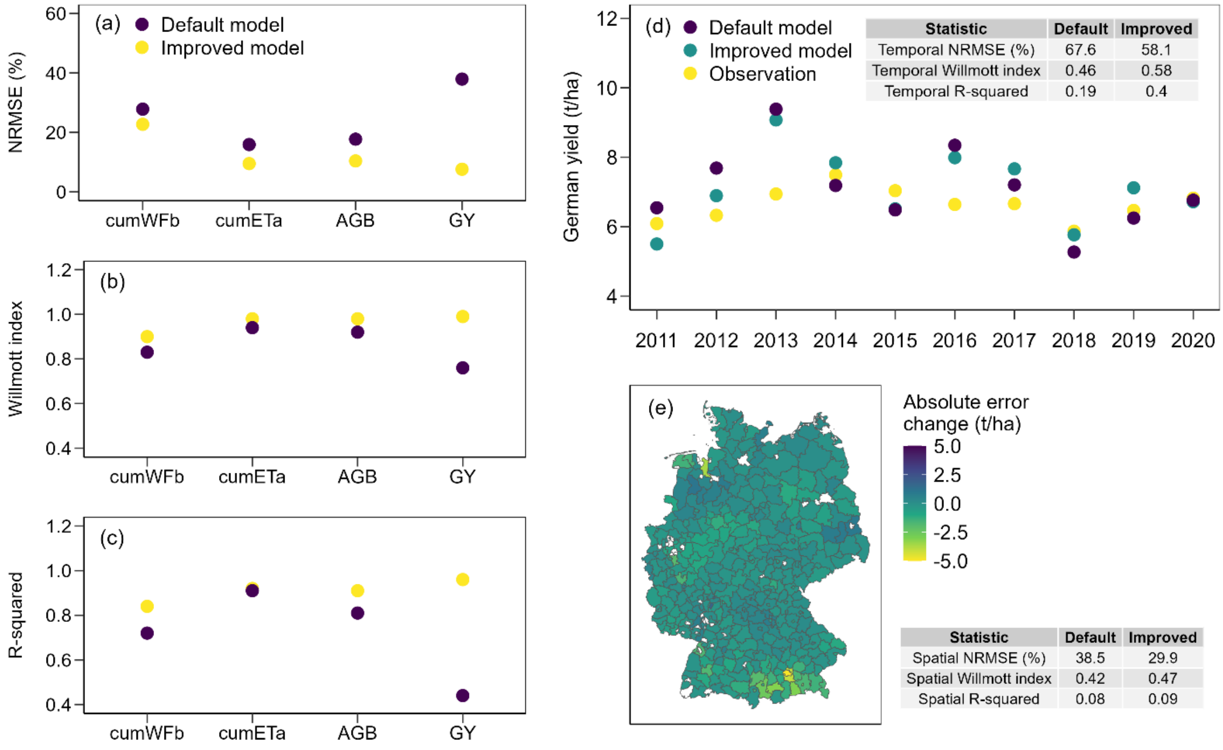
Materials and Methods

We first improved the default SIMPLACE <LINTUL5, SLIM> process-based crop model by integrating new modules that simulate the influences of groundwater on root-zone water balance. Second, we used lysimeter data to evaluate the performance of both the default and improved models in simulating net water flux at the bottom of the lysimeter (i.e., 1.5m below soil surface), actual evapotranspiration, aboveground biomass, and grain yield. Afterwards, we conducted nationwide simulations across Germany with both models and compared the results to winter wheat yield statistics to assess whether incorporating groundwater improves the model's explanatory power for spatiotemporal yield variability.

Results and Discussion

Model evaluation with the lysimeter data showed that incorporating groundwater effects significantly improved the model's skill in simulating water balance and crop growth (Figure 1a-c). Before the improvement, the simulated net bottom water flux was always negative (i.e., loss to deeper layers), whereas the observed net bottom water flux ranged from -101 mm per season to +52 mm per season. After the improvement, the simulated net bottom water flux aligned more closely with the observations, with a maximum simulated value of +36 mm per season. This more accurate representation of water balance at the bottom boundary, improved the simulation of actual evapotranspiration. The improved simulation of actual evapotranspiration led to a more realistic representation of drought stress, which is calculated as actual evapotranspiration divided by potential evapotranspiration, ultimately resulting in better simulations of aboveground biomass and yield.

Nationwide simulations indicated that incorporating groundwater effects improved the simulations of spatiotemporal variability in winter wheat yield across Germany (Figure 1d-e). The default model underestimated yields during the hot and dry year of 2018, while the improved model reduced this bias by capturing the buffering effect of shallow groundwater against drought. Conversely, the default model significantly overestimated yields in the wet years of 2013 and 2016. Although the improved model slightly reduced this error, the simulated yields remained much higher than the observations. These results highlight the need to improve crop models to capture various stresses due to excess rain, including not only waterlogging, which is partially represented in the improved model, but also submergence, lodging, pests, and diseases, which are not yet considered. Although the improved model performed slightly better in simulating spatial yield variability, both models still failed to adequately capture it. This outcome is expected, as the simulations do not account for local practices such as the use of cultivars with varying drought and waterlogging tolerances, irrigation strategies, and drainage systems, primarily due to a lack of high-quality and fine-resolution spatial data.



Statistic	Default	Improved
Temporal NRMSE (%)	67.6	58.1
Temporal Willmott index	0.46	0.58
Temporal R-squared	0.19	0.4

Statistic	Default	Improved
Spatial NRMSE (%)	38.5	29.9
Spatial Willmott index	0.42	0.47
Spatial R-squared	0.08	0.09

Figure 1. Evaluation of the default and improved crop models. Field-scale evaluation with lysimeter data (a–c) including cumulative net water flux at the bottom of lysimeter (cumWFb), cumulative actual evapotranspiration (cumETa), aboveground biomass (AGB), and grain yield (GY). National-scale evaluation of temporal (d) and spatial (e) variability in German winter wheat yield. NRMSE denotes normalized root mean square error. The absolute error change is calculated as the absolute error of the improved model minus that of the default model. The temporal statistics are calculated across the years 2011–2020, while the spatial statistics are calculated across NUTS3 districts.

Conclusions

Here, we provide evidence highlighting the importance of incorporating groundwater impacts on crop growth to better capture spatiotemporal variability in crop yields. However, several limitations remain that should be addressed in future research. First, since shallow water tables play a more significant role during extreme dry and wet years compared to normal years, it may be necessary to conduct further analysis using large ensembles of climate model outputs, which better capture interannual variability, rather than relying solely on historical records. Second, we did not consider the effects of crop management on water table depth, as we relied on static monthly data from groundwater modeling. To simulate the feedback loop between crops and groundwater, it would be necessary to dynamically integrate a process-based crop model with a hydrological model that includes both surface water and groundwater processes.

Acknowledgements

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Swap-Snomin-Lingra: a modular crop-soil model for grassland growth and nitrogen

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Keywords: modular crop-soil model, soil N dynamics, organic fertilizer

Introduction

We present a novel modular crop growth simulation model 'Swap-Snomin-Lingra' composed of the water balance module of the SWAP model (Heinen, 2024), the soil organic matter module SNOMIN (Berghuijs 2024) and the LINGRA grass model (Schapendonk, 1998). The new model was especially designed for simulating specific conditions in Dutch grassland management. Grass in the Netherlands is produced mostly in the wetter soils, often below sea level, with high groundwater levels and with drainage canal systems ensuring the top soil layer is not completely saturated throughout the year. The SWAP model component with associated data sources is particularly suited for simulating these conditions. The Netherlands has a large animal sector and animal manure is an important input for intensively managed grassland. The SNOMIN model component can simulate mineral and organic nitrogen (N) dynamics in the soil and simulate N release from organic manures. The LINGRA crop component can simulate grass growth in response to weather, water availability and nitrogen. The Digital Future Farm (DFF) (van Evert, 2021) presents a modelling framework for coupling the components, allowing them to automatically exchange simulated variables between the components. Crop modeling can give insight in current status of crop and estimate the effect of different management (fertilizer application, mowing timing) choices. Swap-Snomin-Lingra gives insight in the interaction between soil water dynamics, organic fertilizer and SOM mineralization, grass N uptake and grass growth and environmental impact (N leaching). The new model was validated with two experimental datasets.

Materials and Methods

The 'Zode bemesting' experiment was with 3 cattle manure levels. The 'Amazing Grazing' experiment included destructive measurements at 4 timepoints each cut. In both experiments there were 3 locations, 3 years, 4-6 grass growing cycles per year (each ending with mowing) and 3 mineral fertilizer levels. The two experimental datasets contain measurements on biomass (kg dry matter ha^{-1}), N content of the biomass (%) and total N in biomass (kg N ha^{-1}). The Amazing Grazing dataset also contains measurements on groundwater level (cm below ground level).

In the DFF framework, modular soil-plant component models are set up as a standardized interaction between 5 components: a soil water component (in this application: SWAP), a soil nitrogen component (SNOMIN), a crop growth component (LINGRA), a meteo component (TipstarMTC) and a soil temperature component (TipstarSTC). The exchange between these components is limited to a couple of variables, including potential and actual (evapo)transpiration rates, nitrogen uptake rate, water fluxes between soil layers, LAI and root depth.

Results and Discussion

Included is the comparison between experimental observations and simulation output for N content of the biomass. Similar plots were made for biomass, total N in the biomass and groundwater level. As expected, the Swap-Snomin-Lingra model shows increasing N uptake with higher N application, roughly in accordance with measured levels. The simulated produced biomass has more deviance compared to the experiment observations. This might be due to the distinction between live and dead biomass, where the experimental data combine both but the simulation output gives only live biomass. Simulated groundwater level roughly follows observed trends, but it shows larger deviation from the observed groundwater level at lower levels than when groundwater depth is shallow.

Table 1. RMSE of compared variables in both datasets

	AmazingGrazing	**ZodeBemesting**
Biomass (kg dm ha$^{-1)}$	967	657
N in biomass (kg N ha^{-1})	29.26	31.08
N content (%)	0.75	0.76
Ground water level (cm below surface)	42.45	

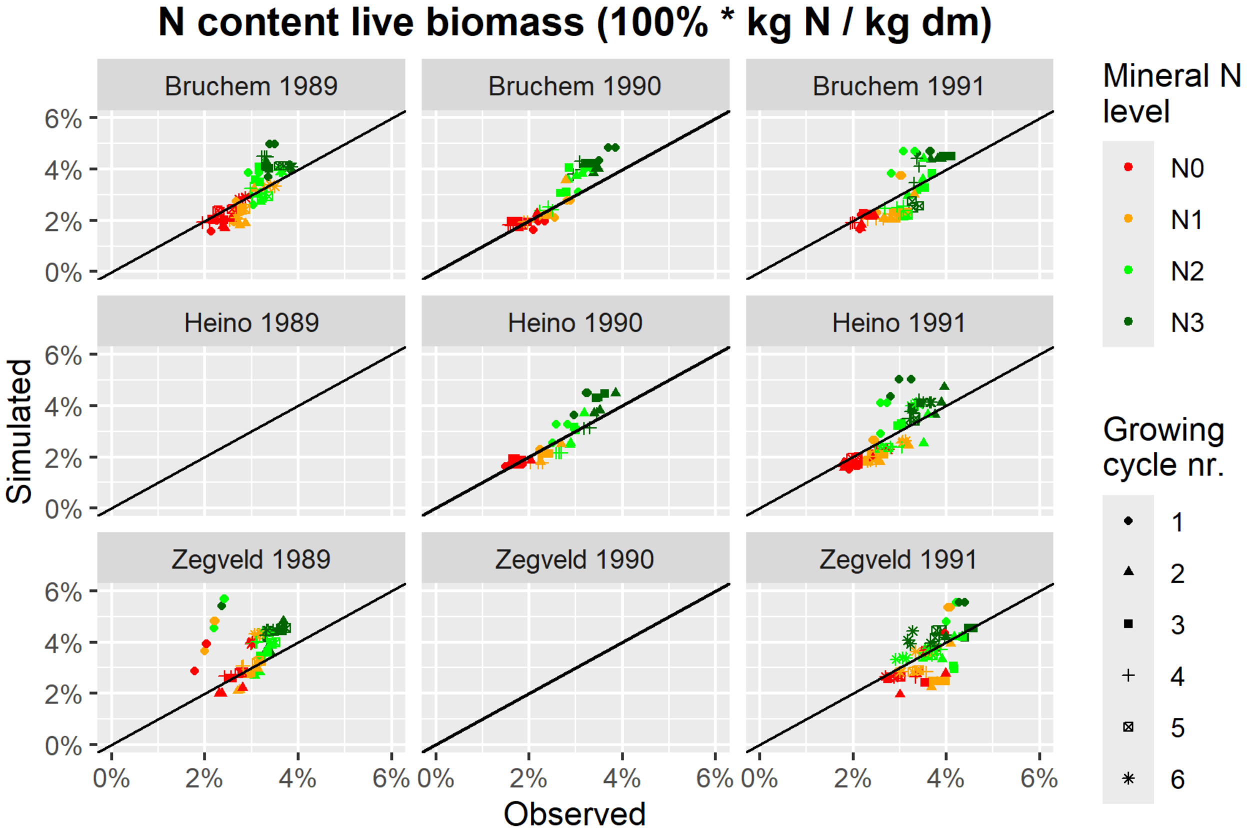

Figure 1. Simulated vs observed nitrogen content of the live biomass (kg N kg dm^{-1}) per location and year in the zodebemesting experiment.

Conclusions

The concept of a modularly designed crop growth simulation model with exchangeable components presents a powerful concept of model design tailored for specific conditions and building of a large knowledge base embedded in existing modules. Validation of Swap-Snomin-Lingra model simulations with observed biomass and observed nitrogen showed first promising results.

Acknowledgements

This study was commissioned and financed by the project “Assessment of synergies and tradeoffs - integrating data, models and scenarios across scales (MAST)” in the context of the Wageningen University & Research program "Circular and climate neutral society” supported by the Dutch Ministry of Agriculture, Fisheries, Food Security and Nature (LVVN) (project number KB-34-004-001).

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Methods to isolate contributions to crop growth of individual stressors and their interactions in agroforestry systems

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Keywords: agroforestry, multiple stressors, microclimatic gradients, SIMPLACE, model calibration

Silvoarable agroforestry, the integration of trees or shrubs into cropland, is increasingly promoted also in temperate regions to enhance biodiversity, carbon sequestration and reduce soil erosion (Veldkamp et al., 2023). Furthermore, it can have several benefits for crop production, potentially improving resilience in the face of extreme weather events (Dobhal et al., 2024). However, it is challenging to predict the influence of trees on crops growing nearby. Trees influence different biotic and abiotic crop stressors, and this influence varies with increasing distance from the trees (Jacobs et al., 2022) and throughout the growing season. The intensities of stressor exposure are expected to display gradients perpendicular to the tree rows (Figure 1), resulting in different relative stressor intensities at each distance from the tree row. Here, we explore methods to investigate how crop responses to irradiation, temperature, as well as water availability change with the distance from trees using statistical and process-based crop models.

