



Assessing the transport matrix method with HAMOCC

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Our goal is to reduce the spin-up time of the ocean biogeochemistry in NorESM, which uses our version of MICOM and HAMOCC as the physical model and the biogeochemistry model respectively. We want to use the matrix-free Newton-Krylov method, and to facilitate this, we will use the transport matrix method to timestep and transport the marine tracers. In this method the advection and diffusion are represented by a series of sparse matrix-vector products that can efficiently be performed on a distributed memory system. The matrices needed can be recorded from an equilibrium run of the physical model, but for now we have chosen to use pre-recorded transport matrices from an alternative physical model.

We are comparing the time-stepping and transport of the tracers by a MICOM-HAMOCC run with a TMM-HAMOCC run to evaluate the integration of the latter.

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