Marine Biology, Oceanography, Computer Science and Computational Science working together.

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T1:

Here we simulate phytoplankton cells as individuals in a well mixed reactor, like a lab experiment.

1. Import packages

```julia
begin
    using PlanktonIndividuals, Plots, JLD2
    using Plots.PlotMeasures
    using PlutoUI
end
```

2. Grid Setup

First we generate grid information (one grid box, 256m thick, and 128x128 in width) and the computational architecture (CPU).

```
arch =  CPU()
```

```julia
arch=CPU()
```

```
grid =
RegularRectilinearGrid{Float32, PlanktonIndividuals.Grids.Periodic, PlanktonIndividuals.(
domain: x ∈ [0.0, 128.0], y ∈ [0.0, 128.0], z ∈ [0.0, -128.0]
topology (Tx, Ty, Tz):     (Periodic, Periodic, Bounded)
resolution (Nx, Ny, Nz):   (1, 1, 1)
halo size (Hx, Hy, Hz):    (2, 2, 2)
grid spacing (Δx, Δy, Δz): 128.0, 128.0, [min=128.0, max=128.0])
```

```julia
grid = RectilinearGrid(size=(1,1,1), x = (0, 128meters), y = (0,128meters), z =
(0,-128meters))
```

3. Model Setup

Next we setup the individual-based model by specifying the computational architecture, grid, and plankton community.

```
model =
PlanktonModel:
├── floating point data type: Float32
├── grid: RegularRectilinearGrid{Float32, PlanktonIndividuals.Grids.Periodic, PlanktonInd
├── PlanktonIndividuals.QuotaMode() is selected for phytoplankton physiology
├── individuals: 1 phytoplankton species with 1024 individuals for each species
└── maximum number of individuals: 16384 per species
```

```julia
model = PlanktonModel(arch, grid; N_species = 1,
                                  N_individual = [2^10],
                                  max_individuals = 2^10*16)
```

And we setup diagnostics.

```
diags = PlanktonDiagnostics:
        ├── diagnostics of tracers: (:PAR, :NH4, :NO3, :DOC, :T)
        ├── diagnostics of individuals: (:num, :graz, :mort, :dvid, :PS, :BS, :Chl)
        └── save averaged diagnostics every 1 timesteps
```

```julia
diags = PlanktonDiagnostics(model; tracer=(:PAR, :NH4, :NO3, :DOC),
                                   plankton = (:num, :graz, :mort, :dvid, :PS, :BS, :Chl),
                                   iteration_interval = 1)
```

Then we setup the duration of the model simulation, a run directory location, and the kind of output we want.

```
sim = PlanktonSimulation:
      ├── ΔT: 300.0s
      ├── model time: 0.0s
      ├── simulation stops after: 288 iterations
      ├── no velocity provided
      ├── diagnostics:
      │   ├── diagnostics of tracers: (:PAR, :NH4, :NO3, :DOC, :T)
      │   ├── diagnostics of individuals: (:num, :graz, :mort, :dvid, :PS, :BS, :Chl)
      │   └── save averaged diagnostics every 1 timesteps
      └── output writer: nothing
```

```julia
sim = PlanktonSimulation(model, ΔT = 300.0seconds,
                                iterations = 288,
                                diags = diags)
```

Finally we setup the output writer.

```
PlanktonOutputWriter:
├── files are saved at ./results
├── diagnostics are saved as ./results/diags.jld2
├── individuals are not saved
├── write log: false
└── Maximum file size: Inf YiB
```

```julia
sim.output_writer = PlanktonOutputWriter(save_diags = true)
```

4. Model Run

```
update!(sim)
```

5. Access Results

Results have been stored in a `jld2` file. Let's open the file, look inside, and retrieve results.

```
file = JLDFile /home/cl/Downloads/results/diags.jld2 (read-only)
        └─📂 timeseries
           ├─📂 t
           │  ├─🔢 1
           │  ├─🔢 2
           │  ├─🔢 3
           │  ├─🔢 4
           │  ├─🔢 5
           │  ├─🔢 6
           │  └─ ⋯ (282 more entries)
           └─ ⋯ (6 more entries)
```

```
file = jldopen(sim.output_writer.diags_file, "r")
```

```
["t", "PAR", "NH4", "NO3", "DOC", "T", "sp1"]
```

```
keys(file["timeseries"])
```

Extract a vector of iterations

```
iterations =
 [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,   more ,279, 280, 281
```

```
iterations = parse.(Int, keys(file["timeseries/t"]))
```