First, statistical models that can consider temporal and, where needed, spatial autocorrelation are used to investigate to which degree the irradiation gradient (i.e. tree shade) is a predictor for the gradient in soil water availability and temperature. Second, a process-based crop model within SIMPLACE (Enders et al., 2023) based on Lintul 5 is calibrated using crop development and growth data as well as abiotic stressors measured at a large distance from the tree row or at a reference field without trees. A standardized calibration protocol is developed to make the method reproducible for different sites. Using this model, its performance in simulating crop growth closer to the tree when only the irradiation hitting the canopy, or only the soil water availability, or both are adapted to measured values close to the tree row are assessed. The model output can be compared to the observed crop growth using regression models like the ones described from the first methodological step. These methods can help to understand which (combination) of environmental gradients is most decisive for crop growth close to trees.

To avoid the need to model the water uptake by the tree roots explicitly, measured soil moisture data is assimilated into the process-based model. Furthermore, a model for the crop canopy temperature is included as crop canopy temperature results from a non-linear interaction of air temperature, irradiation, the plant water status, wind speed and atmospheric stability conditions. This allows assessing possible improvements in model predictive skill when this interactive effect is accounted for.

Later, the methods will be tested by using data from wheat and maize at two agroforestry sites in Germany where stressor exposure is monitored over time by measuring irradiation, soil moisture, wind speed, and crop canopy temperature. Crop responses are monitored by measuring phenological development and leaf area index over time as well as final biomass and grain yield. The results will support understanding whether crops close to trees respond to abiotic stressors in the same way as expected in sole cropping, i.e. trees mainly change the stressor exposure, or whether unique stressor responses resulting from the presence of the trees should be considered in agroforestry models.

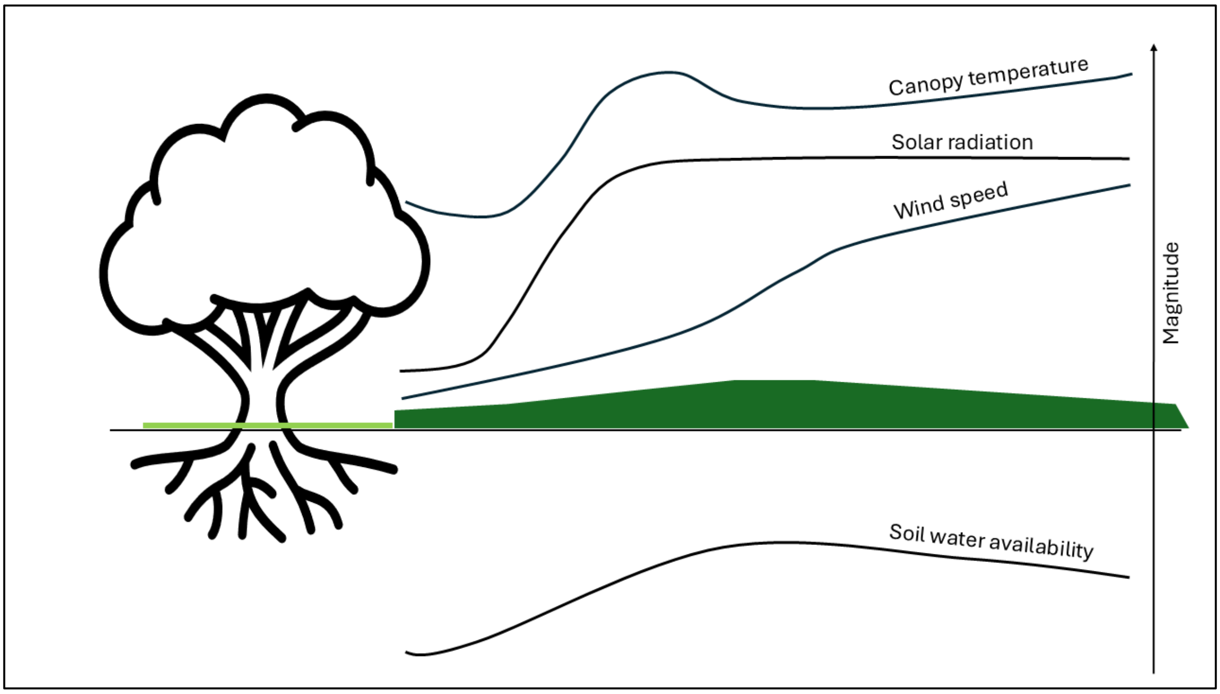

Figure 1. Hypothetical example of gradients of microclimatic variables, i.e. abiotic crop stressors perpendicular to tree rows. The shape of the gradients is based on available evidence and/or personal expectations. The gradients have no scale and no common zero point. Adapted from Jacobs et al., 2022.

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Disentangling environmental and structural drivers of evapotranspiration simulation errors in wheat of semi-arid and Mediterranean region

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Keywords: Evapotranspiration error; Wheat crop model; Wind speed; ET simulation method

Introduction

Accurate simulation of daily evapotranspiration (ET) is essential for assessing water stress and irrigation management in wheat. Previous multi-model ensemble studies have revealed a systematic underestimation of winter wheat ET and proposed preliminary explanations(Webber et al., 2025), but the environmental drivers of simulation errors remain unclear. This study investigates which factors shape ET simulation accuracy in semi-arid and Mediterranean wheat systems.

Materials and Methods

We analyzed daily ET from multi-model ensembles benchmarked against ET observation records in Bushland (Texas, USA) and Avignon (France). Simulation error was quantified as the difference between modeled and observed ET. Beyond error decomposition, we applied linear mixed-effects models to examine how environmental factors influence ET error across crop development stages and ET estimation methods.

Results and Discussion

Error decomposition revealed clear structural differences between rainfed and irrigated conditions: higher mean squared error (MSE) under irrigation was primarily driven by variance rather than systematic bias(Hodson et al., 2021). Mixed-effects modeling further showed that vapor pressure deficit (VPD) and wind speed are the dominant environmental drivers of ET error. We also labeled the simulation results based on the ET simulation method into three groups: results simulated using the ET0 method (ET0), results simulated using the Priestley-Taylor method for PET (PET_PT), and results simulated using other methods for PET (PET_other).Under rainfed conditions, ET errors were most sensitive to VPD during full canopy cover (ET0 and PET_Other slopes ≈ –0.87), weaker during senescence, and negligible at early vegetative stages. Wind speed effects peaked at early vegetative stages (e.g., PET_PT slope ≈ –0.43) but declined towards senescence. Under irrigation, both VPD and wind speed exerted stronger and more consistent negative influences. VPD sensitivity peaked at senescence (slopes < –1.2), while wind speed significantly reduced errors across all methods, particularly for PET_PT (–0.55 to –0.94). PET_PT-based simulations were least sensitive to VPD but most sensitive to wind speed, whereas ET0 and PET_Other were more strongly driven by VPD.

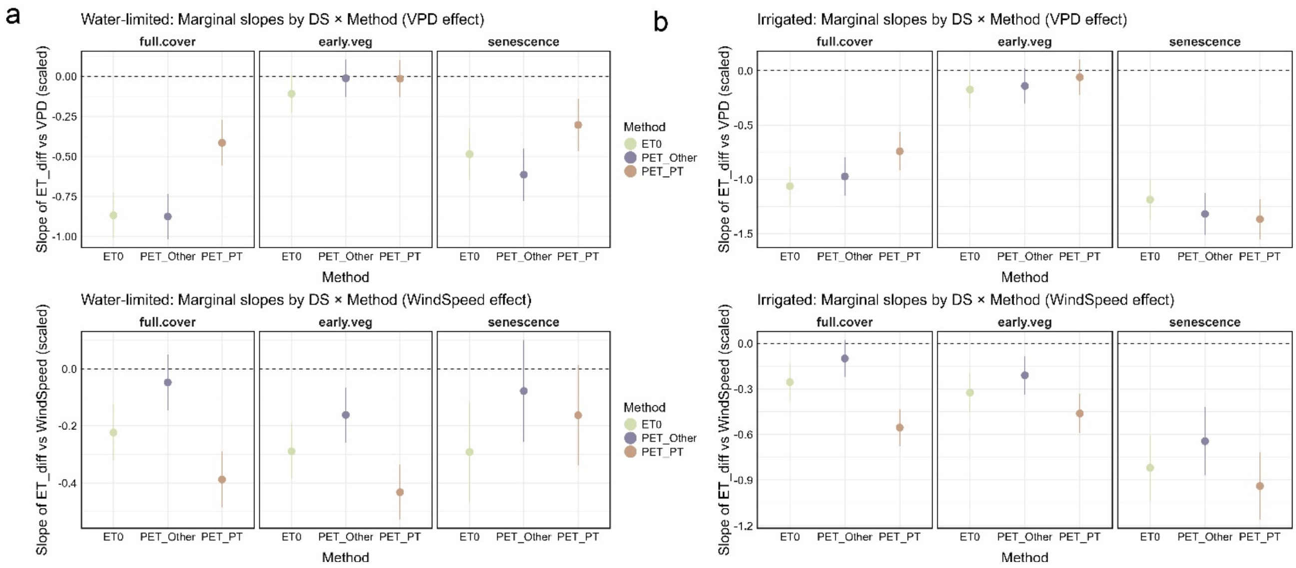

Figure 1. Marginal effects of vapor pressure deficit (VPD, top) and wind speed (bottom) on daily evapotranspiration (ET) simulation errors under a.rainfed (water-limited) conditions and b. irrigated conditions, estimated from linear mixed-effects models. Points represent slopes of ET error with respect to standardized VPD or wind speed (±95% CI), stratified by crop development stage

These findings indicate that the dominant error drivers shift from stomatal/soil-limited control under rainfed conditions to aerodynamic/atmospheric control under irrigation. The significant DS × Method × Environment interactions explain why model performance diverges under contrasting water regimes and emphasize the need to refine aerodynamic and stomatal regulation processes in crop models.

Conclusions

The magnitude and direction of wheat ET simulation errors are jointly shaped by crop development stage, ET estimation method, and atmospheric drivers, with distinct patterns under rainfed and irrigated management. Incorporating stage-specific aerodynamic and stomatal controls could improve model realism and reduce systematic ET underestimation.

Acknowledgements

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From metabolomics to models: predicting functional traits and water-use strategies for crop resilience

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Keywords: Machine-learning, Metabolism, leaves

Introduction

Plant species adopt contrasting ecological strategies ranging from fast-growing annual herbs to long-lived evergreen trees, reflected in traits such as leaf mass per area (LMA), carbohydrate storage, and stomatal conductance (g_{min}). The latter is a particularly critical trait under climate change, as it controls residual water loss when stomata are closed and thus strongly influences drought survival (Burlett et al., 2025). Since metabolites are the biochemical building blocks of plant traits, metabolomics provides a promising entry point for linking molecular processes with functional ecology (Dussarrat et al., 2022). However, the integration of metabolomic data into trait-based and modelling frameworks remains limited. Here, we combined non-targeted metabolomics, functional trait measurements, and machine-learning approaches to assess whether metabolic profiles can predict plant functional traits, including complex physiological traits such as g_{min}, and how these relationships may support modelling of plant strategies under climate stress.

Materials and Methods

A wide range of plant species was sampled in the Bordeaux area including trees, shrubs, and herbs (annuals and perennials) across angiosperms and gymnosperms. Fully developed leaves were collected at comparable phenological stages. Metabolites were extracted from 10 mg of lyophilized plant material using an ethanol fractionation protocol and profiled by UHPLC–LTQ-Orbitrap MS in negative ion mode. Raw data were processed in MS-DIAL v4.9, yielding 4725 curated features after QC correction. Annotation relied on in-house metabolite libraries and ClassyFire ontology. Leaf functional traits (LMA, leaf area, water content, stomatal area and density, g_{max}, g_{min}) were measured and used as prediction targets. Machine-learning models, consisting of Elastic-Net and LASSO Regression or classification, were trained to predict traits from metabolite profiles. Feature selection methods were used to identify key metabolic variables associated with each phenotype while adequate cross-validation and data splitting was used to reduce the risk of overfitting.

Results and Discussion

Trees displayed conservative metabolic strategies, with high investment in lignans, carbohydrates, and storage amino acids, while herbaceous plants, particularly annuals, exhibited metabolic profiles rich in TCA intermediates and nitrogen-rich amino acids, supporting rapid growth. Evergreen trees showed enrichment in glycosyl conjugates and prenol lipids, whereas deciduous species accumulated flavonoids and coumarins, reflecting possible seasonal shifts in defence allocation.

Machine-learning models successfully predicted multiple functional traits from the metabolomic data. They showed for example that species with low LMA accumulate primary metabolites that sustain rapid growth and metabolic activity, whereas high-LMA species are enriched in structural and defence-related compounds that enhance tissue density, protection, and resilience. Importantly even g_{min}, a complex physiological trait linked to leaf structure and cuticle composition, was predicted with good accuracy. This demonstrates that metabolome embed information linked to water-use strategies, offering a novel tool for modelling drought responses.

By linking metabolite fingerprints to traits underpinning resource use and climate resilience, our study highlights metabolomics as a bridge between omics-scale data and crop models. Predicting traits like $g_{min}$from metabolomic data can reduce reliance on labour-intensive physiological assays, could improve parametrization of ecophysiological models and could help identify resilient genotypes for breeding under climate change.

Conclusions

Our findings demonstrate that the building blocks of functional traits are encoded in metabolism and that metabolomic data, combined with machine learning, can robustly predict both simple and complex traits such as g_{min}. This approach offers a powerful addition to trait-based ecology and crop modelling, enabling more accurate integration of molecular level information into simulations of plant adaptation and resilience under global change.

Acknowledgments

This work received financial support from the Bordeaux University in the framework of the GPR Bordeaux Plant Sciences. This work was supported by the MetaboHUB infrastructure funded by the Agence Nationale de la Recherche under the France 2030 program (MetaboHUB ANR-11-INBS-0010 ; MetEx+ ANR-21-ESRE-0035; MetaboHUB (JVCE) ANR-24-INBS-0012) and the PHENOME (ANR-11-INBS-0012) project.

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Sensitivity and uncertainty analysis of WOFOST crop phenology parameters and simulation of Brassica napus for climate-resilient cultivar development

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Keywords: temperature response, calibration, cultivar specific, maturity group specific.

