

# SHAREMED - WP3.1

Developing a relocatable high-resolution  
short-term forecasting system  
for the marine environment

## Document Control Sheet

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| Project title:   | Sharing and enhancing capabilities to address environmental threats in Mediterranean Sea |

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## Introduction

This report describes the high-resolution, relocatable modelling system for short-term forecasts developed within Sharemed and provides the basic instructions to implement this numerical tool in different areas of the Mediterranean Sea. The relocatable system is based on the coupled hydrodynamic-biogeochemical model MITgcm-BFM, and it is initialized and forced by the Copernicus Marine Environment Monitoring Service (CMEMS-CMS) and other available operational products (e.g., satellite data, in-situ measurements). The package has been designed for expert users, with a suite of scripts and procedures for downloading initial, boundary and forcing data and for model set up, once the user has selected a specific geographical domain in the Mediterranean. The whole code is publicly available on specific GitHub repositories, while further details on model setup, implementation and upgrades are provided in a dedicated online wiki page ([https://github.com/inogs/MITgcm\\_BFM\\_chain/wiki](https://github.com/inogs/MITgcm_BFM_chain/wiki)) in which the description of the modeling system can be updated according to its evolution and further developments.

The forecasting system was designed to be easily relocatable: it was firstly implemented in operational mode in the northern Adriatic study site, then it was further tested and applied in a cluster of transnational coastal areas in the Mediterranean Sea (i.e., Sicily Channel -WP4.5- and North Western Med and sub-basins -WP5.1-). All the local implementations were customized by adapting the python and bash scripts developed for the pre- and post-processing phases of each operational system, which shapes up to be an effective regional downscaling of the Copernicus Marine Service (CMS) Analysis and Forecast products.

## General description of the relocatable forecasting system

The relocatable forecasting system was developed by OGS and it is built upon the coupled hydrodynamic-biogeochemical model based on the MITgcm and BFM open-source codes (Figure 1), both of which keep up to the state-of-the-art in the scope of ocean modelling. It is nested into the CMEMS Analysis and Forecasting

system, and it includes the whole operational chain for running the simulations on a daily basis.

The general documentation for the coupled (hydrodynamic-biogeochemical) model MITgcm-BFM can be found at the following links:

- hydrodynamic model: <http://mitgcm.org>
- biogeochemical model: <https://cmcc-foundation.github.io/> - [www.bfm-community.eu/](http://www.bfm-community.eu/)
- coupler (MITgcm-BFM): <https://gmd.copernicus.org/articles/10/1423/2017/>

The “relocability” means that an experienced user should be able to implement and run the forecasting system on his/her own HPC platform without too many efforts. Indeed, the operational chain includes pre-processing, launch and post-processing steps, i.e.:

- selection, “cut” and interpolation of the initial (ICs) and open boundary conditions (OBCs) from CMEMS;
- integration of river contributions into the open boundary condition (OBCs: sections/”slices” derived from CMEMS);
- definition of surface and bottom biogeochemical fluxes;
- creation of model namelists containing all the runtime parameters;
- various scripts in order to manipulate meteorological forcings originating from different sources/services.

