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

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Software

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Summary

AquaCrop is a simulation model that forecasts the growth and yield of crop plants under different environmental and management conditions (Steduto et al., 2009). As a process-based model, it can be used to optimise farm management, forecast regional yields, or study climate change impacts and sustainable farming practices. Originally developed by the Food and Agricultural Organization of the United Nations (FAO), it has been widely applied in agricultural research.

Here, we present an expanded reimplementation of the model, translating it from Fortran to Julia (Bezanson et al., 2017) and focussing on improving its interoperability with other software and models. With `AquaCrop.jl`, we want to make AquaCrop available to the growing number of environmental modellers working in Julia, and contribute to the creation of integrated, interdisciplinary models in the environmental sciences.

Statement of need

All agriculture is dependent on the growth of plants, which provide food, fodder, fibre, and other resources. Forecasting and optimising crop growth is therefore vital to address global food system challenges, including widespread malnutrition, agriculture-related environmental degradation, and global impacts of climate change (Foley et al., 2011). In this context, predictive crop models can be used to inform decision-making. These models use information about environmental parameters (e.g. temperature, rainfall, soil quality) and knowledge of plant biology to simulate crop growth over time and estimate yield.

Crop models range from simple statistical regression approaches to highly complex numerical simulations (Pan & Chen, 2021). Some concentrate on modelling the growth of the plant itself (e.g. EPIC, Williams et al., 1989), while others provide submodels for many different aspects of agricultural systems, such as farm management, livestock, soil processes, or water quality (e.g. APSIM, Holzworth et al., 2014).

AquaCrop is an intermediate-complexity crop model. Its aim is to be complex enough to be accurate but simple enough to be widely usable (Steduto et al., 2009). Indeed, over the past years, it has been used to model numerous crops worldwide (Mialyk et al., 2024), and has been shown to produce reliable estimates of crop phenology and yield for multiple crop species (Kostková et al., 2021). 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 currently these are not up-to-date with the most recent version (7.2) of the original Fortran model (Camargo Rodriguez & Ober, 2019; Foster et al., 2017; Kelly & Foster, 2021).

`AquaCrop.jl` expands this portfolio to contribute to the emerging ecosystem of environmental research software in Julia. To our knowledge, this is the first process-based crop model available

in this language. Our purpose is also to provide a package that can be readily integrated into other scientific software, in order to facilitate the creation of multidisciplinary models of socio-environmental systems (Cabral et al., 2023; Vedder, Fischer, et al., 2024). Specifically, we developed the package to use it as a component within `Persefone.jl`, a process-based model of agricultural ecosystems (Vedder, Matthies, et al., 2024). The aim of this model is to study the impact that agricultural management and policy has on biodiversity, for which the growth of crop plants is an important mediating factor.

Comparison to original implementation

We decided to reimplement the full source code of the model rather than simply providing a wrapper to the original software (though we do this too, see below). The most important reason was that we needed to modify the structure to enable better interoperability when coupling the model to other software. In addition, a native Julia implementation allows a better integration with other Julia libraries, as well as allowing researchers who are familiar with Julia but not with Fortran to work with the model code. In our reimplementation, we followed a two-layered approach:

The core code of `AquaCrop.jl` was translated verbatim from the original Fortran implementation, which allows us to quickly integrate changes and updates to the original `AquaCrop` code. `AquaCrop.jl` supports the original input file formats, and is tested to ensure its output conforms to that of the original software (using the data files in the `extended-tests` branch).

On top of this core code, we developed a wrapper layer with an API that improves the interoperability of `AquaCrop.jl` when used as a package with other software. First, we added support for standardised input and output file formats (TOML and CSV), and for loading input data from memory rather than disk (for example using output from a coupled model). Second, we bundled all state variables for a simulation in one struct (`AquaCropField`), thereby eliminating global state and allowing multiple simulations to be carried out in parallel, as well as making serialisation and data transfer easier. Third, we enabled the model to be updated one day at a time, rather than being executed as a singe batch job. This allows state variables to be inspected and changed on the go, which makes it possible to use the package for bidirectional model coupling as well as interactively.

