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

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Biophysical processes are important factors to account for in the soil-plant-atmosphere continuum to predict the fluxes of energy, CO_2 and H_2O in the system. They include processes such as photosynthesis, evapo-transpiration, energy balance, temperature, or stomatal conductance. Biophysical models have been continuously developed for several decades to better understand and predict those processes, but they are still either complicated to use (*e.g.* compiled monolithic models) or slow to compute (*e.g.* implemented in R or Python), and very often the sub-processes included in those models are complicated to extend and evaluate independently. Furthermore, there are often many implementations to simulate the same process (*e.g.* see stomatal conductance models reviewed in Buckley (2017)), mostly only differing by a slight correction or improvement in their formulation. For example, Schymanski and Or (2017) corrected the model of Penman-Monteith by clarifying the number of sides exchanging sensible and latent fluxes in leaves. Those model implementations are developed for various reasons, including improvements in the knowledge about a process, different constraints for the simulation scale, data availability, or computational intensity. In this context, it can be difficult to choose one model over another, or even to evaluate their accuracy or applicability considering the particular objectives of the simulation. Besides, current tools only propose a limited set of models, without the possibility to easily add or compare external models.

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

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

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

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

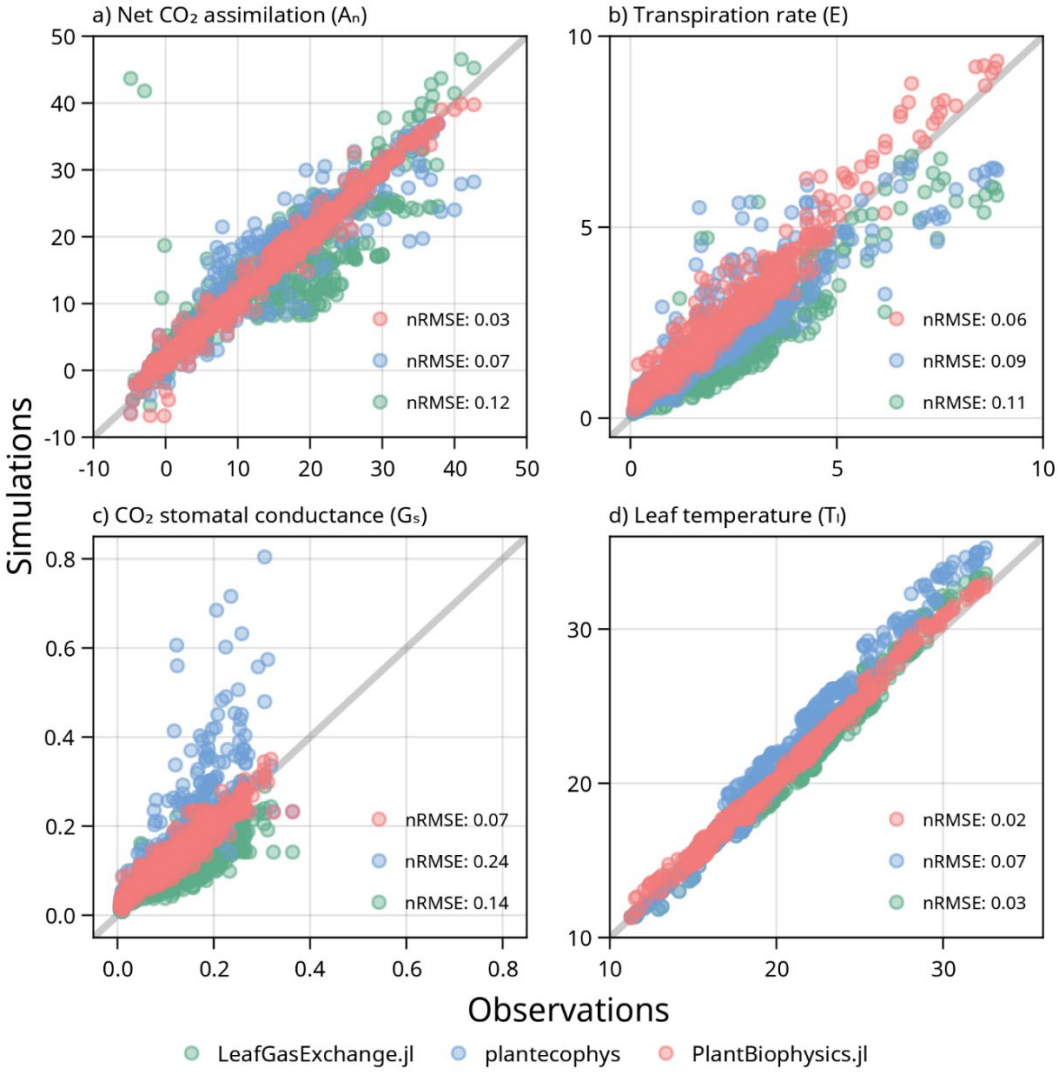

Figure 1: Measured data for *Eucalyptus delegatensis* (Medlyn et al., 2015) plotted against simulations of: net carbon assimilation (a), net transpiration rate (b), stomatal conductance for CO2 (c) and leaf temperature (d). All simulations were performed using a photosynthesis-stomatal conductance-energy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

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