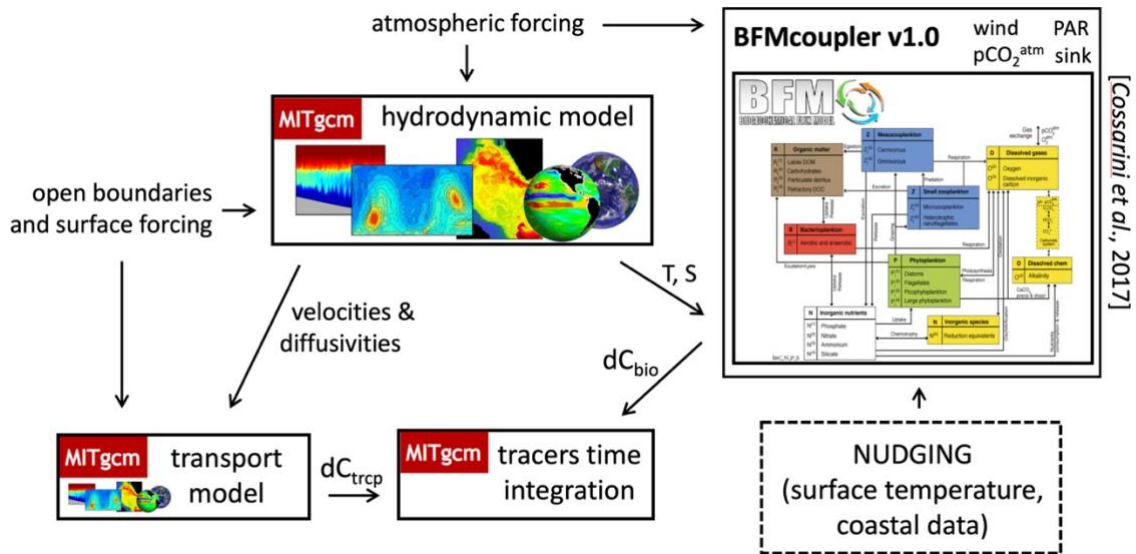


Figure 1 - Description of the MITgcm-BFM coupling used in SHAREMED.

The forecasting system was initially developed by OGS on the northern Adriatic Sea (at  $1/128^\circ$  resolution) and it is running operationally since several years, providing 72-hour forecasts (<http://medeaf.ogs.it/adriatic>). The implementation of the relocatable system relies on code sharing through GitHub repositories and, during the project, different customized configurations were developed at each study site (Figure 2).

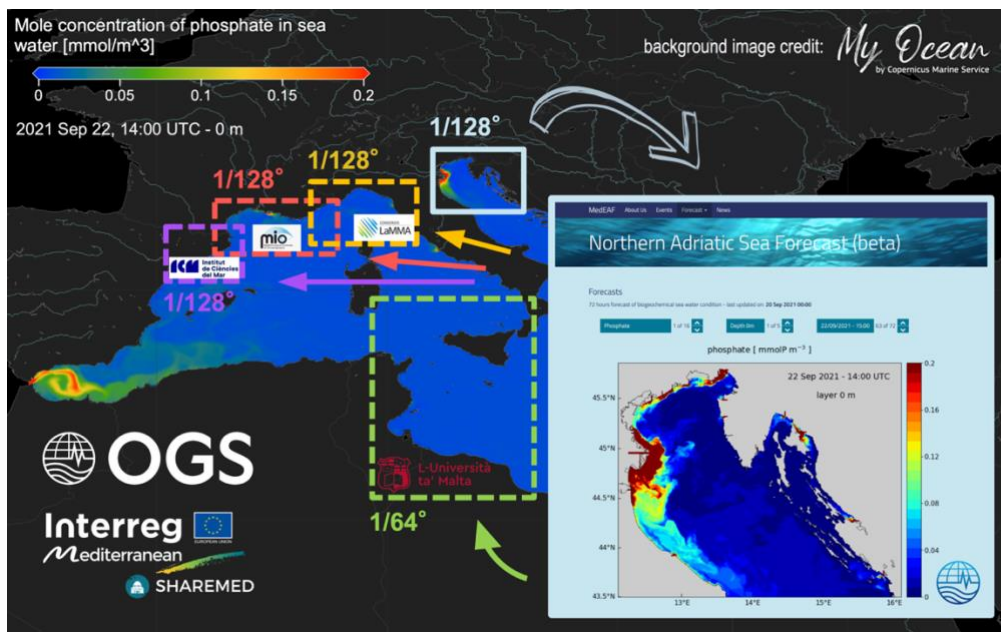


Figure 2 - The different configurations of the relocatable forecasting system in SHAREMED.

## Instructions to compile and build the coupled MITgcm-BFM executable

In order to build the MITgcm-BFM executable, the user must follow the steps below.

Define your `ModelBuild` directory and clone from the GitHub repository the tool for building the model:

```
DIR=ModelBuild  
git clone git@github.com:inogs/MITgcmBFM-build.git $DIR
```

Download the source code of **BFM**, of the **coupler** and of **MITgcm**:

```
cd $DIR  
git checkout main  
./downloader_MITgcm_bfm.sh
```

Edit `builder_MITgcm_bfm.sh`, to set debug mode or not, compiler, modules, etc...