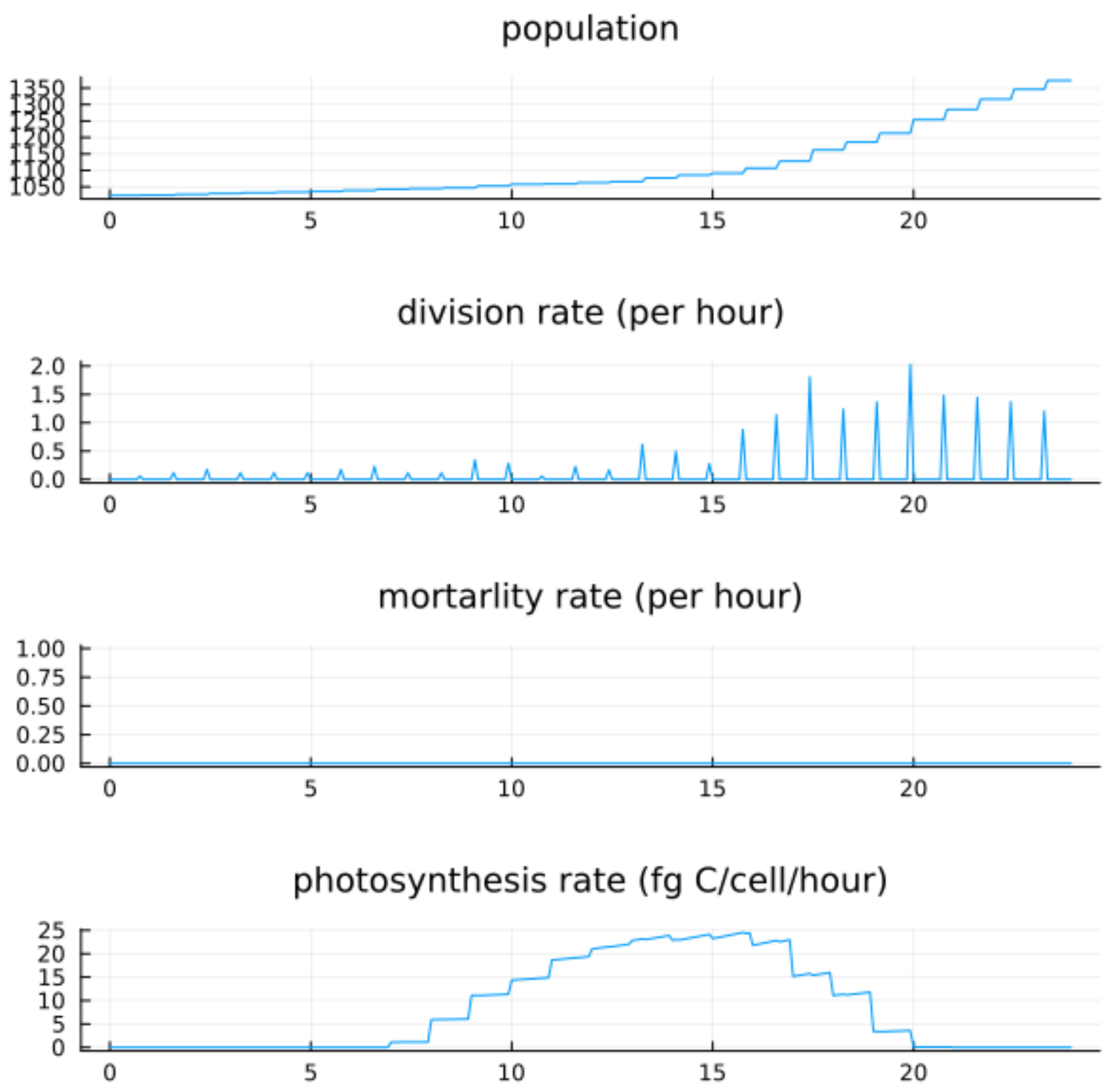
Read results into arrays and close file.

```
begin
    (PAR, NH4, NO3, DOC) = (zeros(288),zeros(288),zeros(288),zeros(288))
    fil2 = sim.output_writer.diags_file
    get_time_series!(fil2,"PAR",PAR)
    get_time_series!(fil2,"NH4",NH4)
    get_time_series!(fil2,"NO3",NO3)
    get_time_series!(fil2,"DOC",DOC)
end
```