Overall, we leave the scientific core of the model unchanged, but make it easier for environmental modellers using Julia to integrate the model into their own work, interface with other libraries for the Julia ecosystem, or adapt the model to suit their needs.

Examples

Multiple tutorials for different use cases are provided in the documentation. A simple demonstration of a basic run using the data from the `AquaCrop.jl/test/testcase` directory is shown here:

```
using AquaCrop
using CairoMakie
using Unitful

# First, we specify the input file format:
# NormalFileRun(): use the original AquaCrop file format
# TomlFileRun(): use TOML and CSV formatting
# NoFileRun(): provide input data via the API
runtype = NormalFileRun();

# Then specify the directory containing the necessary input files
```

```
parentdir = AquaCrop.test_dir;

# Now we can do a simulation run and plot the results
outputs = basic_run(; runtype=runtype, parentdir=parentdir);
function plot_basic_out(cropfield, cols)
    x = cropfield[!, "Date"]
    aux_sz = round(Int, sqrt(length(cols)))
    f = Figure()
    for (i, coli) in enumerate(keys(cols))
        ii, jj = divrem(i-1, aux_sz)
        ax = Axis(f[ii, jj],
                title = cols[coli][1],
                xlabel = "Date",
                ylabel = cols[coli][2]
                )
        lines!(ax, x, ustrip.(cropfield[!, coli]))
        ax.xticklabelrotation = π/4
        ax.xticklabelsize = 8
        ax.yticklabelsize = 8
    end
    return f
end

f = plot_basic_out(outputs[:dayout],
    Dict("CC"=>["Canopy Cover","%"],
         "Tavg"=>["Temperature","K"],
         "Biomass"=>["Biomass","ton/ha"],
         "Rain"=>["Rainfall","mm"]))
```