Introduction

Climate change is adversely impacting the production of food and oilseed crops (AAFC, 2025). An accurate prediction of plant development can help agronomists to evaluate the impact of different crop management practices and help plant breeders to predict cultivar performance in the target population of environments or help select robust cultivars for future target environments impacted by climate change.

The aim is to evaluate the WOFOST model prediction accuracy for three prediction problems faced by most breeding programs and defined in the following scenarios: the first scenario is a hold-out location scenario to simulate a known cultivar in an untested novel location, the second hold-out cultivar scenario simulates a new cultivar in a known test location using crop parameters calibrated with observations from cultivars belonging to a similar maturity group, and the third hold-out combined cultivar & location scenario simulates a new cultivar in an untested novel location. The obtained results will help to understand the possibility to simulate the two key plant developmental stages, flowering and maturity, for each of the defined scenarios.

Materials and Methods

In this spring oilseed rape (Brassica napus, canola) case-study, ten spring oilseed rape cultivars have been evaluated in ten different field trials. The ten cultivars have been selected carefully for their differences in phenology or more specifically time to flowering and time to maturity.

The WOFOST (WOrld FOod STudies, de Wit A. et al., 2019) simulation model is used to simulate the impact of different environments, exposed to different abiotic stresses, on the spring oilseed rape phenology. For the calibration of the crop phenological development model, we followed the 6-step protocol defined by Wallach et al. 2023. To determine the key input parameters involved in the simulation of crop development we are using a systematic approach for the study of the combined effect of all inputs on the output called uncertainty analysis and the study of the contributions of components to the uncertainty of the model called sensitivity analysis (Saltelli A. et al., 2010). The key crop parameters identified in the sensitivity analysis are then used for calibration of the WOFOST and Beta-Distribution Method (BDM, Zhou & Wang, 2018) adapted WOFOST models. To find the optimized parameter values for the identified key crop parameters, we performed a two-step approach. In the first step, a global optimization algorithm is used for finding the feasible value that minimizes the objective function over the entire feasible region. And in a second step the optimized parameters from the global optimization algorithm are used as the starting point for a local derivative-free optimization subplex algorithm.

For the evaluation of the model performance, all available observations for the same cultivar or for the same maturity group are used for the calibration of the identified key crop parameters. And ultimately, the model prediction accuracy is evaluated for the three most relevant prediction problems in plant breeding as defined in the introduction.

Results and Discussion

The performed sensitivity and uncertainty analysis is indicating that the oilseed rape phenology is mainly temperature driven, and two crop parameters (TSUM1 & TSUM2) have been identified explaining most of the variability in the crop model output. As illustrated in the Top Marginal Variance (TMV) composition plot for the evaluation of the parameter sensitivity changes over time during the crop growing period (Figure 1).

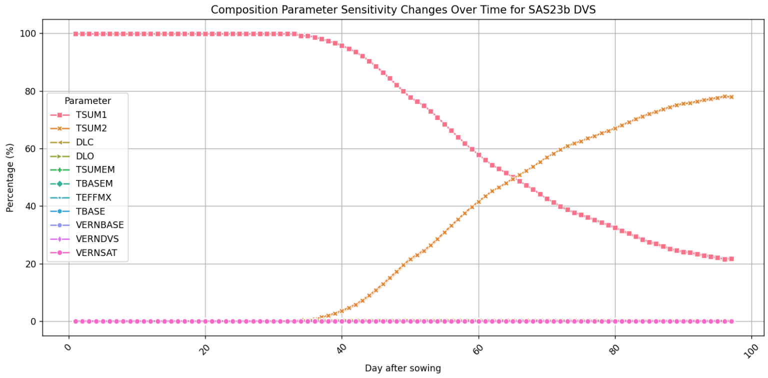

Figure 1. Plot daily TMV composition for evaluation of parameter sensitivity changes over time during the crop growing period using SAS23b weather data. For WOFOST model (IDSL = 0) only parameters TSUM1 & TSUM2 are sensitive, all other non-sensitive parameters stay close to zero.

The WOFOST model performance evaluation results confirm a good performance for the DOA simulation with a RMSE value of 4 days. However, a moderate estimate was obtained for DOM with a minimum RMSE of 12 days. Improved prediction accuracy for the predicted DOA and DOM dates can be obtained when a well-represented selection of locations is included in the training set for calibration (HO_2024, Table 1).

Table 1. Overview of RMSE and Willmott refined index of agreement calculations obtained per scenario for the best and the worst DOA simulations.

Scenario	Training set	Average data points	↓ Min RMSE	Max RMSE	↑ Max Willmott ref.	Min Willmott ref.
performance	all observations	41	2.57	8.15	0.89	0.56
hold-out cultivar	cultivar hold-out (HO_entry)	57	9.12	18.32	0.48	-0.26
hold-out cultivar	cultivar hold-out Canada only (HO_entry_CAN)	48	9.38	18.18	0.26	-0.30
hold-out location	year 2024 hold-out (HO_2024)	18	7.26	12.50	0.50	-0.33
hold-out location	20% locations hold-out (HO_20%)	22	9.12	18.43	0.48	-0.27
hold-out location	location hold-out Canada only (HO_location_CAN)	14	10.38	14.27	-0.17	-0.76
hold-out cult. & loc.	combination cultivar location hold-out Canada only	42	9.00	18.75	-0.89	-1.00

Conclusions

The proposed systematic approach for uncertainty and sensitivity analysis highlighted the critical role of temperature in driving the phenological development of spring oilseed rape, as modeled by WOFOST. Cultivar- and maturity group-specific calibrations showed promise, especially when the training dataset used for calibration is aligned with environmental variability of the target environments. DOM predictions are expected to be more challenging due to the complexity of genotype × environment interactions. The potential benefits from crop developmental stage-specific temperature functions and possible influence of additional variables warrant further validation and may offer opportunities to improve the DOM simulations. Future research should explore advanced calibration techniques, including Bayesian and machine learning approaches, to enhance model reliability and scalability.

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Ozone impacts on wheat yields and soil carbon stocks: insights from crop modeling

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Keywords: Farquhar, stomatal conductance, crop physiology, biomass

Introduction

Wheat is one of the world's major staple crops, providing much of the global calorie intake. However, it is highly sensitive to tropospheric ozone (O_3), a secondary pollutant formed from nitrogen oxides, volatile organic compounds, and other precursors. O_3 exposure reduces primary production and crop yields, yet its impacts on soil organic carbon stocks remain poorly studied, and most climate models omit O_3 effects, introducing biases in future projections.

Materials and Methods

The CERES-O3 cropping system model (Lebard, 2005), an extension of CERES-EGC (Gabrielle et al., 2006), simulates crop development and associated fluxes of carbon, water, and energy using meteorological forcing data and information on agricultural management practices (e.g., crop rotations, residue management, organic inputs). It integrates Farquhar's photosynthesis equations (Farquhar et al., 1980) as well as equations accounting for ozone impacts on photosynthetic assimilation, and hence on yields and biomass production. O_3 impacts are represented through a flux-based Phytotoxic Ozone Dose with an 8 nmol m^{-2} s^{-1} threshold (POD8), computed from hourly modeled stomatal O_3 flux and accumulated over the growing season (mmol m^{-2} leaf). POD8 then drives reductions in photosynthetic capacity (e.g., Vcmax/Jmax) and earlier senescence. Unlike most existing studies using crop models to assess O_3 impacts on yields only, our flux-coupled framework extends the impact assessment of soil carbon dynamics, a link rarely quantified in crop–climate assessments.

Model calibration relied on a 2009 field experiment conducted in Grignon, France, where two wheat varieties were exposed to different O_3 concentrations generated at varying distances from a fumigation ramp. Observed O_3 levels served as treatments to assess physiological responses, which were then extrapolated to yields, biomass, and soil carbon pools. Model validation was extended to several years by using wheat yield and biomass data from the same site, with ambient O_3 concentrations and management practices retrieved from the ICOS carbon portal.

Results and Discussion

Simulations suggest that O_3 reduces carboxylation, electron transport, and stomatal conductance, while increasing dark respiration and accelerating senescence. These processes decrease assimilation, biomass accumulation (≈ 20%), and yield (≈ 11%). In addition, long-term simulations (10 years) indicate a decline in soil organic carbon stocks under elevated O_3.

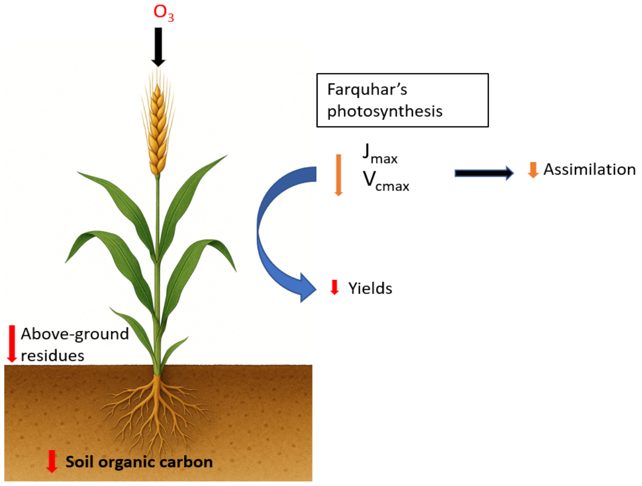

Figure 1. Impacts of ozone on plant production and soil organic carbon stocks

Conclusions

Overall, tropospheric ozone (O_3) poses a dual threat — not only by reducing wheat yields, thereby compromising food security, but also by weakening the capacity of agroecosystems to store carbon, and thus our ability to mitigate climate change. Our findings underscore the need to integrate O_3 effects into cropping system models at larger scales to better assess yield losses and soil carbon decline in European wheat systems, both under current conditions and across future scenarios of climate change and air pollution.

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Evaluating the impact of temporal resolution in a crop model for garlic (*Allium sativum*)

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Keywords: temporal resolution, garlic, crop modeling, Cropbox

Introduction

Crop simulation models are widely used to predict crop growth and yield under varying environmental conditions. However, most studies have relied on fixed temporal resolutions, often at daily or sub-daily scales, but rarely with systematic evaluation of how alternative temporal scales affect prediction accuracy and computational demand. Since physiological processes such as photosynthesis and carbon assimilation are nonlinear, coarse temporal resolution may lead to biased estimates. Despite recognition of these issues, few studies have quantified the biases arising from different temporal resolutions and their implications for model performance. This study addresses this gap by testing multiple temporal resolutions in a garlic model implemented within the Cropbox framework.

Materials and Methods

Hourly weather data were obtained for the study site and period. These data were resampled into multiple temporal resolutions ranging from 1 hour to 168 hours using Julia (TimeSeries.jl). Meteorological variables were aggregated by mean or by sum. Missing values, if present, were interpolated from daily means to preserve continuity.

Simulations were conducted using the garlic crop model implemented in the Cropbox framework (Hsiao et al., 2019, Yun et al., 2022). Cropbox provides explicit specification of physical units for all variables, allowing flexible adjustment of simulation time steps via configuration (Yun & Kim, 2023). For each resampled weather dataset, the model was initialized at the first timestamp of the series, and the simulation time step was set to match the aggregation interval.

Model outputs included dry yield, carbon assimilation, leaf appearance, leaf area, and bulb mass. Simulation results from each temporal resolution were compared against the baseline 1-hour simulation using RMSE and MAE. Computational cost was quantified by measuring model runtime from initialization to completion in a specified computing environment (Mac mini, 2023; Apple M2 chip; 16 GB RAM; macOS 14).

The overall workflow of the experiment, from input data to trade-off evaluation between accuracy and computational cost, is illustrated in **Figure 1**.

Results and Discussion

Coarser temporal resolutions tended to overestimate carbon assimilation due to the nonlinear light-response of photosynthesis and accumulated numerical integration errors, especially when diurnal variation was smoothed.

In contrast, morphological traits such as leaf area and leaf appearance were relatively insensitive to resolution, as they are governed by thermal time functions, namely growing degree days (GDD) and the Beta function, which robustly captured temperature variation regardless of step size. This underscores the differing sensitivity of radiation-driven growth processes vs. temperature-driven morphological processes.

Thus, while radiation processes were more sensitive to changes in temporal resolution and temperature processes remained relatively stable, larger time steps substantially reduced computational cost, ultimately confirming the inevitable trade-off between accuracy and efficiency.

Conclusions

This study highlights the crucial role of temporal resolution in crop modeling. While hourly data ensure higher accuracy, they demand greater computational resources. Coarser resolutions reduce cost but can introduce significant biases in carbon dynamics and stress responses. By quantifying both prediction accuracy and computational demand, this research can provide practical guidelines for selecting appropriate temporal resolutions in crop modeling applications.