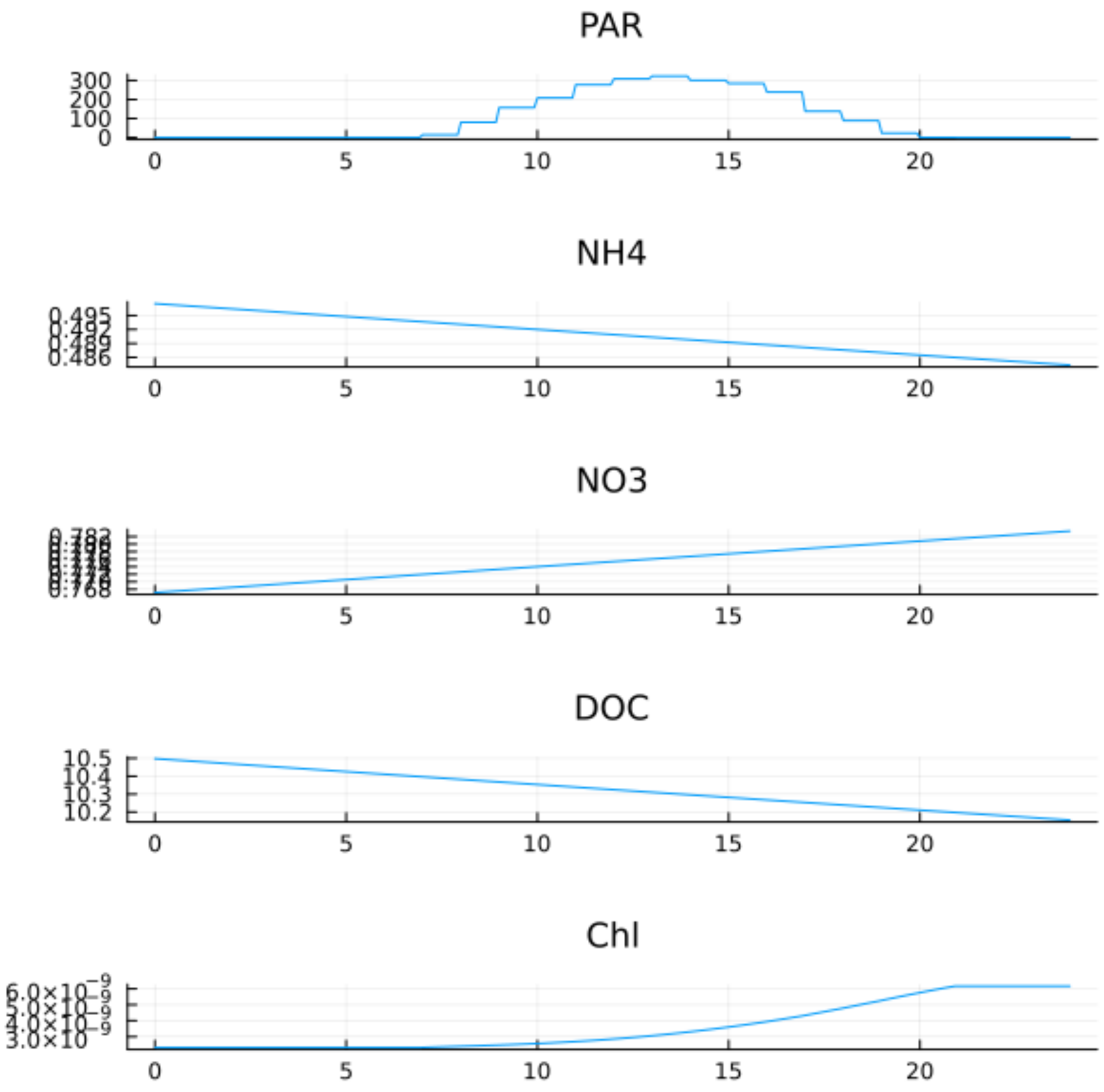
```
begin
    (num,dvid,mort,PS,Chl) =
    (zeros(288),zeros(288),zeros(288),zeros(288),zeros(288))
    fil = sim.output_writer.diags_file
    get_time_series!(fil,"sp1/num",num)
    get_time_series!(fil,"sp1/dvid",dvid)
    get_time_series!(fil,"sp1/mort",mort)
    get_time_series!(fil,"sp1/PS",PS)
    get_time_series!(fil,"sp1/Chl",Chl)
end
```

6. Vizualize Results

Now we plot the plankton population as function of time.



And then the environmental variables.



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Appendix: Helper Functions

```
get_time_series! (generic function with 1 method)
```