For example:

```
MIT_COMPILER=intel (gfortran)  
export MODULEFILE=$PWD/compilers/machine_modules/g100.intel  
(fluxus.gfortran, yourmachine.yourcompiler)
```

Put your HPC-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
```

Decide the number of cores and the domain decomposition of your model run, configuring your `SIZE.h` (e.g., choosing among the various options of the northern Adriatic benchmark experiment). E.g., for 95 cores:

```
cp presets/NORTH_ADRIATIC/SIZE.h_095p presets/NORTH_ADRIATIC/SIZE.h
```

Configure/customize the setup:

```
./configure_MITgcm_bfm.sh
```

If needed, update the MYCODE directory with your own modified routines (different OBCs, meteorological forcing files, etc...).

Put your HPC-platform-specific *INC\_FILE* for MITgcm in:

```
$PWD/compilers/$INC_FILE (e.g., x86_64.LINUX.gfortran.inc).
```

Compile and build MITgcm: use the same builder used for compiling BFM (i.e., *builder\_MITgcm\_bfm.sh*)

```
./builder_MITgcm_bfm.sh -o MITgcm
```

The executable (*mitgcmuv*) is in *\$PWD/MITGCM\_BUILD*.



## Instructions to install the operational chain

In this section we describe the main dependencies in the code pipeline and we provide a primer for the production workflow, from the download of the code to the installation of the chain.

Clone the operational chain from the GitHub repository.

```
git clone git@github.com:inogs/MITgcm\_BFM\_chain.git
```

The installation of the chain relies on the script called `mit_setup_chain.ksh`. In order to run it, the user must set properly the `mit_profile__machine.src_inc`, where *machine* is the name of the host, as set up in the `MIT_HOSTNAME` variable.

With this configuration script, the user must set some variables and run some commands, depending on the *machine* used (i.e., the available computing facility). The structure of this file is explained below, so that the user/installer can configure it without difficulties.

### Variables

- `MIT_NETCDF_PATH`: is the path of folder containing the NetCDF library on the machine (one can locate easily, for instance, loading the proper module, and spotting the folder in the `LD_LIBRARY_PATH` env variable);
- `MIT_DATE_PATH`: the path of `date` command (almost certainly will be `/usr/bin/date`);
- `MIT_NCKS_PATH`: the path of `ncks` on the machine;
- `MIT_NCFTPGET_PATH`: the path of `ncftpget` on the machine;
- `MITGCMUV_PATH`: the path of the executable produced during the compilation of the model (see section above). This will be located in the `MITGCM_BUILD` subfolder of the model folder;
- `MOTUCLIENT_UNPACK_DIR`: a path where the tool `motuclient` will be unpacked (usually set to `$MIT_BINDIR/motuclient`);

- `PYTHON3_PATH`: the path of a valid `python3` interpreter. It is used just to create virtual environment, the interpreter included in this environment will be used.

## Functions

- `mit_mkdir <dir>`: creates the directory `<dir>` with all its parents and checks for the success;
- `symlink_if_not_present <path> <link>`: symbolic links the `<path>` to `<link>` if `<link>` is not already present. If it is so, the function does nothing. If `<path>` it not present, it returns an error state;
- `clone_or_update <git_link> <path> <branch>`: if `<path>` is not present, it clones the `<git_link>` repo to `<path>` checking out branch `<branch>` (notice: if `<path>` is present it does nothing, the 'update' part has still to be implemented);
- `download_and_unpack <url> <path> <filename> <extraction_dir>`: downloads file at `<url>` placing it to `<path>/<filename>`. Then it creates the directory `<extraction_dir>` and extracts the contents to it. If some step fail, the function returns an error status;
- `set_python_environment <python3_path> <requirements>`: uses `<python3_path>` to create an environment according to the variable `$MIT_VENV_1` (set in `mit_profile.src_inc`). Then it activates the environment, and uses `pip` to install all the requirements specified in `<requirements>` (the `python3` path is set for convenience in the variable `PYTHON3_PATH`. The requirements are listed in the file `$MIT_HOME/requirements.txt`).

Note that all the functions above are idempotent up to an upgrade coming from online repositories. This means that a script containing these function can be safely executed n times without spoiling the setup.

## Commands

Although the exact command depends on the specific machine (i.e., modules to load, particular env variable to set) the structure of the file is the following:

```
# env variable section
mit_batch_prex "export
LD_LIBRARY_PATH=${MIT_LIBDIR}:${MIT_NETCDF_PATH}:${LD_LIBRARY_PATH}"
mit_batch_prex "mit_mkdir $MIT_BINDIR"
# symlink section
mit_batch_prex "symlink_if_not_present $MIT_DATE_PATH
$MIT_BINDIR/date"
mit_batch_prex "symlink_if_not_present $MIT_NCKS_PATH
$MIT_BINDIR/ncks"
mit_batch_prex "symlink_if_not_present $MIT_NCFTPGET_PATH
$MIT_BINDIR/ncftpget"
mit_batch_prex "symlink_if_not_present $MITGCMUV_PATH
$MIT_BINDIR/mitgcmuv"
# git section
mit_batch_prex "clone_or_update $MIT_BITSEA_REPO $MIT_BITSEA
$MIT_BITSEA_BRANCH"
mit_batch_prex "clone_or_update $MIT_POSTPROC_REPO $MIT_POSTPROC_DIR
$MIT_POSTPROC_BRANCH"
mit_batch_prex "clone_or_update $MIT_BC_IC_REPO
$MIT_BC_IC_FROM_OGSTM_DIR $MIT_BC_IC_BRANCH"
# motuclient section
mit_batch_prex "download_and_unpack $MIT_MOTUCLIENT_URL $MIT_BINDIR
motuclient.tar.gz $MOTUCLIENT_UNPACK_DIR"
mit_batch_prex "symlink_if_not_present
$MOTUCLIENT_UNPACK_DIR/src/python $MIT_BINDIR/motuclient-python"
# python3 section
mit_batch_prex "set_python_environment $PYTHON3_PATH
$MIT_HOME/requirements.txt"
# module section
# ad libitum
```

After setting `mit_profile__machine.src_inc`, create a script (e.g., `chain_env.sh`) with the following content (export and alias).

NOTE: given the example below, you could put it in `/yourpath/`.

```
-----  
# MIT_HOME is your MITgcm_BFM_chain directory, the root of the git  
repository  
export MIT_HOME=/yourpath/MITgcm_BFM_chain  
# your machine name  
export MIT_HOSTNAME=fluxus  
# your work-launch (e.g., "scratch" area) directory in a parallel  
filesystem  
export MIT_WORKDIR=/yourpath/WORK  
export MIT_VERSION_NUMBER=1  
export MIT_STAGE=devel  
alias mitcd="cd $MIT_HOME ; pwd"  
-----
```

Then do:

```
source chain_env.sh  
cd $MIT_HOME/bin/src
```

For a first check that everything works, compile and install all the scripts:

```
make  
make install
```

Add a line referring to your `mit_profile__<yourmachinename>.inc` in the *SCRIPTS* list of the Makefile (`$MIT_HOME/bin/src/Makefile`) and perform another (updated) installation:

```
make  
make install
```

Once the job scheduler options are set (consult your IT manager for these details), you can launch your model run (with bulletin date: 19/10/2021, as an example).