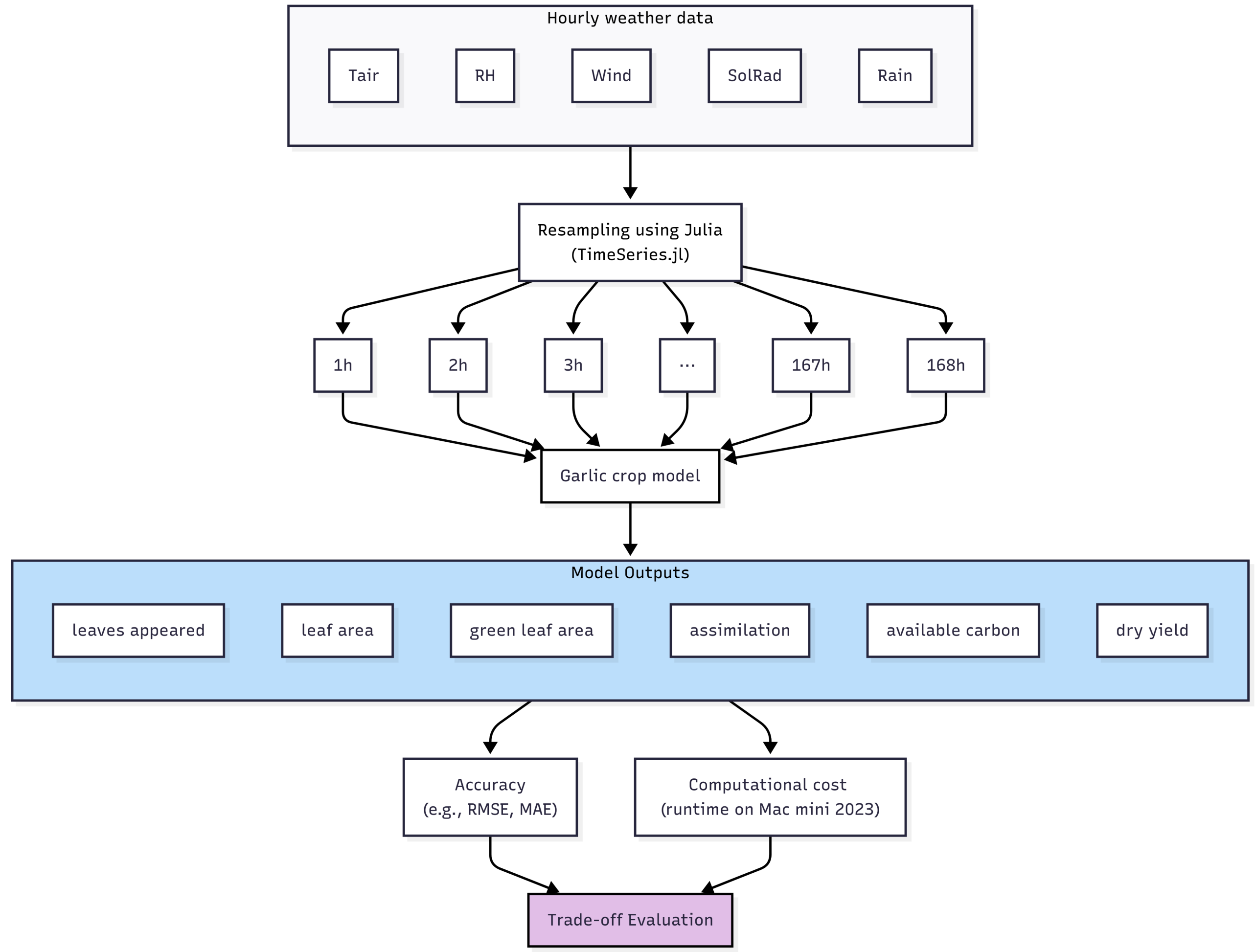

Figure 1. Workflow for evaluating temporal resolution in the garlic model

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Implementing crop heat stress effects in the Community Land Model (CLM5)

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Introduction

Global land surface models (LSMs) describe vegetation growth in detail, with a photosynthesis module allocating the carbon and nitrogen concentrations to each part of the plant (leaves, stem, roots), while simulating the energy use and plant hydraulics and connecting fluxes to the environment (soil, atmosphere) of the plants. Crop modules to simulate global yield for different crops are one of the most recently added components to LSMs (Fisher and Koven, 2020). LSMs usually take more a generic approach compared to process-based agronomy models, which were mainly developed for field-scale applications and model detailed growth stages, different stresses and various management practices. The coarse spatial resolutions (0.5-2.0◦ lat/lon) and lack of detailed crop information at the global level, make crop implementations in LSMs challenging, resulting in simplifications of crop growth stages and land management practices (Levis, 2014). However, the need for more accurate representation of crops on a global scale increases with increasing threats to global production, such as climate extremes. As heatwaves are already becoming more frequent, we present some model implementations to target heat stress effects on crop production and evaluate them for the some major crops in the Community Land Model (CLM5).

Materials and Methods

A new module is introduced for this study to the CTSM5.2 code, called *CropHeatStress*. This module contains several functions to keep track of heat stress days during the crop growth phase. Several implementations and parameterizations are assessed to target the leaf area index (LAI) or crop grain production directly. To define heat stress thresholds, the mean vegetation daytime temperature is used ($T_{veg,day}$), which is considered to be a more direct indicator of heat stress compared to air temperature (Siebert et al., 2014), and also includes the reduced impact for irrigated crops due to leaf cooling.

The main aim of this study is to improve the crop representation on the global level by including yield sensitivity to heat stress, hence a global analysis approach is used here. The model adaptations are evaluated in terms of i) model impact and ii) large-scale model accuracy. Model adaptations are based on similar approaches used in process-based agronomy models. The yield simulations are compared with gridded yield data and for the different IPCC regions during the period of 1980-2014.

Results and Discussion

Research is still ongoing, but some preliminary findings can already be presented in this abstract. First of all, using vegetation temperature to define critical temperature thresholds results in reduced effects of heat stress for irrigated crops compared to rainfed crops over the same region, as expected. This also shows the strong link between drought and heat stress of vegetation, as rainfed crops often do not have the capacity of self-cooling due to limited soil water availability during warm periods. Several test simulations were done to apply heat stress in different ways, either to accelerate leaf senescence and reduce grain production, or alternatively, only reduce the carbon allocation to grains during the grain production phase in CLM5. Preliminary results suggest that targeting the grain production directly gives a better accuracy compared to the indirect measure of accelerating LAI senescence (figure 1), however this experiment shows also little change over most regions. The current tests only consider an absolute critical temperature value, which results in overprediction of stress in mid-latitudes and an underrepresentation of stress in high latitudes. Ongoing model implementations include testing other stress functions and including a climatology-based critical temperature threshold rather than absolute temperature values, with the aim of improving the temperature stress representation globally.

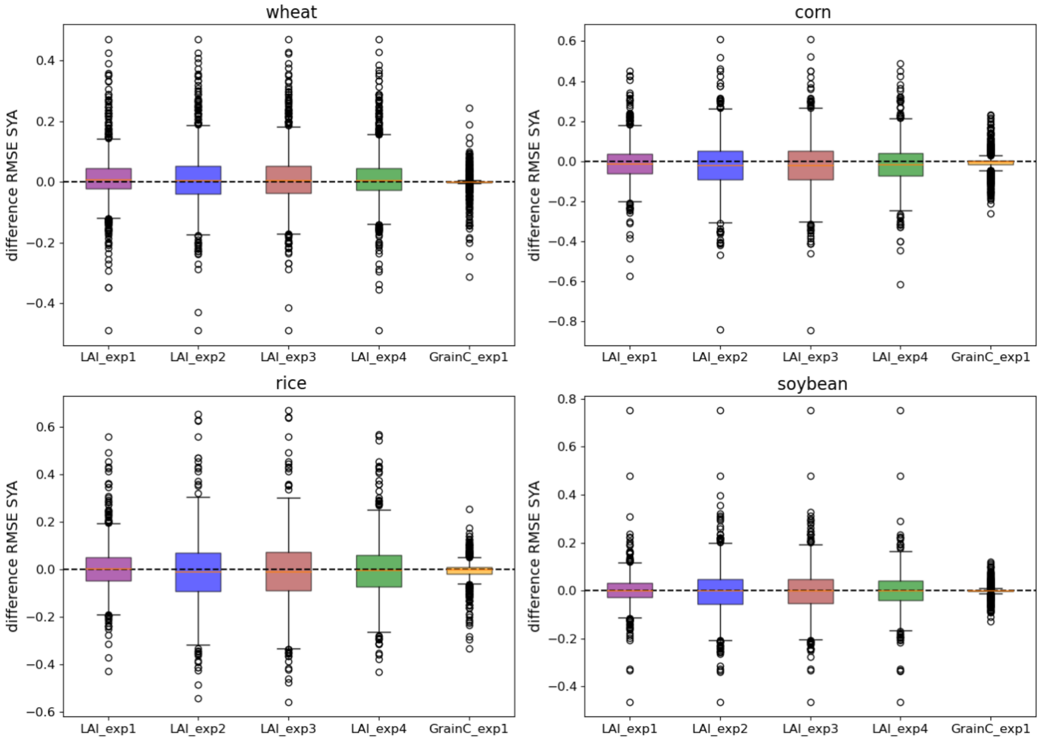

Figure 1. Difference between the Root Mean Square Error (RMSE) of CLM experiment standard yield anomalies (YSA (-)) and the CLM control run, in which the RMSE for each experiment and control run is calculated with the Earthstat-FAO gridded annual yield dataset (also used in Lombardozzi et al., 2020). Negative values indicate the experiment had a lower RMSE with the reference data, and thus a higher accuracy, compared to the control run.

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Interpretable machine learning for explaining wheat and maize yields from high-resolution farm- and plot-level observations

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Keywords extreme gradient boosting, random forest, explainable AI, feature importance, crop modelling

Introduction

Understanding the drivers of agricultural yields is critical for ensuring food security in the face of climate change, shifting land-use pressures and consumer demands. The growing availability of high-resolution data has created new opportunities for applying machine learning (ML) to this challenge (van Klompenburg et al., 2020). Despite not modelling biophysical processes, ML approaches have often achieved higher predictive accuracy than process-based biophysical models. At the same time, concerns remain about the limited interpretability of many ML models. Recent advances in interpretable ML, including SHapley Additive exPlanations (SHAP; Lundberg and Lee, 2017), provide ways to trace model predictions back to underlying drivers and reveal nonlinear relationships that are difficult to capture with traditional methods. This "explainable ML" is gaining traction in agronomic research (e.g. Tamayo-Vera et al., 2025).

Along with methodological advances, data availability also shapes how ML can be applied in studying yields. Yield modeling often relies on field trials, or aggregated regional data (e.g. Lischeid et al., 2022). While field-trial data minimize measurement error, they do not capture actual farmer behavior also shaped by market conditions and coordination issues. In this study, we assess the potential of machine learning to analyze and predict yield variation in two major crops – winter wheat and maize – using observational Austrian farm- and plot-level panel data covering 2015-2023. Our objectives are (1) to evaluate the out-of-group predictive performance of several commonly used ML algorithms, and (2) to identify which biophysical and management features contribute most to predicted yield variability.

Materials and Methods

We fit four tuned ML models – two regression-based (Elastic Net; Multivariate Adaptive Regression Splines, MARS) and two tree-based (Random Forest (RF), Extreme Gradient Boosting (XGB)). Farm yields and management data (expenditures on pesticides and fertilizers, livestock density, plus binary indicators for organic farming and irrigation) were obtained from the Farm Accountancy Data Network (FADN). From hourly INCA weather rasters (Haiden et al., 2011), we extracted plot-level monthly summaries of temperature (minimum, maximum, average), precipitation sum, and maximum wind speed using plot geometries from the Integrated Accounting and Control System (IACS). The plot-level soil contents of sand, silt, clay, organic matter, and lime, together with soil pH, were obtained from the 1x1 km grid "ebod2". The analysis was conducted at three aggregation levels: (i) farms with only a single plot of wheat or maize (*single plots*), (ii) all plots considered individually (*all plots*), and (iii) farm-level area-weighted averages across multiple plots (*weighted averages*) to compare model performance across different spatial scales. We tested three sets of explanatory features: (i) management, (ii) biophysical (weather, soil, topography), and (iii) all features combined. We applied SHAP to quantify global variable importance and explore variable-specific response patterns in yield predictions.

Results and Discussion

Across 72 model specifications, wheat yields were predicted more accurately than maize yields, with best-performing models yielding R^2 values of 0.57 for wheat and 0.38 for maize. Models using combined biophysical and management features consistently outperformed those using only management or only biophysical features. Predictive performance was best at farm-level aggregation for wheat, but plot-level aggregation for maize. Among algorithms, tree-based methods (XGB and RF) generally outperformed regression-based models across crops and aggregation levels.

SHAP analyses highlighted clear differences in yield drivers (Figure 2). Wheat yields were strongly shaped by management practices, with pesticide application, organic farming status, and livestock density among the top predictors. Maize yields, in contrast, were more sensitive to meteorological and soil factors, particularly summer rainfall, maximum temperatures, and soil texture. Elevation and soil texture, particularly silt content, were important for both crops, showing nonlinear yield responses — for instance, an S-shaped effect of silt, inverted U-shaped effects of pesticide expenditure, and rainfall and temperature thresholds beyond which maize yields declined. Seasonality was also important: maize yields depended heavily on summer weather extremes, whereas wheat yields were influenced by winter vapor pressure, spring rainfall, and early-summer soil moisture.

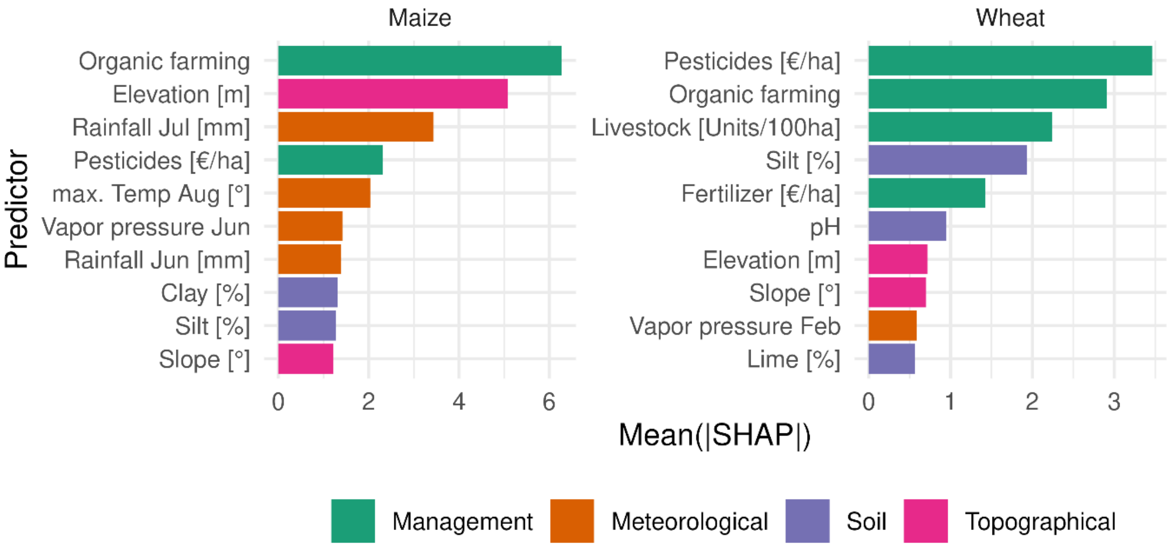

Figure 2: SHAP importance plots of the ten most important features for maize and winter wheat

Conclusions

Machine learning models, particularly tree-based methods, provided robust out-of-group predictive performance, with wheat yields generally more predictable than maize yields. Interpretable ML analyses indicated that management variables play a central role in explaining wheat yield variation, whereas maize yields are more strongly influenced by weather and soil. Importantly, SHAP analyses revealed nonlinearities and threshold effects that point to yield responses that are not proportional to inputs or weather conditions, and thus highlight critical tipping points where small changes in management or weather can have large impacts. These results highlight the potential of ML approaches not only to enhance yield prediction but also to generate insights into the relative importance of different yield determinants across crops.

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Implementation and comparison of grapevine phenology models (CF and DTS) using the Cropbox framework

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Keywords: phenology, simulation, Cropbox, Julia, process-based model

Introduction

Accurate prediction of grapevine phenology is critical for optimizing vineyard management, especially under changing climatic conditions. Process-based phenology models provide a mechanistic understanding of development stages and are widely used for decision support in perennial crops. This study implements two process-based models, the Chilling and forcing model (CF) (Cesaraccio et al., 2004) and Days Transformed to Standard temperature (DTS) (Ono & Konno, 1999), using the Cropbox framework implemented in the Julia programming language. Cropbox offers a declarative modeling interface that simplifies the development and comparison of crop models, supporting modular and structured specification of physiological processes (Yun & Kim, 2023).

