

AquaCrop.jl: A Process-Based Model of Crop Growth

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Summary

All agriculture is dependent on the growth of plants. Crop plants provide food for humans, fodder for domestic animals, and fibre and other resources for our manufacturing economy. Therefore, understanding how plants grow under different conditions is important not just for farmers themselves, but also for the rest of society. Crop models based on physical and physiological processes use information about environmental parameters (e.g. temperature, rainfall, soil quality) and knowledge of plant biology to simulate how crop plants grow over time and estimate the resulting yield. Such models can be used to optimise farm management, forecast regional or national yields, or study climate change impacts.

Statement of need

AquaCrop.jl is an independent Julia translation of the AquaCrop model (version 7.2), originally developed by the FAO (Steduto et al., 2009). This is a well-established crop growth model that has been used to model numerous crops worldwide (Mialyk et al., 2024), and is known to produce reliable estimates of crop phenology and yield (Kostková et al., 2021).

AquaCrop is already available in multiple languages. First implemented in Delphi, it was later open-sourced in a Fortran version (de Roos et al., 2021; Remote Sensing and Data Assimilation Research Group, 2021/2024). There are also versions available in Matlab, Python, and R, although these are not up-to-date with the most recent version of the original model (Camargo Rodriguez & Ober, 2019; Foster et al., 2017; Kelly & Foster, 2021). With AquaCrop.jl, we want to expand this portfolio to make the model more easily accessible to the growing number of environmental modellers working with Julia.

Beyond just adding another language, our purpose is also to provide a package that can be readily integrated into other scientific software. Recent research has emphasised the need for the creation of interdisciplinary models that consider the multiple processes inherent in global challenges such as climate change or biodiversity loss (Cabral et al., 2023). This will require the use of model coupling, and the adaptation of existing models to be usable as components in integrated models (Vedder, Fischer, et al., 2024).

Specifically, we developed the package to use it as a component within Persefone.jl, a model of agricultural ecosystems (Vedder, Matthies, et al., 2024). The aim of this model is to study the impact that agricultural processes have on biodiversity, for which the growth of crop plants is an important mediating factor.

The core code of AquaCrop.jl closely follows the FAO's Fortran implementation, which allows us to quickly integrate changes and updates to the original AquaCrop code. On top of the core code, we developed an API that makes it easy to configure and run the simulations in several ways. It enables exploring and interacting with state variables at run time, opening up the possibility of dynamic, bidirectional model coupling. These new features increase the

interoperability of the model compared to its original implementation. In addition, they allow complementing the code with other libraries from the Julia ecosystem, like `DataFrames.jl`, `Makie.jl`, `StatsModels.jl`, or `Optimisers.jl`. All of this makes `AquaCrop.jl` a reliable and versatile tool for simulating and studying crop growth.

Example

The following tutorials are provided in the documentation:

- [Basic run](#) shows how to set up a model run using the original `AquaCrop` configuration file format, simulating a complete vegetation period in one go.
- [Intermediate run](#) shows how to configure the model with TOML and CSV files, how to advance the simulation one day at a time, and how to access crop variables at run time.
- [Advanced run](#) shows how to configure the model via the API (i.e. using Julia variables), and how to change variables at run time.

A simple demonstration of the basic run using the data from the `AquaCrop.jl/test/testcase` directory is shown here:

```
using AquaCrop
using CairoMakie
using Unitful

runtype = NormalFileRun();
parentdir = AquaCrop.test_dir; #".../AquaCrop.jl/test/testcase"

outputs = basic_run(; runtype=runtype, parentdir=parentdir);

f = Figure();
ax = Axis(f[1,1],
    title = "Biomass vs Day",
    xlabel = "Day",
    ylabel = "Biomass",
)
lines!(ax, 1:size(outputs[:dayout], 1) , ustrip.(outputs[:dayout][!, "Biomass"]))
```