```
cd $MIT_HOME/bin  
./mit_start.ksh --pass --job-multiple --force --try-resume --without-kill --rundate 20211019
```

`mit_start.ksh` generates the `log` directory, where the single jobs and/or the single executables can be submitted or launched one by one for each of the three “stages” of a forecast run: preprocessing, model run, postprocessing.

To conclude, the compilation phase will produce an executable (MITgcm-BFM) called `mitgcmuv`. For running the model:

- **option 1 - full operational chain**

`mit_start.ksh` should run the whole model chain (if there are no setup/runtime errors). The job produced by `mit_start.ksh` (which needs the machine-specific scheduler options) will look for the MITgcm-BFM executable located in `$MIT_HOME/HOST/$MIT_HOSTNAME/bin/` (together with the other executables: `date`, `ncks...`).

The executable can be renamed "`mitgcmuv_<number_of_cores>`", where the number of cores is specified in `mit_mpi__intelmpi.src_inc`.

- **option 2 - test simulation**

copy the `mitgcmuv` executable in your run directory and run the simulation using a customized job for your local scheduler.

## Model output

Model output is dumped in the native MITgcm format, in png images or in NetCDF products, organized in the same way as the CMS modelling products for the Mediterranean Sea. Figure 3 shows an example of model output published on a dedicated web page (<https://medeaf.ogs.it/adriatic>).

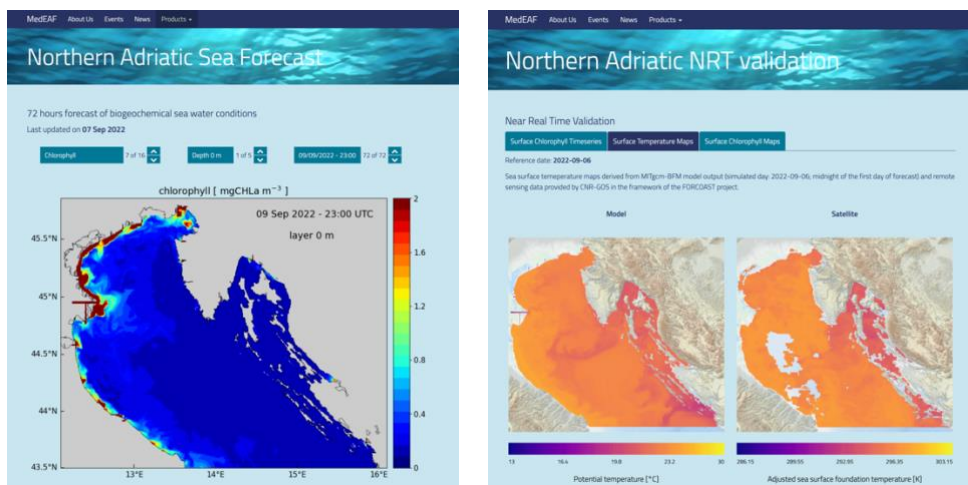


Figure 3 - Examples of model output published on dedicated web pages: chlorophyll forecast fields (left) and SST comparisons with satellite data (right).

NetCDF products can be also stored on specific web services, like the THREDDS server shown in Figure 4.

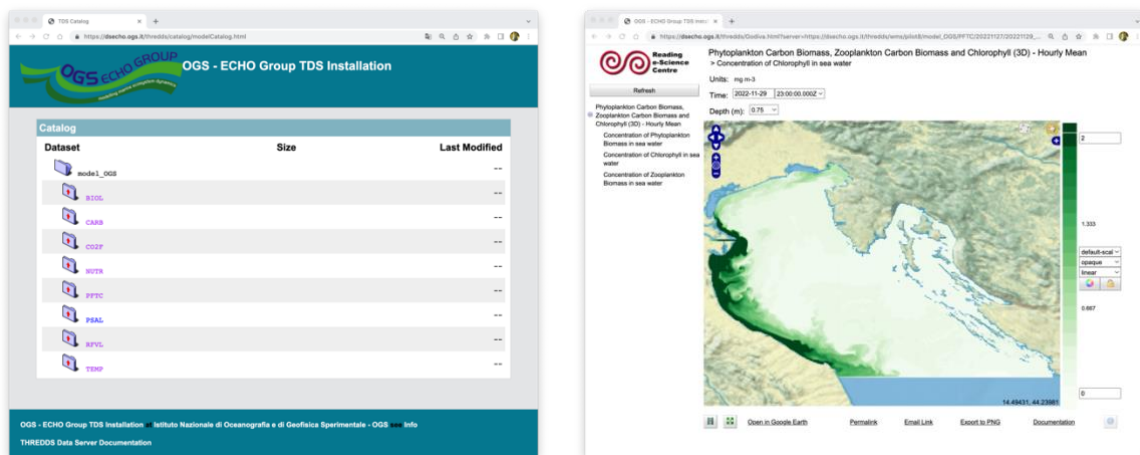


Figure 4 - Example of model output stored on a dedicated THREDDS server and visible through the "preview" tools available.

## Conclusions

In the framework of SHAREMED, we developed a short-term forecasting system for ocean hydrodynamics and biogeochemistry in a cluster of transnational coastal areas in the Mediterranean Sea.

Model development has been carried out in the northern Adriatic Sea (AS). The system was subsequently tested in the Sicily Channel (SC), and finally transferred to the northwestern Mediterranean Sea (NWM), where the domain has been further subdivided into three transnational sub-basins: the Ligurian Sea, the Gulf of Lion and the Catalan Sea.

At present, the system is running in operational or pre-operational mode on a daily basis in all the study sites, providing 2- to 3-day forecasts of the main physical and biogeochemical variables (e.g., currents, thermohaline properties, nutrients, chlorophyll, dissolved oxygen). The results are published on dedicated SHAREMED portals and site-specific webpages, while the source code of the modelling system and of the operational chain described in the present report is available on public GitHub repositories.



## References

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