The primary goal is to evaluate and compare the performance of the CF and DTS models for predicting grapevine flowering dates across cultivars and regions in Korea. A simple ensemble model, combining CF and DTS predictions, was also tested as a preliminary step(Yun et al., 2017). The central focus, however, is to demonstrate how the Cropbox framework enables systematic and flexible analysis of process-based phenology. A schematic overview of the modeling workflow is presented in Figure 1.

Materials and Methods

The analysis was conducted for two grapevine cultivars: Campbell Early (*Vitis labrusca* × *Vitis vinifera*) and Kyoho (*Vitis vinifera*), across three major cultivation sites in South Korea: Naju, Okcheon, and Jinju. For each cultivar–site combination, observed flowering dates (full bloom) and daily mean temperatures were collected from 1997 to 2024, with the number of years varying by data availability. The CF and DTS models were implemented in Julia using the Cropbox framework. Predictive performance of CF, DTS, and their simple average ensemble was evaluated against observed flowering dates using root mean square error (RMSE).

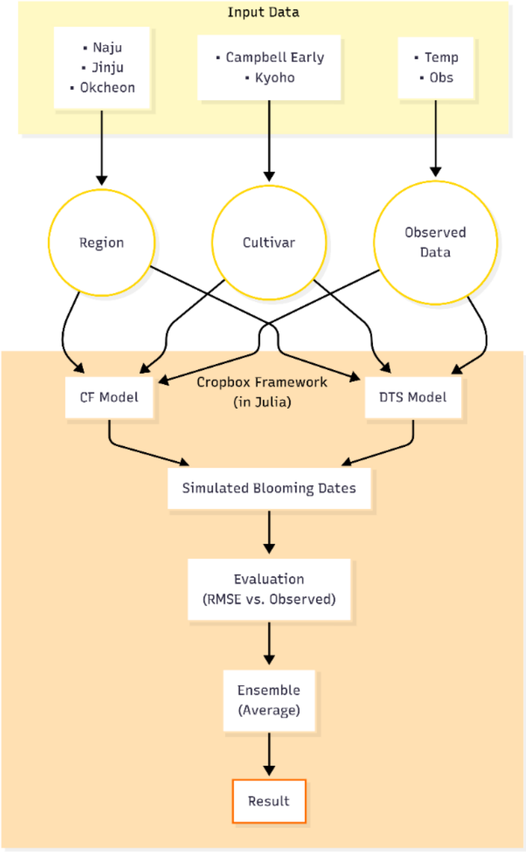
Results and Discussion

The CF model generally outperformed the DTS model in terms of RMSE across most combinations. Ensemble predictions consistently fell between the CF and DTS values and never produced the worst performance. However, the ensemble rarely surpassed the best-performing individual model. Campbell Early showed more consistent responses to temperature signals than Kyoho, suggesting cultivar-specific sensitivity. Differences in model performance across regions suggest a potential influence of local climate variations or observation uncertainty.

Conclusions

This study demonstrates the effectiveness of the Cropbox framework in implementing and comparing phenology models for grapevine flowering. While the simple ensemble of CF and DTS models showed moderate error reduction in some cases, its benefit was not consistently superior to that of the individual models. Future work will explore broader ensembles that include additional phenology models, building on previous multi-model ensemble studies. Ultimately, this research aims to construct a robust platform for grapevine phenology modeling capable of integrating diverse approaches and adapting to future climate variability.

Figure 3. Schematic diagram of the proposed phenology modeling workflow using the Cropbox framework.



Acknowledgements

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Model-based identification of physiological traits to improve yield of irrigated maize

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Keywords: crop modeling, breeding, phenological traits, genotype-by-environment interaction, irrigated systems

Introduction

Among strategies to increase yield potential, modifying crop physiological traits to develop improved genotypes is a promising strategy (Asseng et al., 2019). **Identifying traits that contribute to possible yield increases** is an important step in breeding high-performing cultivars. While crop simulation models have been effective in evaluating such traits under diverse environments, most applications have focused on water-limited conditions and assumed a non-limiting nitrogen supply (e.g. Xiao et al., 2020). This leaves a critical gap for irrigated systems, where trait performance interacts with nitrogen dynamics. To address this gap, we utilized the SSM-iCrop model to identify and prioritize physiological traits that can enhance irrigated maize yields in four major maize-growing sites in Iran.

Materials and Methods

The SSM-iCrop model (Soltani et al., 2013) was parameterized and evaluated using multi-environment data (2001–2022), showing nRMSE values of 6–23% and correlations of 0.80–0.98 for key traits, indicating satisfactory performance under diverse nitrogen scenarios. For each study site, daily weather data from 2001 to 2022, including minimum and maximum temperature, precipitation, and sunshine duration, were obtained from the Iran meteorological organization. Site-specific soil information was extracted from the HC27 soil database. Crop management practices were defined according to regional agronomic recommendations. Irrigation was automatically applied when 45% of available soil water had been depleted to avoid water stress during the growing season. Nitrogen management was adjusted by an automated algorithm to define site-specific optimal strategies, which were then fixed and applied across all years.

To explore genetic improvement, 53 genotype-specific parameters in SSM-iCrop were screened for sensitivity, and traits with consistent positive yield effects were selected for in-silico modification. The modified trait values reflected the observed genetic variation reported in previous studies. Yield responses of single-trait genotypes were assessed across environments (2008–2022) relative to a reference cultivar, providing a basis for identifying traits with the most significant potential to raise irrigated grain maize yields.

Results and Discussion

Accelerated leaf area expansion (PLAPOW) was the most influential trait, resulting in a 20% yield improvement across sites (Fig. 1). Faster canopy closure enhanced radiation interception and early N uptake, confirming the central role of early vigor in irrigated maize (Trachsel et al., 2017).

Extending vegetative (bdEMREJU) and grain-filling duration (bdSILPM) ranked second, raising yields by 17% (Fig. 1). Longer assimilate deposition supported higher kernel weight, consistent with evidence that grain filling duration is a key determinant of maize yield potential (Li et al., 2020). However, practical constraints such as fixed cropping calendars may limit its applicability.

Increasing radiation use efficiency (RUE) and the slope of the harvest index (PDHI) ranked third in importance, reflecting 6 to 10% yield improvement across sites. Their effects were most pronounced in short and medium-season environments, aligning with earlier findings that improved light conversion efficiency and assimilate partitioning remain viable targets for yield improvement.

Nitrogen-related traits showed minor but significant yield gains (<3%). Among the nitrogen-related traits investigated, the maximum rate of nitrogen uptake (MXNUP) made the most substantial positive contribution to yield, promoting greater leaf area at silking, increasing post-silking radiation interception, and enhancing grain filling capacity (Fig. 1).

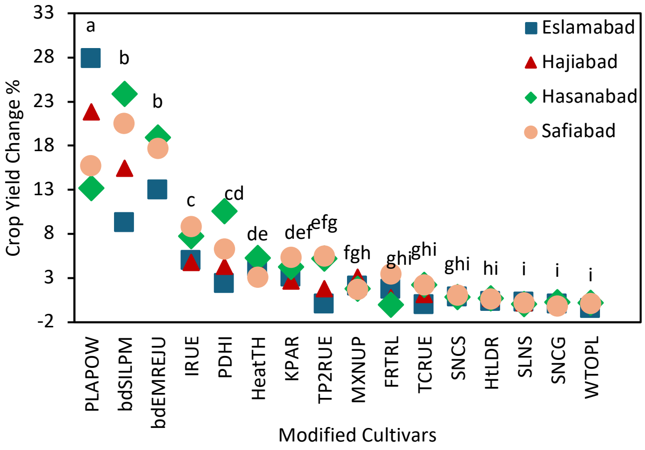

Figure 1. Percentage change in crop yield of the in silico genotype across study sites during 2008–2022. Letters indicate statistical groupings; genotypes sharing a letter do not differ significantly according to LSD test at P = 0.05. Model parameters modified in SSM-iCrop included PLAPOW (leaf area expansion exponent), bdSILPM (days silking to maturity), bdEMREJU (days emergence to juvenile), IRUE (radiation-use efficiency), PDHI (slope of harvest index increase during grain filling), HeatTH (critical maximum temperature for leaf destruction), KPAR (light extinction coefficient), TP2RUE (upper optimum temperature for dry matter production), TCRUE (upper ceiling temperature for dry matter production), MXNUP (maximum N uptake rate), FRTRL (initial crop mass for seed growth), SNCS (N in senesced stems), SLNS (N in senesced leaves), SNCG (N in green stems), HtLDR (leaf death rate by heat shock), and WTOPL (crop mass threshold for leaf partitioning).

Conclusions

In conclusion, trait effectiveness varied across environments due to strong genotype-by-environment interactions. Considering the challenges of extending the growing period owing to cropping systems constraints, accelerated leaf area development in grain maize is the most promising trait for achieving higher yields in irrigated conditions. These findings provide novel insights into potential breeding targets for irrigated grain maize under the growth conditions of Iran and similar arid and semi-arid production environments.

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How does waterlogging contribute to yield losses, and can it be quantified?

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Keywords: Remote sensing, MONICA, Edge-Otsu, Time Under Anoxia, Critical Oxygen Content

Introduction

Waterlogging (WL) affects 10–12% of global cropland (Bailey-Serres et al., 2012). Most studies rely on field data and point-scale models, which don't fully capture WL dynamics (Garcia-Vila et al., 2025; Nóia-Júnior et al., 2025). Remote sensing (RS), especially SAR and multispectral data, enables large-scale monitoring. This study validates RS methods for estimating WL-related yield losses in Germany and integrates them into a crop model to improve impact assessment.

Materials and Methods

Sentinel-1 SAR and Sentinel-2 MSI imagery (Copernicus program, ESA) were pre-processed using SNAP, Google Earth Engine, and Python. Study areas included Bremen, Brandenburg, and Bavaria. WL detection combined edge-based Otsu thresholding of SAR backscatter (< -18 dB), Gamma distribution fitting, and Markov Random Field smoothing to ensure spatial and temporal consistency. RS-derived WL masks were merged with crop maps and used as oxygen deficit (OD) forcing in the MONICA crop model (Nendel et al., 2011). MONICA represents WL stress through Critical Oxygen Content (COC) and Time Under Anoxia (TUA) thresholds, enabling yield simulations under WL conditions.

Results and Discussion

RS(A-C) and MONICA(D-F) consistently identified WL in low-lying areas, in line with the DEM (Figure 1). Their overlay showed strong spatial agreement, with WL stress concentrated in depressions. MONICA simulations indicated yield reductions of 21.9%, from 4234.6 to 3538.8 kg ha^{-1}, consistent with earlier reports (Zaidi et al., 2007; Herzog et al., 2016). While MONICA captures oxygen stress processes, its point-based nature restricts spatial coverage. RS, particularly SAR, improves detection of WL extent and severity, making it a valuable complement to process-based models.

Conclusions

WL poses a significant risk to crop productivity. Integrating RS-based WL monitoring with MONICA simulations enhances yield impact assessments and supports adaptation strategies under increasing extreme rainfall.

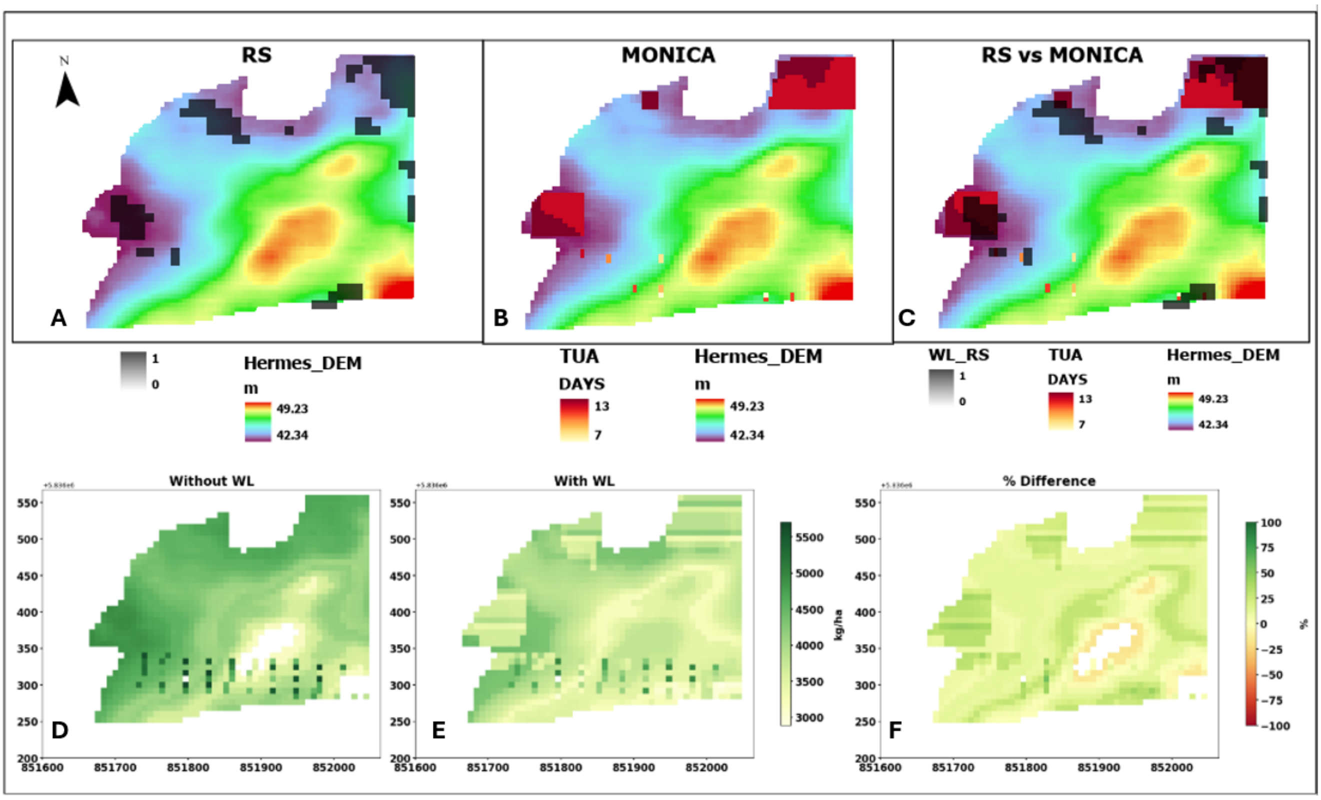

Figure 1.Comparison of WL detection and MONICA yield simulations **A**: RS-derived WL distribution **B**: WL stress simulated with MONICA (TUA) **C**: RS vs MONICA overlap **D**: With WL (kg/ha) **E**: Without WL (kg/ha) **F**: Relative yield difference (%).

