Coupling BFM with ocean models:

the MITgcm model

S. Querin, G. Cossarini, P. Lazzari, G. Bolzon

Release 1.0, April 2023
—— BFM Report series N. 5 ——

http://bfm-community.eu
bfm_st@cmcc.it

BFM
BIOGEOCHEMICAL FLUX MODEL

This document should be cited as:
Querin S., Cossarini G., Lazzari, P., Bolzon, G. (2023). Coupling BFM with MITgcm model. BFM Report series N. 5, Release 1.0, April 2023, Trieste, Italy, http://bfm-community.eu

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1 Introduction

1.1 The MITgcm and BFM models and the basic coupling equations

The MITgcm-BFM is an online coupled hydrodynamic-biogeochemical model: ocean dynamics and tracers transport are solved by the MITgcm, while biogeochemical reactions are handled by the BFM (Figure 1.1). The MITgcm (Massachusetts Institute of Technology general circulation model; Marshall et al., 1997) is a 3-D, finite volume, general circulation model used by a wide scientific community. It can be customized to obtain different configurations by modifying its available packages and parameters, according to the user's needs and to the design of the numerical experiment (Campin et al., 2023). The code and documentation of the MITgcm are under continuous development: the modular Fortran77 code is open source and it can be downloaded from the MITgcm Git repository (https://github.com/MITgcm/MITgcm). Further information and useful links can be found on the MITgcm website (http://mitgcm.org/). The Biogeochemical Flux Model (BFM) is an open-source, modular, Fortran90 numerical model designed to describe the dynamics of the major biogeochemical processes that occur in marine ecosystems (Vichi et al., 2023). The software described in this document is essentially the coupler (BFMCOUPLER) between the MITgcm ocean circulation model and the BFM biogeochemical reaction model (Figure 1.1). The BFMCOUPLER code has been designed as an additional MITgcm package that handles the exchange of information between the hydrodynamic and the biogeochemical compartments. The coupled numerical model solves the transport-reaction equations, where the reaction terms are defined within the BFM framework. Specifically, the set of partial differential equations for a generic tracer concentration C can be written as:

$$\frac{\partial C}{\partial t} = -\mathbf{u}\cdot\nabla C + \nabla_H\cdot(A_H\nabla_H C) + \frac{\partial}{\partial z}A_V\frac{\partial C}{\partial z} - w_B\frac{\partial C}{\partial z} + \left.\frac{\partial C}{\partial t}\right|_{bio} \tag{1.1.1}$$

where $\mathbf{u}\equiv(u,v,w)$ is the three-dimensional current velocity and (A_H, A_V) are the horizontal and vertical turbulent diffusivity coefficients, respectively. w_b is the sinking velocity of living or dead organic particulate matter. The first three terms on the right hand side (advection and diffusion terms) are solved by the PTRACER package of the MITgcm. Additionally, the BFMCOUPLER handles the sinking process and the computation of the biogeochemical derivatives, which are the reaction terms described in BFM as a set of ordinary differential equations that express the transformation fluxes of biogeochemical properties in the marine environment. The BFM formulation and the standalone implementation are fully described in the BFM manual (Vichi et al., 2023).

1.2 Main features of the coupled model code

The MITgcm–BFM coupling was achieved by upgrading a few routines of the MITgcm GCHEM package (Geo-CHEMistry), which handles the evolution of tracers, and by developing the additional package BFMCOUPLER, which was specifically designed as the interface with the BFM model. The

