GOTM goes biogeochemical:
Application to Gotland Sea

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Motivation

- To create an environment within which any biogeochemical model can be implemented without technical problems.
- To allow for direct plug-in of the GOTM-BIO module into GETM and other three-dimensional models.
- To offer a wide choice of advection schemes (for vertical motions) and solvers for the ODE (sources and sinks) part.
Literature used


GOTM is a one-dimensional numerical model developed and supported by a core team of ocean modellers. GOTM aims at simulating accurately vertical exchange processes in the marine environment where mixing is known to play a key role. GOTM is freely available under the GPL (Gnu Public License).

The interested user can download the source code, a set of test cases (Papa, November, Flex, ...) and a comprehensive report.

You are warmly invited to join the GOTM mailing list and send any comments/questions to the GOTM team or become a GOTM contributor. The GOTM developers are grateful to their sponsors.
Stiff versus explicit solvers

Surface nutrient content in Northern North Sea seen with numerical different solvers:

Explicit solver at long time steps (left) does not obey nutrient limitation. Stiff solver (right, Burchard et al. [2003]) is stable and accurate. Note the different scales.
Neumann et al. 2002 model
Gotland Basin setups

1. Basic experiment

2. Experiment with reduced background turbidity (Jerlov class II instead of Jerlov class III)

3. Experiment with no feedback of bio-turbidity to the temperature equation (no feedback versus feedback)

4. Experiment with increased diapycnal mixing

\[ k_{\text{min}} = 4 \cdot 10^{-6} \text{ J kg}^{-1} \text{ instead } k_{\text{min}} = 1 \cdot 10^{-6} \text{ J kg}^{-1} \]

5. Experiment with increased wind forcing in February and March (factor 2 applied to wind speed in February and March)
Base run: temperature
Base run: Chl-a

CHLα: Modelled data and observations

Chl [mg m⁻³]

Base run: DIN

DIN: Modelled data and observations

DIN [mmol m$^{-3}$]

Base run: DIP

DIP: Modelled data and observations

DIP [mmol m⁻²]

Base run – Turbidity run: Temp.

Temperature: sensitivity to water turbidity
Base run – no feedback run: Temp.

Temperature: sensitivity to turbidity feedback
Conclusions

- 1D models for ecosystem studied need extra parameterisations for lateral processes (important e.g. for Gotland Basin studies)
- Nonetheless: 1D models help to understand model sensitivities and support ecosystem model development
- Improvements in physical parameterisations often require changes of ecosystem model parameters.
- Various other biogeochemical models have already been implemented into GOTM-BIO.
- Module can also be used for models for early diagenesis (sediment models).
- The new modified Patankar approach for solving the ODE part enables solution of stiff problems.