Acknowledgements

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Evaluation of oryza2000 model in simulating anthesis and maturity dates of rice varieties in multi-locations in Bangladesh

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Keywords: SIMPLACE, sensitivity analysis, Morris scanning, temperature, uncertainty

Introduction

Accurate simulation of phenological stage is crucial in the application of crop growth models to predict eco-physiological and yield processes. ORYZA2000 (Bouman et al., 2001) is the most widespread crop model for simulating rice growth in different rice cropping systems where the phenological output is driven mainly by temperature and by eight crop parameters. However, significant spatial variability in climatic conditions, along with the cultivation of diverse rice varieties, introduce substantial uncertainty in model applications. Determination of crop phenological parameters are important for the simulation of other crop growth processes and for modeling upscale.

Materials and Methods

We integrated the ORYZA2000v2v13 model to the SIMPLACE modelling framework then investigated model sensitivity and performance in predicting phenological stages in Bangladesh which is one of the top rice producers worldwide. The field measured data includes dates of anthesis and maturity of 20 rice varieties grown over 3 seasons (2020–2022) and 4 locations (Cumilla, Mymensingh, Rangpur, and Sunamganj). The Morris and Extended FAST methods were used to perform the sensitivity analysis of different phenological crop parameters in simulating anthesis and maturity dates. Variety-specific model calibration was carried out based on the observed anthesis and maturity dates in Cumilla in 2020 then the modeling validation was performed for the data from remaining seasons and locations.

Results and Discussion

The observed anthesis (and maturity dates) varied among varieties, locations, and seasons which could be explained due to the differences in sowing and transplanting dates as well as the difference in local temperature and daylength. Sensitivity analysis using the Morris and Extended FAST methods revealed that the parameter cDVRP (development rate during panicle development, °Cd^{-1}) significantly influenced anthesis prediction, with total effect (μ^*) and interaction effect (σ) values of 55 and 59 days, respectively. Similarly, cDVRJ (development rate during the juvenile phase, °Cd^{-1}) had even higher sensitivity, with $\mu^* = 67$ and $\sigma = 85$ days. In contrast, cDVRR (development rate during the reproductive phase, °Cd^{-1}) was found to be most critical for simulating maturity, with $\mu^* = 43$ and $\sigma = 86$ days. Variety-specific model calibration based on different combinations of those three parameters in 2020 in Cumilla shows a good simulation of anthesis and maturity dates with average root mean square error (RMSE) of 5 and 3 days, respectively. However, model validation across the remaining seasons and locations showed variable prediction accuracy, with RMSE ranging from 8–25 days for anthesis and 9–32 days for maturity (Figure 1). With the higher heat unit (HU) as results of the higher air temperature from transplanting to anthesis, the model showed the earlier simulated anthesis dates in Rangpur in 2022. Thus, compared to the observed data, there was a systematic underestimatimation of simulated anthesis and maturity DOY for all varieties in this location (Figure 1d). The opposite performance of the model was found in Sunamganj (Figure 1e).

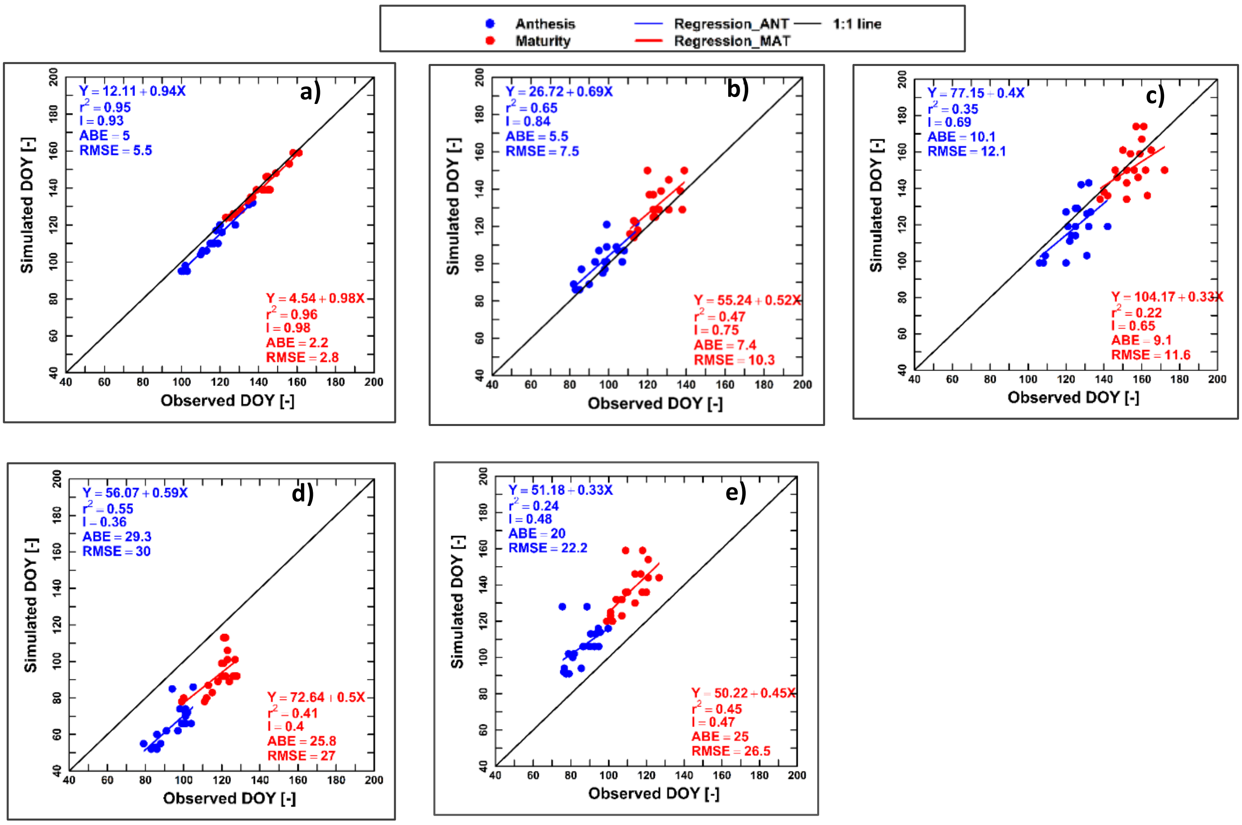

Figure 1. Comparison of simulated and observed anthesis (blue) and maturity (red) DOYs (day of the year) for twenty rice varieties from modeling calibration using data from Boro season in 2020 in Cumilla (a) and modeling validation using data from Boro season 2022 in Cumilla (b), Mymensigh (c), Rangpur (d) and Sunamganj (e). Blue and red lines indicate the linear regression between the observed and simulated anthesis and maturity DOY, respectively. The abbreviation I (unitless), r (unitless), ABE (number of DOY) and RMSE (number of DOY) are agreement index, correlation coefficient, absolute bias error, and root mean square error, respectively. Data showing here is only for selected growing seasons and locations.

Conclusions

The oryza2000 has been implemented in SIMPLACE and tested with field measured anthesis and maturity data from 20 rice varieties. Use of variety-specific parameters derived from one season and location reasonably simulated the anthesis and maturity DOY for that selected location and season, however is not generic enough for other seasons and locations. This indicates that the model requires the local specific parameters which captures the interaction of genotype with location and seasonal temperature change.

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AgriSegment: A Web-based Multi-modal Segmentation Suite for Crop Modeling Support and Dataset Preparation

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Keywords: data preparation, interactive refinement, deep learning, plant phenotyping, precision agriculture

Introduction

Crop modeling and digital twin concepts benefit from semantic information directly obtained from images of living plants, e.g., branch count, leaf area index, and the number of flowers. Plant segmentation is required to separate the plant from the background and from other plants, as well as to identify its various parts. Existing tools remain inaccessible to most agronomists due to required programming skills and fragmentation limiting synergy. SegFormer can automatically detect plant regions, while SAM allows for interactive refinement. These refinements can be fed back to improve SegFormer's training, creating a cycle of continuous dataset improvement. Current workflows treat them separately, breaking this loop. AgriSegment (Tarif, 2025) addresses this gap with (1) a web-based platform that makes advanced models accessible to agricultural researchers, and (2) a hybrid workflow where automatic detection supports interactive refinement, producing high-quality phenotyping data essential for parameterizing and validating crop models.

Materials and Methods

We developed four web apps using advanced segmentation models. These include SegFormer for semantic segmentation (Elmessery et al., 2024), SAM (Kirillov et al., 2023) for interactive corrections, Mask2Former for panoptic segmentation (Darbyshire et al., 2023), and a hybrid method that combines SegFormer's automatic point generation with SAM's interactive tools. The system is built with FastAPI and works in real time, supporting different image formats and output options. Users can start with automatic detection and then switch to interactive refinement if higher accuracy is needed. Apps provide plant area measurements, confidence scores, and results (binary masks, overlays, transparent PNGs) to support detailed agricultural analysis.

Results and Discussion

The hybrid SegFormer-SAM workflow combines automatic and interactive segmentation. First, SegFormer automatically creates seed points with semantic segmentation. Then SAM refines them with user-guided boundary corrections. This method outperforms single-model workflows, especially when the canopy shapes are complicated and the field conditions change. Processing speeds ranged from 2-3 seconds per image for automatic workflows to 8-12 seconds for interactive refinement on NVIDIA RTX 3060 GPU. Users can export refined masks to retrain SegFormer, enabling continuous improvement. This distinguishes our approach. Evaluation on 40 field images showed the interface removes programming barriers, enabling agronomists to generate training data. Users can select fast batch processing or precise interactive analysis based on research needs. The source code of AgriSegment is freely available at https://github.com/mehran-tarif/AgriSegment

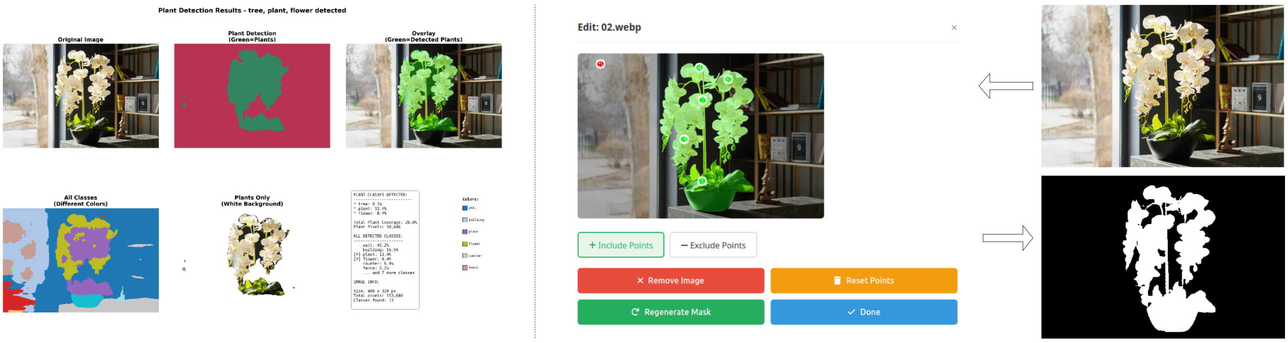

Figure 1. Automatic plant detection (left) and interactive refinement interface (right).

Conclusions

AgriSegment successfully combines automatic detection with interactive refinement, providing agricultural researchers with accessible tools for high-throughput phenotyping. The feedback loop mechanism, where user refinements improve the model over time, represents an important advance over fragmented workflows. By making advanced segmentation models accessible through web interfaces, AgriSegment speeds up high-quality phenotyping data generation essential for crop modeling research, supporting both breeding research validation and digital twin development for precision agriculture.

Acknowledgements

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Integrating a dynamic pest model to improve crop model performance

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Keywords: Biotic stress, Dynamic pest damage, Yield loss, Pesticide reduction, Expert-N

Introduction

Crop models are powerful tools for assessing the impact of changes in temperature, precipitation, and atmospheric CO_2 on crop growth and productivity. While the effect of resource-driven growth limitations such as nutrient and water availability is generally modelled in present crop models, other factors are often overlooked. Pests—including weeds, insects, and fungal pathogens—are a major source of yield loss (Hossard et al., 2014; Mack et al., 2023). Yet, many crop modelling studies sidestep these effects by assuming optimal pest control, an assumption that cannot always hold in practice.

To assess the pest damage in crop models, a dynamic pest module was implemented into the crop model Expert-N and evaluated using 14 years of field experiments from a site in Baden-Württemberg, Germany.

Materials and Methods

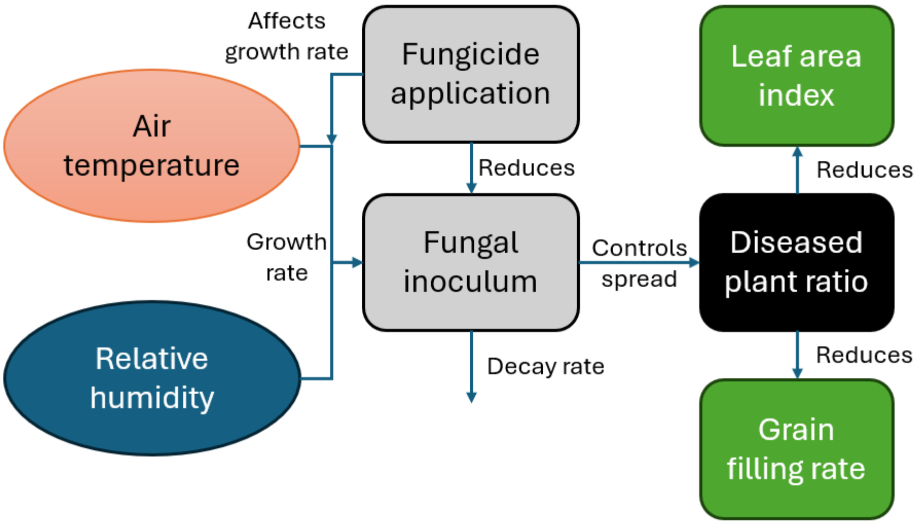

Figure 4. Schematic flow chart of pest damage interactions in the implemented pest module

To account for the effects of fungal damage on winter wheat, the generic pest model developed by Rasche and Taylor (2017) was integrated into the crop model Expert-N. The implemented mechanisms are illustrated schematically in Figure 1. The dynamic pest module simulates fungal inoculum growth as a function of daily temperature and relative humidity. The resulting inoculum dynamics drive the progression of diseased plant area, which can reduce the leaf area index (LAI) or grain filling rate, depending on the selected damage function. In this study, two damage pathways were considered: leaf blight, which decreases LAI, and Fusarium, which reduces grain filling.