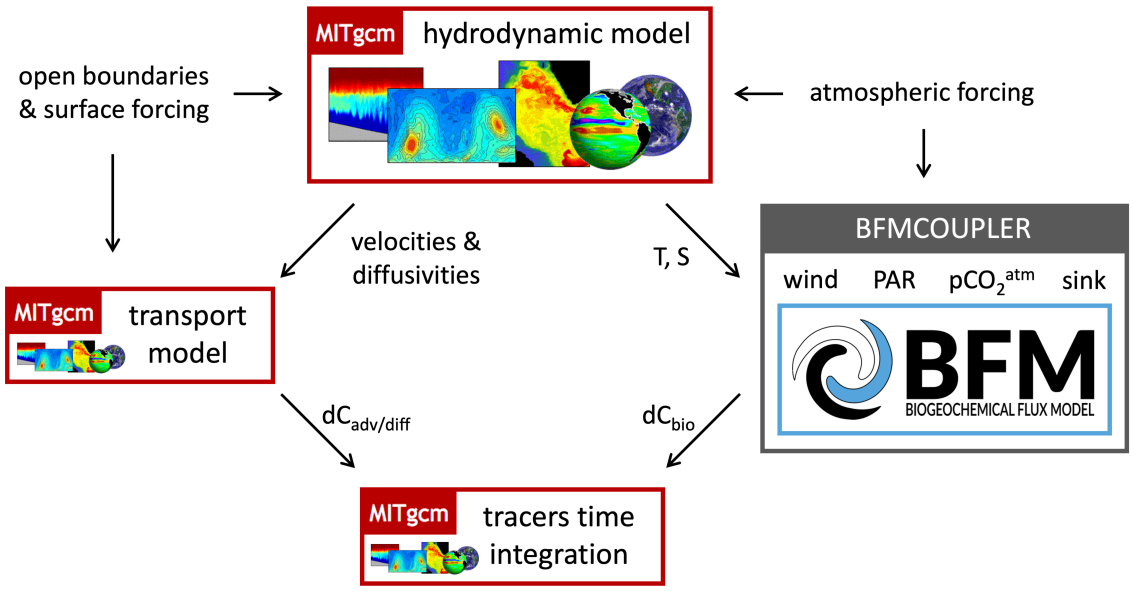

Figure 1.1: Scheme of the numerical integration of the MITgcm-BFM online coupled model.

BFM is called by the MITgcm as an external library; therefore, the BFM must be compiled separately using the same compiler used for the MITgcm.

The key routines of the BFMCOUPLER package that drive the initialization, the internal time stepping, the external fields loading, and the diagnostics setting are listed in the following paragraphs.

1.2.1 Initialization

BFMCOUPLER_VARS.h contains the common blocks for the list of the BFM state variables and diagnostic variables (BFM_var_list.h) and for the parameters and fields that are required to calculate the carbonate system solution, carbon dioxide air–sea exchange, PAR, light extinction, sinking, and nutrient air deposition and bottom fluxes. Forcing fields can be initialized either with a background value by BFMCOUPLER_INI_FORCING.F or read from external fields. BFMCOUPLER_READPARAMS.F reads the data.bfmcoupler namelist, which contains the names of the files for the above fields. The parameters that manage the time intervals for reading, interpolating, and applying the external forcing are read from the above mentioned namelist. The input namelist also contains specific parameters for the processes solved by the BFMCOUPLER: sinking speed for detritus, self-shading coefficients for different phytoplankton groups, and background values of the seawater light extinction factor. The allocation of memory used by the BFM is set (at this point) here by the BFM BFM_initialize routine. The BFMCOUPLER_READPARAMS.F routine is called from the conveniently modified GCHEM_READPARAMS.F routine (a call statement to BFMCOUPLER_READPARAMS must be added). Accordingly, GCHEM_INI_VAR.F must contain a call statement to BFMCOUPLER_INI_FORCING.F.

1.2.2 Time stepping routine

The core of the present coupling scheme is the BFMCOUPLER_CALC_TENDENCY routine, which is called by the MITgcm native routine GCHEM_CALC_TENDENCY. The approach adopted in

this coupling scheme is to loop in space and to call the BFM as a subroutine to calculate the derivative terms of each biogeochemical tracer for each computational grid point. The BFMCOUPLER_CALC_TENDENCY routine solves some additional processes such as light penetration, sinking of phytoplankton and detritus, and the exchange processes across the surface and bottom layers of the water column.