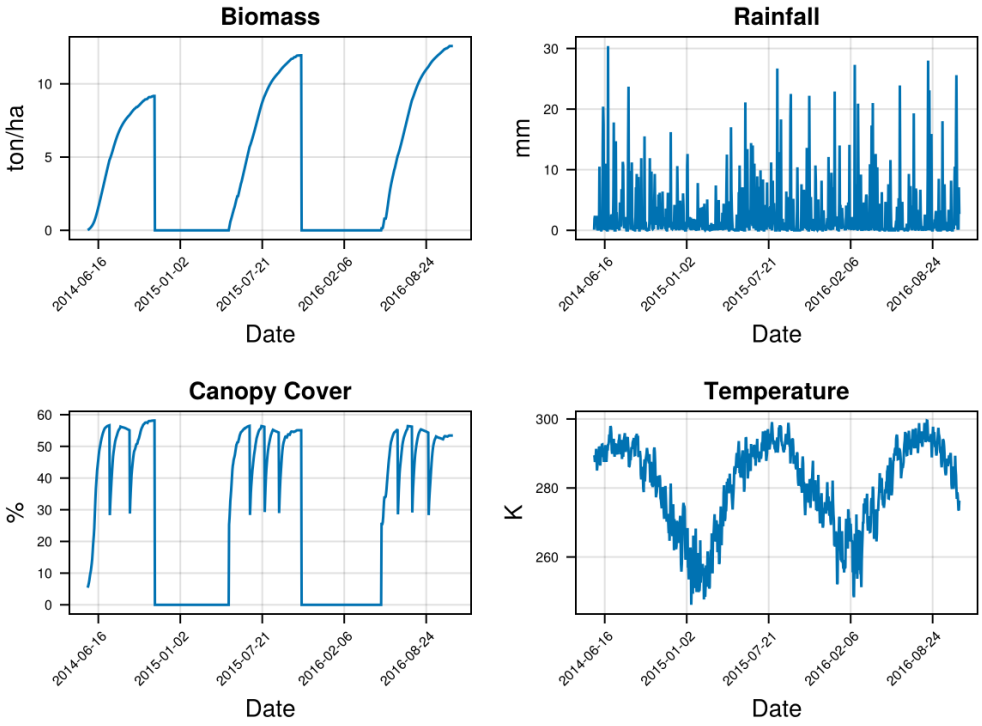

Figure 1: Simulated canopy cover and biomass of an alfalfa crop over time, together with daily temperature and rainfall.

The resulting graph is shown in Figure 1. Canopy cover increases during the growing season, with regular harvests taking place. Biomass is shown accumulated over the whole season.

Figure 2 shows a simulation of the growth of beans (*Vicia faba*) based on environmental data from Thuringia, Germany, with historical yield data shown for comparison. This showcases that when well parameterised, `AquaCrop.jl` forecasts the development of yields over time quite reliably (cf. Kostková et al., 2021). As the issue of parameterisation is a complex one, we provide a separate tutorial for this here, using publicly available crop data from Germany as an example.

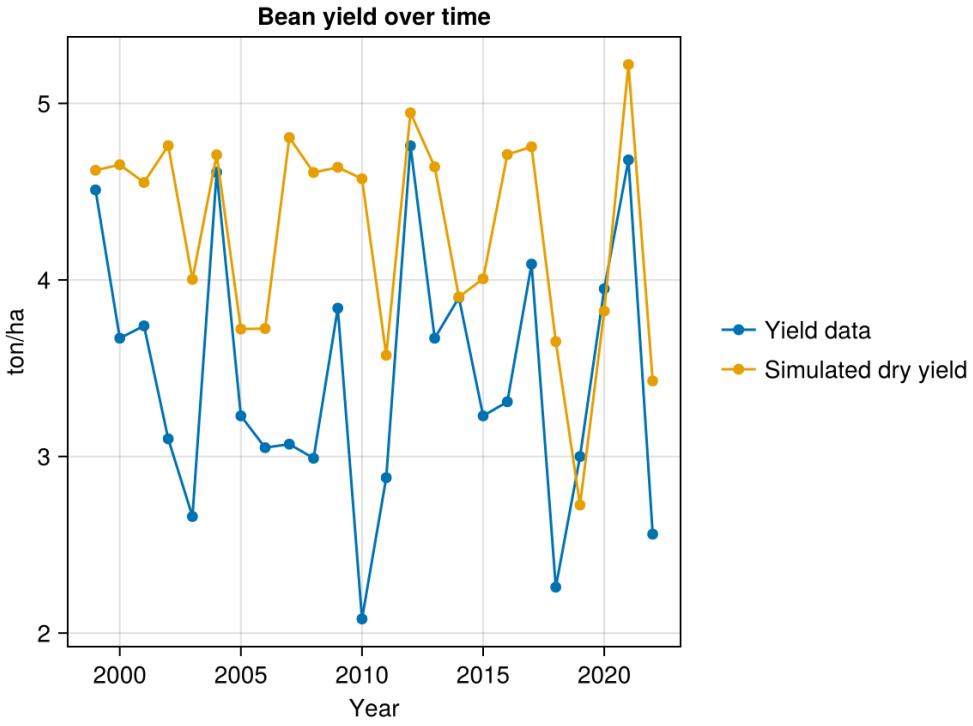

Figure 2: Simulated yield of beans (*Vicia faba*) compared to observed yields in Thuringia, Germany.

To facilitate comparisons between the Fortran and Julia versions, we made the original version available as a compiled binary using a Julia library package (JLL). This can be called as follows:

```
import Pkg
Pkg.add("AquaCrop_jll")
import AquaCrop_jll
# setup AquaCrop Fortran code input directories and files
run(AquaCrop_jll.aquacrop())
```

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