On calibration

April 10, 2020

Parameters to calibrate

Regarding calibration on real data, we first thought of assessing the effect of the parameters on which we had the most uncertainty. We first called it a sensitivity analyses, but if we also plan to use the best results afterwards for the rest of the simulations, this may be simply called a calibration (with a few words on the variability of the results with other parameters, which could be used in the discussion).

As a reminder, the first parameters we wished to calibrate

- sinking rate $\{0.1; 0.3; 0.5\}\beta(0.55, 1.25)$
- cyst mortality and burial $\approx 10^{-4}/10^{-5} \times 0.01; 0.1; 0.3$
- germination/resuspension $0.1; 0.01; 0.001 * 10^{-5}, 0.1$

This already means 10*11 parameters if we don't consider ranges.

Then, when designing new models, we considered calibrating on interactions too.

Calibration by quadratic programming is only possible for linear

However, this would mean scanning a space of 49 parameters. In the best case scenario, if we vary one parameter after the other (OAT, Morris-style?) with only two values around the calculated interactions (+/- 10 %, for instance), this still mean 49*48*3=7056 simulations. If we want to vary all parameters together (for instance $a_{11}^{'} = 1.1a_{11} \cap a_{12}^{'} = 1.1a_{12}$ with all other parameters at their first value, etc.), this means $C_{49*3,49}$.

Each simulation is very short, but we at least need to discuss this before lauching all simulations.

Diagnostics

We first considered:

- SAD
- direct calibration on annual dynamics ("burn-in" on first 10 years with synthetic temperature data, then using actual temperature to compare the dynamics)
- phenology based on the beginning of the bloom (maybe duration and number)

However, I think this could be too restrictive if we just want "phytoplankton-like" dynamics, and not the exact simulation of all species. Instead, we could simply have

- average abundance
- amplitude of the cycles
- beginning of the bloom