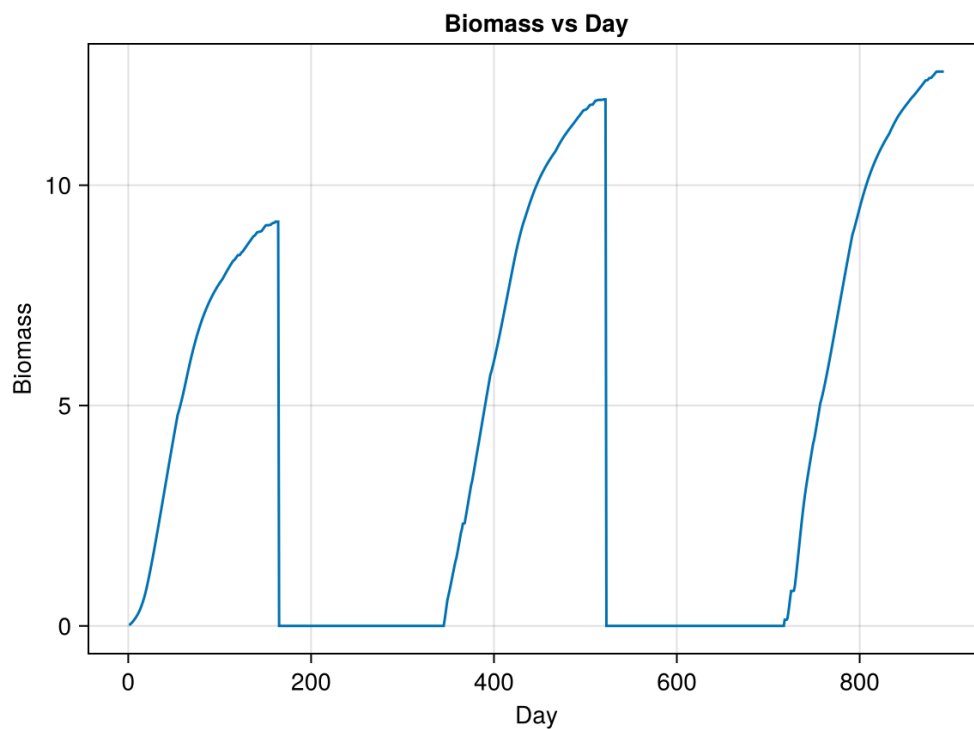


Figure 1: Biomass of crops over time in a generic simulation run.

56 **Figure 1** shows the biomass increase over time during three growing seasons, as generated by
 57 the basic run demonstration above. **Figure 2** displays the results a more realistic use case. Here,
 58 AquaCrop.jl was used to simulate the growth of beans (*Vicia faba*) based on environmental
 59 data from Thuringia, Germany, with historical yield data shown for comparison.

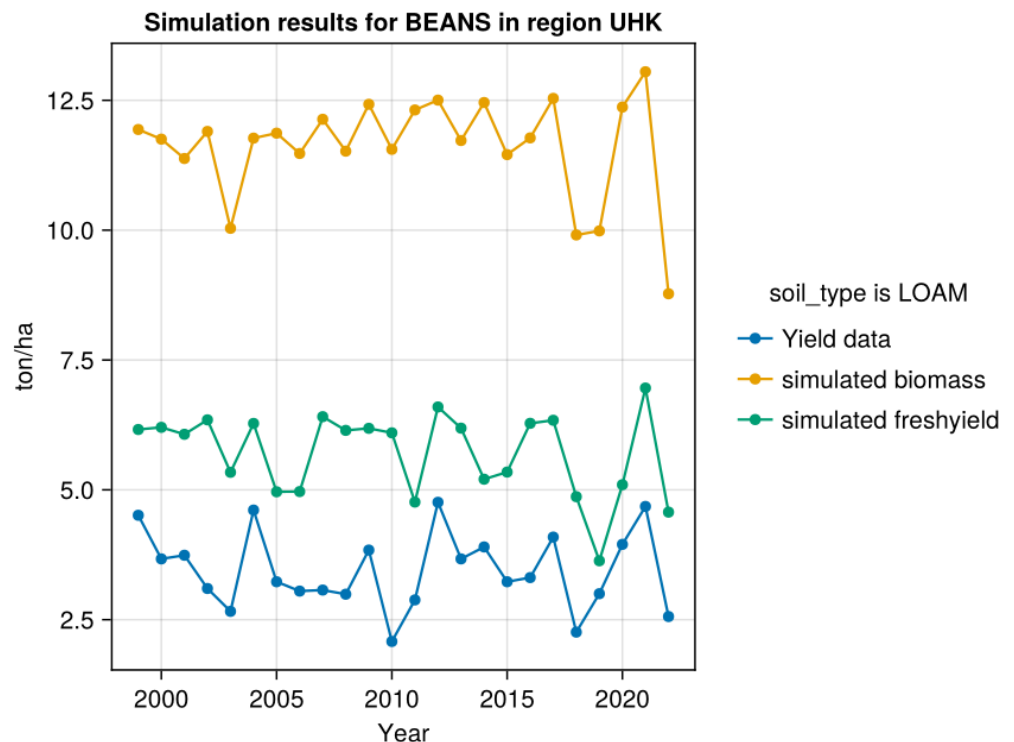


Figure 2: Simulated yield of beans (*Vicia faba*) compared to observed yields in Thuringia, Germany.

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