1.2.3 Loading fields

The external forcing fields used by the BFMCOUPLER (i.e., CO2 air concentration, PAR, light extinction factor, nutrient air deposition, and bottom fluxes) are read by the BFMCOUPLER_FIELDS_LOAD.F routine, which is called from the modified GCHEM_FIELDS_LOAD.F routine (a call statement must be added). Input/output directives are based on the native MITgcm I/O package (MDSIO), a set of Fortran routines for reading and writing direct-access binary files.

1.2.4 Diagnostics

The BFMCOUPLER package uses the MITgcm's DIAGNOSTICS package. The definition of new specific diagnostics from the BFM's fluxes and variables is managed in BFMCOUPLER_DIAGNOSTICS_INIT.F, which is called from BFMCOUPLER_INIT_FIXED.F. The new diagnostics quantities are calculated in BFMCOUPLER_CALC_TENDENCY.F through a list of files (BFMcoupler_VARDIAGlocal.h, BFMcoupler_VARDIAGcopy_fromD.h, and BFMcoupler_VARDIAG_fill_diags.h) that use the variables from the BFM0D_output_ecology BFM routine and specific instructions from the diagnostics package (DIAGNOSTICS_FILL.F routine). New diagnostic quantities are listed in the namelist in the data.diagnostics parameter file, which specifies the frequency and type of output, the number of levels, and the names of all the separate output files. The coupled MITgcm–BFM model can use a large number of tracers; therefore, increasing the ndiagMax parameter in diagnostics_size.h may be necessary. The initialization of BFMCOUPLER diagnostics is provided by adding a call statement to BFMCOUPLER_INIT_FIXED.F in the GCHEM_INIT_FIXED.F routine.

1.2.5 Long-step option

The LONGSTEP MITgcm package allows the tracer time step to be longer than the time step used by the hydrodynamic model. When this package is activated along with the BFMCOUPLER package, a new specifically developed version of the LONGSTEP_THERMODYNAMICS.F routine has to be used. The new version of this routine includes a call to BFMCOUPLER_CALC_TENDENCY. The BFMCOUPLER routines use the hydrodynamic variables stored in the LONGSTEP variables, which are either the averages or the temporal sub-samplings of the variables of the master hydrodynamic model, depending on the when_to_sample parameter set in the data.longstep namelist file.

A full description of the BFMCOUPLER package is provided in Cossarini et al. (2017).

2 Installation, configuration and compilation

In order to build the MITgcm-BFM executable, the following steps have to be performed.

```
# Download the source codes from GitHub:
% git clone git@github.com:inogs/MITgcmBFM-build.git
% cd MITgcmBFM-build
% git checkout bfm-release-5.3
% ./downloader_MITgcm_bfm.sh

# The downloader is configured to retrieve the checkpoint66j version of the
    MITgcm and the dev_mitgcm branch of the BFM, which contains the BFMCOUPLER
     code.

# Edit builder_MITgcm_bfm.sh, to set debug mode or not, compiler paths,
    modules, etc. For example:
# MIT_COMPILER=intel (gfortran)
# export MODULEFILE=$PWD/compilers/machine_modules/g100.intel (yourmachine.
    yourcompiler)
# Put your platform specific INC_FILE for BFM in: $BFMDIR/compilers/$INC_FILE
    (e.g., x86_64.LINUX.gfortran.inc)


##########  Compile and build bfm  ##########
% ./builder_MITgcm_bfm.sh -o bfm
#############################################

# Set the number of cores and the domain decomposition of your model run,
    configuring SIZE.h
# and choosing among the various options of the experiment.
# E.g., the cube test case experiment described in Cossarini et al. (2017).

# Choose the experiment configuration from the presets/ directory.
# For the test case, use the preset CUBE-GMD.


#######  Configure/customize the setup  #########
% ./configure_MITgcm_bfm.sh --preset CUBE-GMD
################################################

# This procedure generates the code in the MYCODE/ directory and the namelists
     (i.e., data.diagnostics and data.ptracers) in the
    READY_FOR_MODEL_NAMELISTS/.
# To customize the experiment, the namelists can be edited by the user, for
    example:
# data.diagnostics is used by the MITgcm DIAGNOSTICS package to manage the
    output of the simulation (see the MITgcm manual);
# data.ptracers in used to set ICs, advection scheme, etc. for each tracer.
```

```
# If needed, the MYCODE directory can be updated with specifically modified
    routines (different OBCs, meteorological forcing files, etc.).
# Platform-specific INC_FILE for MITgcm must be also added in: $PWD/compilers/
    $INC_FILE (e.g., x86_64.LINUX.gfortran.inc)
# Lastly, the executable mitgcmuv can be generated in the MITGCM_BUILD
    directory:

########  Compile and build MITgcm  ############
% ./builder_MITgcm_bfm.sh -o MITgcm
################################################
```

