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Implementing a matrix-free Newton-Krylov method in NorESM

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Quasi-equilibrium ocean biogeochemistry states in Earth system models require prohibitively demanding computational time, especially for when large number of tracers are involved. This so-called spin-up typically is measured in the order of thousands of model years integration. In this study, we implement a matrix-free Newton-Krylov method (Khatiwala, 2008) in the Norwegian Earth system model (NorESM) so the spin-up time can be reduced. The idea is to construct the function $\mathbf{F}(\mathbf{u}) = \Phi(\mathbf{u}(0), T) - \mathbf{u}(0) = \mathbf{0}$, which can be expressed as a matrix in which we can apply Newton-Krylov methods to find the quasi-equilibrium states. Unfortunately the interconnectivity and complexity of the processes leads to a dense matrix, making it expensive and impractical to calculate the necessary Jacobian, $J = \partial\mathbf{F}/\partial\mathbf{u}$.

The Newton-Krylov method remedies this issue through solving the matrix-vector product $J\delta\mathbf{u}$, that can be approximated by $\left(F(\mathbf{u}^n + \sigma\delta\mathbf{u}^n) - F(\mathbf{u}^{n-1})\right)/\sigma$. The differencing parameterσ is typical chosen dynamically, and n is the iteration index. Matrix-free Newton-Krylov method requires a good preconditioner to improve the convergence rate. By exploiting the inherent locality of the advection-diffusion operator, and that in most biogeochemical models, the source/sink term at a grid point depends only on tracer concentrations in the same vertical column, we obtain a good, sparse preconditioner. The performance of this preconditioner can be improved again by applying both outer Broyden updates during the Newton steps and inner Broyden updates during the Krylov steps.

Khatiwala, S., 2008. Fast spin up of ocean biogeochemical models using matrix-free Newton-Krylov. Ocean Model. 23 (3-4), 121-129.