The model was applied to simulate crop yields at the variety trial site Tailfingen in Baden-Württemberg, Germany. The site is located on high-quality loess soil, where water limitations rarely occur. As a result, annual yield differences are driven primarily by fungal diseases, making it an ideal location for such trials. The dataset covers 14 years of yield observations under two management regimes: an 'optimal' treatment with multiple pesticide applications and a 'reduced' treatment with limited fungicide use. The crop model parameters were optimized to minimize the mean absolute error (MAE) in comparison to the measured yields.

Results and Discussion

For the optimal treatment, simulations with the standard crop model resulted in a mean absolute error (MAE) of 930 kg/ha across the 14 years. Although this performance is moderate, it is strongly influenced by a few years with poor fits—most notably 2016, when above-average rainfall led to yield overestimation, as the model cannot account for the effects of prolonged wet conditions and delayed pesticide application. Incorporating the pest module reduced the MAE to 550 kg/ha for the optimal treatment and 330 kg/ha for the reduced treatment. This demonstrates that the model can capture the effects of reduced fungicide application—something not possible with conventional models. Importantly, even though BBCH stages were not explicitly targeted during calibration, including the pest module improved overall performance, as crop development parameters no longer had to implicitly account for pest effects

Conclusions

Incorporating dynamic pest effects into crop models offers several advantages. It enables the estimation of yield impacts under reduced pesticide use—an important consideration given the growing emphasis on precise pesticide reduction. At the same time, including a pest module improves model performance, as it explicitly represents pest damage rather than leaving it to be absorbed indirectly during calibration.

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Title: Modelling the millet and cowpea association in Senegal: the potential of the STICS model for agro-ecological intensification

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Keywords: Millet and cowpea intercropping, STICS model, yield

Introduction

In Senegal, yield declines highlight the close links between population growth, declining soil fertility and ecosystem degradation (Faye et al., 2023). As arable land is limited, the cereal-legume association is one of the prototypes of productive and sustainable ecological intensification cropping systems (Senghor et al., 2023). Because of the variability in the performance of these associated crops, it is essential to use agronomic indicators to assess them (Bedoussac and Justes, 2011). Dynamic crop models are tools that can help to understand and improve the agri-environmental performance of these systems. This study therefore aims to assess the performance of STICS-Combined Crops (STICS-CA) in simulating the growth and development of the millet-cowpea association in Senegal under contrasting experimental conditions.

Materials and Methods

The data used come from trials conducted at the experimental station of the Centre National de Recherches Agronomiques de Bambey (CNRA) under strictly rainfed conditions and with supplemental irrigation during the 2018 and 2019 rainy seasons. Millet, a Souna 3 variety, and cowpea, Baye Ngagne, a local seed variety, and 58-74f, a variety with high fodder potential, were used. Two levels of mineral fertilisation were applied, 0kgN/ha and 68.5kgN/ha. The 20 cropping situations in 2019 were used to calibrate the model, while those in 2018 were used for independent evaluation. Each plot constituted a simulated crop situation based on observed measurements (soil, water, nitrogen, phenology, growth). In 2018, organic nitrogen was estimated on the basis of composite analyses by block, while in 2019 measurements were available by plot. Soil water properties (field capacity and wilting point) were estimated from moisture profiles by selecting the maximum and minimum representative values for each depth. Calibration was based solely on site-specific soil and plant parameters, with the model's generic parameters retained, and was based on a sequence ranging from phenological stages (calibrated according to Affholder et al., 2013) to LAI, then to water and nitrogen dynamics, through to biomass and grain yield. The model's performance was assessed by graphical comparison and using statistical indicators (EF, RMSE, rRMSE).

Results and Discussion

The model reproduced biomass (EF=0.8; rRMSE=30%) and acquired nitrogen (EF= 0.9 and rRMSE= 24%) well during calibration, but its performance dropped during evaluation, particularly for yields (Fig.1). The simulations were more accurate for millet than for cowpea, which showed greater discrepancies between observations and predictions. These results corroborate the work of Traoré et al. (2022), confirming the model's ability to simulate biomass in intercropping.

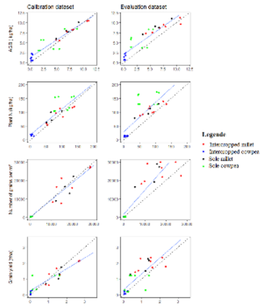

Figure 1. The above-ground biomass (AGB) and plant nitrogen (plant N) at harvest, as well as the number of grains per square meter and the grain yield, were observed and simulated by STICS-AC for the millet and cowpea calibration dataset.
The dotted black line is a straight line with the equation y = 1/1. The blue line shows the regression of the simulated values against the observed values.

The model reproduced the advantage of millet in intercropping over pure cropping, although it tended to overestimate yields (Fig. 2). It also simulated higher humus mineralisation in intercropping (138.15 kg/ha) than in pure cropping (110.15 kg/ha), but the lack of details on the calculation of the 'priming effect' in STICS prevents this difference from being fully explained. The model was able to reproduce the effects on millet performance of the choice of cowpea variety in the associations, of fertilisation and its interaction with the association, and of irrigation. However, it did not capture the variability in millet yield observed between the two years of the experiment.

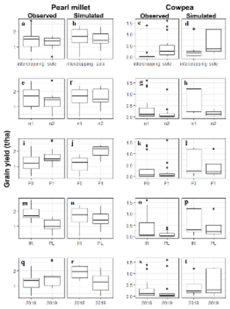

Figure 2. The effect of cropping system, cowpea variety, fertilization, irrigation type and year on the observed and simulated grain yields of millet and cowpea is shown below.

n1: Cowpea grain, n2: Cowpea forage, F1: Mineral fertilization (68.5 kg N ha-1) and F0: No fertilization (0 kg N ha-1).

Conclusions

Overall, STICS-CA reproduces the advantage of millet in intercropping and the effects of fertilisation, variety and irrigation, despite poorly simulated interannual variability. It can still be used for virtual experimentation and evaluation of intercropping systems in the Sahel, taking into account its limitations.

Acknowledgements

This study was funded by AFD, USAID, and the European Union. The authors thank CIRAD's AIDA Research Unit, Gaston Berger University, and ISRA (especially the Bambey Agricultural Research Centre) for their technical support.

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Simulating drought tolerant peanuts by early reduction of transpiration and photosynthesis under mild stress using the DSSAT-CROPGRO Model

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Keywords: ***Arachis hypogaea*** **L, Water saver, Drought adaption, Yield, DSSAT-CROPGRO-Peanut.**

Introduction

Understanding and predicting peanut (*Arachis hypogaea* L.) performance under water-limited conditions is crucial for improving crop resilience in a changing climate. Peanut breeders are developing new water saver cultivars that have low stomatal conductance, and that reduce transpiration and photosynthesis as the plant becomes drought stressed (Zhang et al., 2022). Battisti et al. (2017) proposed methods to incorporate drought adaptive traits into the DSSAT-CROPGRO-Soybean model and used the model to evaluate the impact of these traits on soybean production in Brazil. The objective of this work was to incorporate the water saver trait into the DSSAT-CROPGRO-Peanut model and evaluate the model using two sites and two years of field data in Alabama, USA.

Materials and Methods

The focus of the water saver strategy was to reduce transpiration and daily photosynthesis under water stress. A new genetic coefficient, DT1 was introduced into the Ecotype file to modify transpiration and photosynthesis under drought stress. In the model, once potential transpiration and daily photosynthesis is computed, it is modified based on the equations presented in Battisti et al. (2017) for water-saving varieties

$$EOP = MIN\ (EOP,\ ((1.0-EXP(DT1*TRWUP*10/EOP))\ *\ EOP))$$

$$PG = MIN\ (PG,\ ((1.0-EXP(DT1*TRWUP*10/EOP))\ *\ PG))$$

Where EOP is daily transpiration without water stress (mm/day), DT1 is a calibration parameter in the ecotype file, TRWUP is total potential root water uptake (cm/day), and PG is daily gross photosynthesis (g/m^2/d). For non-water saver varieties, the values of EOP and PG initially computed by the model are not modified. If DT1 has a value of -99, no modification of daily EOP and PG takes place.

Experiments were conducted in 2019 and 2020 at the E.V. Smith Research Center of Auburn University at Shorter, Alabama (EV, 32°29′ N, 85°53′ W) and the Wiregrass Research and Extension Center of Auburn University at Headland, Alabama (HL, 31°22′ N, 85°19′ W) (Table 1). Two peanut varieties (C1: AU-16-28, a water saver, and C2: TUFRunner 297, a drought susceptible variety) were planted each season in irrigated and dryland plots. Biomass including leaf, stem, pod and seed weight, leaf area index and soil water content were collected periodically during the season. Genetic coefficients were calibrated by Zhen et al. (2022) for the irrigated experiments for both locations for phenology parameters. New model ecotype parameter DT1 and morpho-physiological cultivar parameters were re-calibrated to minimize error for phenology, biomass, pod yield, and seed yield under dryland conditions for EV in year 2019/2020, and evaluated for HL in year 2019/2020.

Table 1. Peanut varieties, soil types, water treatments, years of data used for CROPGRO-Peanut model calibration and evaluation.

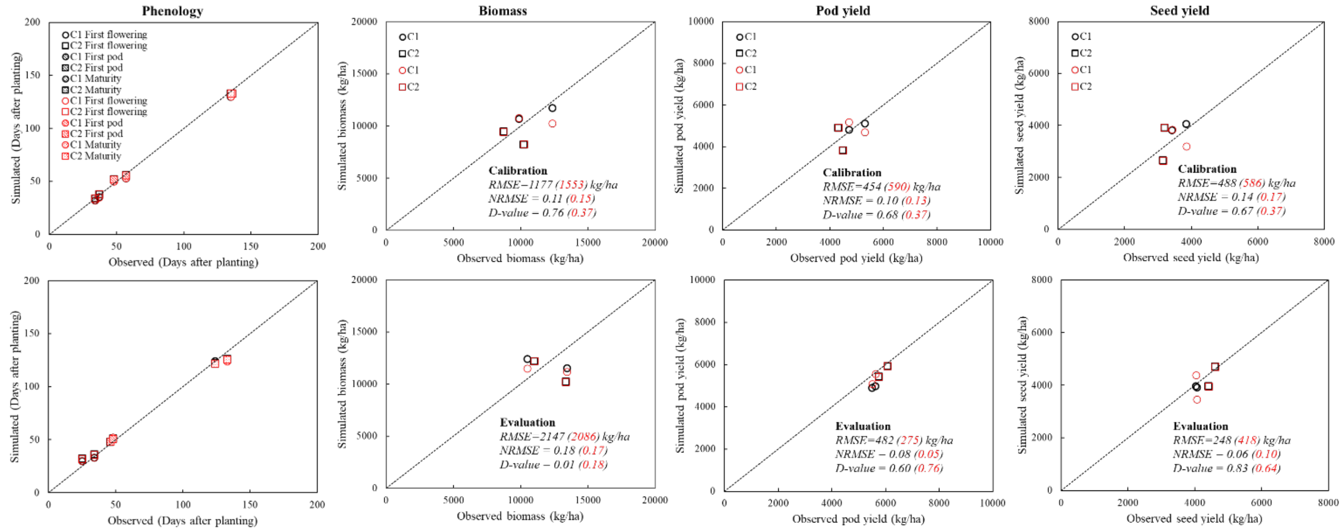
Experiment numbers	Locations	Peanut varieties	Soil types	Water treatments	Years	Data used
Exp. 1	EV Smith research center at Shorter, Alabama (EV)	C1: AU16-28 C2: TUFRunner 297	Loam	Dryland and Irrigation	2019/2020	Calibration
Exp. 2	Wiregrass research and extension center at Headland, Alabama (HL)		Sandy loam	Dryland and Irrigation	2019/2020	Evaluation

Results

Model performance was evaluated for two peanut varieties grown under dry conditions at EV and HL during 2019 and 2020, with and without the drought-tolerant modification (Figure 1). The drought-tolerant version (black points) consistently improved agreement between simulated and observed values compared with the unmodified model (red points). For phenology, both model versions captured key stages well with most of the points falling along the 1:1 line.

Biomass was simulated with RMSE values of 1177 kg ha^{-1} (NRMSE = 0.11, D = 0.76) for calibration and 2147 kg ha^{-1} (NRMSE = 0.18, D = 0.01) for evaluation, compared with 1553kg ha^{-1} (NRMSE = 0.15, D = 0.37) and 2086 kg ha^{-1} (NRMSE = 0.17, D = 0.18) without DT1. Pod yield simulations had an RMSE of 454 kg ha^{-1} (NRMSE = 0.10, D = 0.68) for calibration and 482 kg ha^{-1} (NRMSE = 0.08, D = 0.60) for evaluation, while the unmodified model showed larger errors (590 kg ha^{-1}, NRMSE = 0.13, D = 0.37) for calibration but lower errors for evaluation (275 kg ha^{-1}, NRMSE = 0.05, D = 0.76). For seed yield, RMSE values were 488 kg ha^{-1} (NRMSE = 0.17, D = 0.37) and 248 kg ha^{-1} (NRMSE = 0.06, D = 0.83) for calibration and evaluation with DT1, compared to 586 kg ha^{-1} (NRMSE = 0.17, D = 0.37) and 418 kg ha^{-1} (NRMSE = 0.10, D = 0.64) without DT1. Overall, these results indicate that the drought-tolerance parameter (DT1) enhanced simulation of both phenological stages and yield-related traits under water-limited conditions.

Figure 1. CROPGRO-Peanut model performance for two peanut varieties (C1-C2, listed in Table 1) with (black points) and without (red points) drought tolerant modification grown under dry conditions in EV and HL during 2019 and 2020.



Conclusions

The modified CROPGRO-Peanut model with the new designed DT1 parameter simulated phenological stages of peanut cultivars under drought conditions with high accuracy. The modified model gave improved simulations of biomass, pod and seed yield compared to the original model. These results demonstrate the potential of the new drought tolerant algorighms to improve simulation of drought-tolerant traits for peanut improvement.

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GLOBAL-SCALE SIMULATION OF WINDBORNE CROP DISEASE TRANSMISSION WITH LIVE 3-D VISUALIZATION ENABLED BY GPU ACCELERATION

Authors:

Marcel Meyer, Thomas Gaiser, Frank Ewert

Abstract

The global burden of pathogens and pests on major food crops is estimated at 17-30%. Despite the relevance of diseases and pests many widely used crop models do not yet account for their effects on crop yields. We present results from a method development study on crop disease modelling.