3 Running a MITgcm-BFM test case

A test case for the MITgcm-BFM model is described in Cossarini et al. (2017). The numerical experiment is based on a idealized domain forced by steady winds and a seasonal cycle of surface heat (downward long-wave and short-wave radiation) and mass (precipitation) fluxes. The horizontal shear in the surface wind field maintains a permanent cyclonic gyre, whereas the surface heat fluxes act on the thermohaline properties of the water column. The closed domain is discretized by adopting a uniform grid spacing in the horizontal direction, creating 64 grid cells in both directions. All the peripheral grid points of the bathymetry are land points (closed box), whereas the bottom of the domain is a bowl-shaped pit. In the vertical direction, the model is composed of 30 layers with non-uniform thickness (from 1.5 to 21 m). The time step equals 300 s.

The configuration of the MITgcm includes the following packages (listed in `data.pkg`): cal, exf, kpp, longstep, diagnostics, ptracer and BFMCOUPLER.

Specific runtime options (e.g., free-surface formulation and volume conservation constraints) are set in the parameters contained in the namelist

- `data`

Other package-specific namelists for the MITgcm-BFM runs are:

- `data.ptracer`
- `data.BFMcoupler`
- `data.cal`
- `data.diagnostics`
- `data.exf`
- `data.gchem`
- `data.kpp`
- `data.longstep`

Additional explanation of the MITgcm namelists is provided in Cossarini et al. (2017).

The `input/` directory provides files for a 10-day long simulation.

The atmospheric forcing is provided by the 8 components listed below (summing up to 64 x 64 x 10 x 8 bytes for each variable):

- short-wave radiation: `swdown_64x64_10dx37.dat`
- long-wave radiation: `lwdown_64x64_10dx37.dat`
- precipitation: `precip_bal_64x64_10dx37.dat`
- zonal wind component: `uwind_64x64_10dx37.dat`

- meridional wind component: `vwind_64x64_10dx37.dat`
- air pressure: `apressure_64x64_10dx37.dat`
- air temperature: `atemp_64x64_10dx37.dat`
- air humidity: `aqh_64x64_10dx37.dat`

Further forcing and setup files are provided for the river runoff, the bathymetry and the vertical profiles that characterize the initial conditions:

- runoff: `runoff_64x64_10dx37.dat`
- the bathymetry and grid, which is a 64 x 64 box, with 30 vertical levels (closed_box64x64.bat)
- init/ contains the profiles that can be used to generate the initial conditions for the biogeochemical tracers

A detailed documentation on how to run the MITgcm model can be found at https://mitgcm.readthedocs.io/en/latest/, while the instructions to run the provided test case are reported below.

```
######  Work area generation  ######
% cd testcase
% ./testcase_generator.sh
#####################################

# This script creates the wrkdir/run/ directory and populates it with the
    generated ICs, meteo files, bathymetry and namelists

# Run the test in serial mode
% cd wrkdir/run
% source $MODULEFILE  # the same used for compiling the code

####  Launch of the executable  #####
% ./mitgcmuv
#####################################
```

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