The atmosphere is an important medium for transmission of crop diseases and insect pests, such as, for example, fungal pathogens, insect vectors and migratory pests. Recent advances in massively parallelized GPU computing promise the potential for substantial performance gains in simulating windborne crop diseases and pests that could facilitate also advanced coupling of model components and real-time simulations.

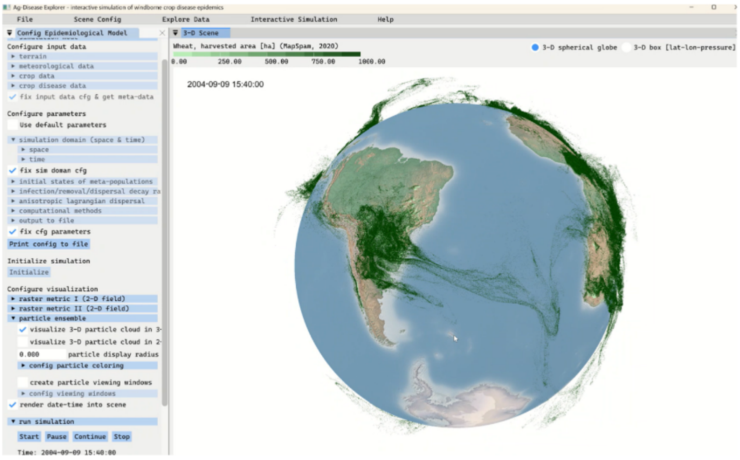
We developed and tested different GPU-based implementations of spatiotemporally explicit crop disease models on landscape to global scales. Our approach is based on customized CUDA C++ implementations for general-purpose GPU computing, linked with methods from computer graphics (OpenGL) to enable live 3-D visualization of simulation data. This facilitates substantial speed-up, scalability and flexibility, and it allows for interactive exploratory visual data analysis of complex feedback between meteorology and pathogen biology during atmospheric transmission.

The prototype for a GPU-accelerated simulation tool that we present allows, for the first time, real-time global-scale simulation of windborne crop disease transmission with live 3-D visualization of simulation data. We report results from method development, including performance estimates and validation, focusing on a new atmospheric transport model dedicated to windborne crop pathogen and pest transmission that can be applied to different crop health threats, such as cereal rusts and potato late blight, and adapted to different insect pests, such as desert locusts and fall army worm. The feasibility of coupling the GPU-accelerated atmospheric transport model with stochastic epidemiological models for simulating complex disease patterns and crop models for yield impact assessments is discussed.

Our results may serve useful as an initial step towards identifying suitable modelling approaches for advancing the representation of crop diseases and insect pests in crop modeling frameworks.

Global-scale simulation of windborne crop disease transmission with interactive 3-D visual data analysis

A. *AgDisease*: graphical user-interface



Configure input data
- ▸ terrain
- ▸ meteorological data
- ▸ crop data
- ▸ crop disease data
- ✓ fix input data cfg & get meta-data

Configure parameters
- ☐ Use default parameters
- ▾ simulation domain (space & time)
  - ▸ space
  - ▸ time
- ✓ fix sim doman cfg
- ▸ initial states of meta-populations
- ▸ infection/removal/dispersal decay ra
- ▸ anisotropic lagrangian dispersal
- ▸ computational methods
- ▸ output to file
- ✓ fix cfg parameters

Print config to file

Initialize simulation

Initialize

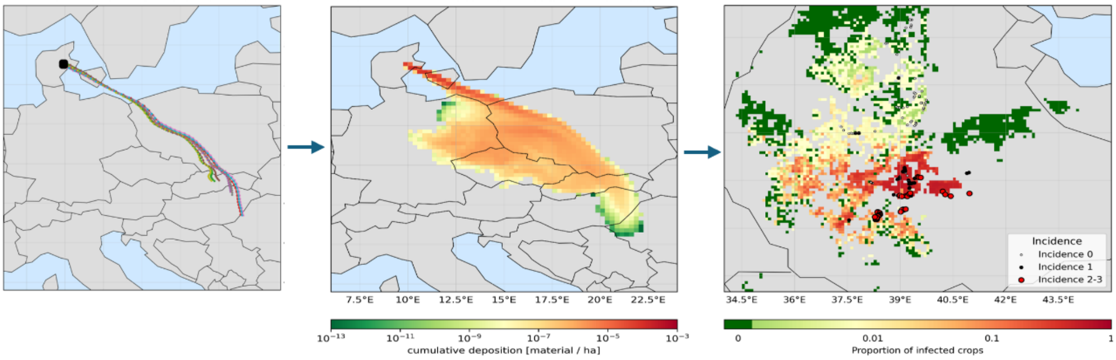
Configure visualization
- ▸ raster metric I (2-D field)
- ▸ raster metric II (2-D field)
- ▾ particle ensemble
  - ✓ visualize 3-D particle cloud in 3-
  - ☐ visualize 3-D particle cloud in 2-
  - 0.000 particle display radius
  - ▸ config particle coloring
  - ☐ create particle viewing windows
  - ▸ config viewing windows
- ✓ render date-time into scene
- ▾ run simulation

Start Pause Continue Stop

Time: 2004-09-09 15:40:00

B. test-case: wheat rusts

C. *AgDisease:* linking atmospheric dispersal and epidemiological models



Importance of reliable soil information for simulation of crop growth and yield from field to regional scale

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Abstract

Model-based assessments of food security risks, future climate change impacts on crop production as well as digital farming require adequate simulation of crop production at different spatial scales. In many cases, process-based 1-D simulation models are used for this purpose and extended to varying spatial domains. Usually, the temporal and spatial resolution of the simulations depend on the availability and resolution of weather data as well as soil and crop management information. In the case of soil information, various data sources are available with different horizontal and vertical spatial resolution as well as recorded soil properties.

The aim of this presentation is to review the sensitivity of crop models to different sources of soil information as found in the literature from regions in Europe as well as in Africa. Therefore, at first, the content of different sources of soil information with respect to their content and spatial resolution is compare and, secondly, the effect of the use of different data sources and resolutions on simulated crop yield is evaluated for different regions in the world

In most cases, soil information has been gathered from field campaigns (reference or ground truth) as well as from secondary soil data with varying spatial resolution. Then the soil information from the different sources has been used as input to crop yield simulations over several years with different field scale crop models combined with the same weather and management information. Simulation results were compared with respect to their simulated mean crop yield as well as their yield stability.

An example of the effect of different spatial resolution of soil information on mean simulated crop yields is shown in Figure 1.

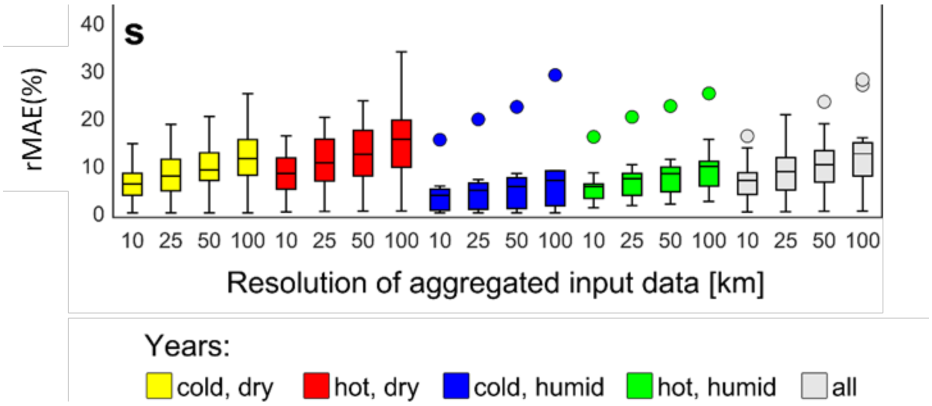

Figure 1. *Relative mean absolute error (rMAE) of simulated silage maize yield for different spatial resolutions of soil input data and years with different weather conditions. Boxplots show the rMAE calculated from n = 11 crop models (middle line indicates the mean rMAE across models, whiskers are Tukey style and extent to 1.5 times the interquartile range) (Hoffmann et al. 2016)*

Implications for the assessment of the impact of climate change or of crop management scenarios at regional are discussed.

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Improving parameterisation of growing degree days: new methods and challenges

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Keywords: Hybrid, probabilistic, regional scale, crop modelling

Introduction

Traditional crop models can be adapted to regional scales for climate impacts analysis but are limited by skill in modelling phenology (Challinor et al., 2018). Phenology parametrisations are generally based on growing degree days (GDD) and temperature response functions. Disagreement on response functions has previously led to uncertainty in predictions and data scarcity continues to limit progress. Accordingly, we present a new method developed using the phenology database of the German Weather Service (DWD, Kaspar et al., 2014), the largest open-source maize phenology dataset in the world. We present challenges and progress in transferring learning beyond German conditions.

Materials/Methods

We compare two methods to improve GDD models for regional scale maize phenology using temperature response functions: (1) the *expected thermal response* derived from probability theory and (2) neural networks (NNs).

The ERA5 product (Hersbach et al., 2020) was used as input data. 26,208 anthesis observations from the DWD were used for calibration, the last three years of which (2022, 2023, 2024) were withheld for evaluation. *Benchmark:* A GDD model was applied with both piecewise linear and curvilinear *Wang-Engel* response functions (Wang et al., 2017).

Method 1: The expected thermal response (ETR) refers to estimation of the mean of the response function over finer scale spatial variation in a grid cell (instead of applying the response function to the mean temperature). The ETR was calculated by numerically integrating existing response functions against a probability density function. The ETR was tested in a GDD model.

Method 2: NNs were used to replace both the response function (as in van Bree et al., 2025) and separately the accumulation step of a GDD model. Maximum and minimum daily temperature, photoperiod and vapor pressure deficit were included as features in the NN response function.

Results and Discussion

- All models performed similarly (R^2 approx. 0.3 - 0.4) when fully calibrated, but calibration often implied implausible parameter values;
- The ETR was optimal at more physically feasible cardinal temperatures (T_opt 26.7°C) than the benchmark model (T_opt 22.2°C);
- NNs gave a physically implausible response function outside the range of temperatures in the dataset.

When cardinal temperatures were taken from the literature, the ETR performed better (R^2 0.39) than the benchmark, where no variance was explained (Figure 1, right panel). Unlike the ETR (model standard deviation 8.9 days), the benchmark produced an overly dispersive model (model standard deviation 11.3 days) - it underestimated low flowering times and overestimated high flowering times.

When the benchmark was optimised to the data, the function had a gentler gradient for higher temperatures. The ETR had a similar shape and performance, but was derived from existing crop modelling knowledge, so should perform better out of sample (Figure 1, left panel).

Neither the NN response function nor the NN accumulation improved on the benchmark or ETR GDD model (Figure 1, right panel). Temperature described most of the variation in the NN response. The NN response was positive for low temperatures and did not decrease above feasible optimal temperatures, so did not always align with physical intuition (Figure 1, left panel). Most daily temperatures (98%) were between 7 and 26°C, so NN response functions may suffer from over-fitting outside these regions. Both NN models had lower spread than the GDD models (model standard deviation 6.3 and 7.0 days for the NN response and NN accumulation respectively).

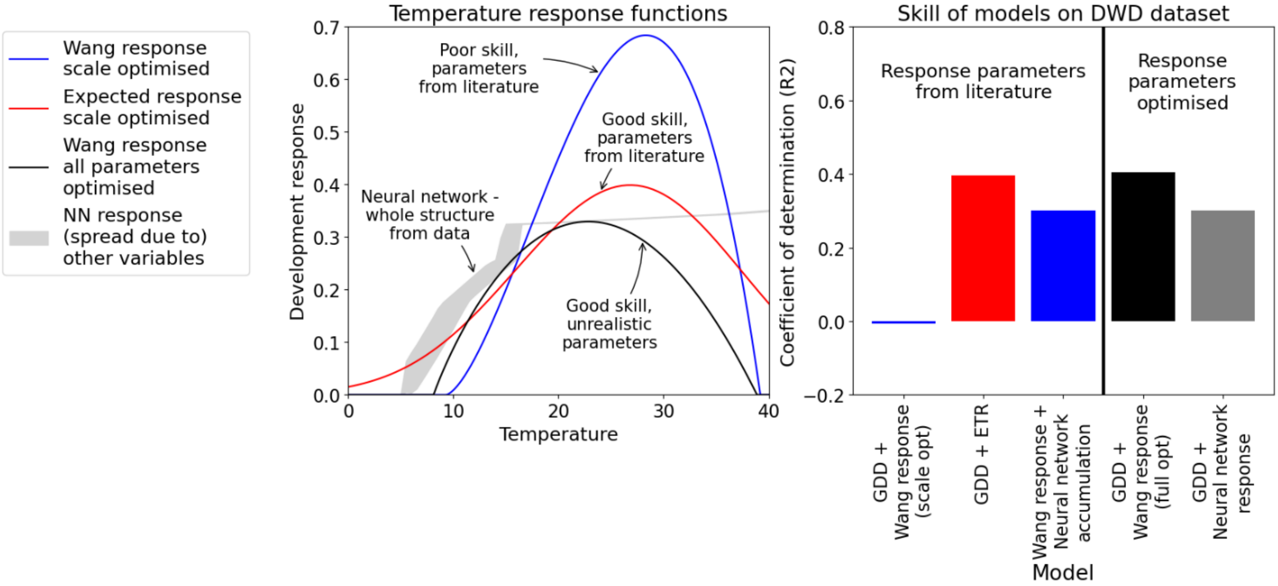

Figure 1. Left panel: Temperature response curves of Wang et al., 2017 (blue) and ETR (red) compared to a neural network response function (shaded grey). The Wang curve and ETR are more physically plausible outside the range of temperatures in the dataset (99th percentile = 26°C). *Right panel:* Skill scores for the different models on the DWD maize phenology database years 2022-2024. The plot is divided by whether models used the response curve of Wang et al. with parameters from the literature.

Conclusions

The ETR performs as well as existing and NN-based response functions but aligns better to laboratory experiments. Improvements in model performance are often accompanied by reductions in variance, a trend which could be attributed to the data averaging effect.

The DWD database is large enough to train complex neural networks but is limited by the range of temperatures in Germany. Given the size of the dataset, we expect indications about the shape of response curves to be reliable, but estimations of optimal temperature to be less conclusive.

We conclude with progress and challenges in implementing the ETR on a broader scale, drawing on transfer learning methodologies. We propose integration of crop modelling knowledge into machine learning as the best way to address data scarcity issues.

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