

ECOSMO E2E v2.0

User Manual

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Purpose of this document:

This user manual provides the information required to obtain, compile, configure, and run E2E models using the archived one-dimensional GOTM-FABM-E2E test cases with different lower trophic level models (ECOSMO, ERSEM & ERGOM). Documentation for GOTM, FABM, and the lower-trophic-level host models is available through the references cited in the associated manuscript.

Associated manuscript:

Vijith Vijayakumaran, Rebecca Millington, Jorn Bruggeman, Josefine Hahn, Helen Powley, Gennadi Lessin, Anja Lindenthal, Corinna Schrum, and Ute Daewel, ECOSMO E2E v2.0: Generic modules of higher-trophic-level fish and macrobenthos functional groups compatible for two-way coupling to lower-trophic-level model hosts through FABM coupler, Geoscientific Model Development, (2026), Submitted.

Source code, reference configurations, forcing, and example output:

<https://doi.org/10.5281/zenodo.20413770>

This document should be cited as:

Vijayakumaran, V. and Daewel, U. (2026). *ECOSMO E2E v2.0 User Manual*. Helmholtz-Zentrum Hereon, Institute of Coastal Systems – Analysis and Modelling, Geesthacht, Germany. Version 1.0, July 22, 2026.

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Funding:

The modularisation of ECOSMO E2E model was funded by NECCTON project, Horizon Europe RIA under Grant Number 101081273.

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This documentation for ECOSMO E2E v2.0 is distributed as supplementary documentation accompanying the manuscript *ECOSMO E2E v2.0: Generic modules of higher-trophic-level fish and macrobenthos functional groups compatible for two-way coupling to lower-trophic-level model hosts through FABM coupler*, submitted to *Geoscientific Model Development*. Permission is granted to copy, distribute and use this document for scientific, educational and non-commercial purposes with appropriate credit or reference.

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1 Introduction

The ECOSMO E2E v2.0 modules represent higher-trophic-level (HTL) functional groups and are designed for online, two-way coupling to lower-trophic-level (LTL) ecosystem models through the Framework for Aquatic Biogeochemical Models (FABM). The model explicitly simulates carbon biomass for fish and macrobenthos. Its process formulations follow the ECOSMO end-to-end framework described by Daewel et al. (2019); the complete equations, assumptions, and evaluation are provided in the associated model-description paper Vijayakumaran et al. (2026).

The distribution of ECOSMO E2E v2.0 contains two generic HTL modules:

- **ecosmofish**: a configurable fish functional-group module that may be iterated more than once, for example as a planktivorous group (feeding predominantly of planktons) and a benthic-piscivorous group (feeding predominantly on planktivorous fish and macrobenthos);
- **ecosmomb**: a macrobenthos functional-group module.

The state variables and diagnostic variables are declared and defined in the fortran source codes (`ecosmofish.F90` and `ecosmomb.F90`). The dependencies of each variable is also given in the fortran scripts.

Each instance receives prey, detritus, dissolved organic matter, nutrients, and oxygen from the selected LTL host. In return, grazing, mortality, excretion, respiration, and other source–sink terms modify the coupled LTL variables. Because the predation, excretion and mortality targets are specified at runtime in `fabm.yaml`, the HTL modules can be connected to different FABM-compatible LTL and HTL compartments without rewriting the HTL source code.

This manual uses GOTM version 6 as a one-dimensional physical host. The archived examples demonstrate coupling to ECOSMO, ERGOM, and ERSEM. This user manual focusses on the steps needed to reproduce the ECOSMO E2E v2.0 simulations listed in Vijayakumaran et al. (2026).

2 Software and archived material

2.1 Archive contents

Download the archived release from <https://doi.org/10.5281/zenodo.20413770> and extract the zip file. The directories are:

src/ Fortran source files and the CMake model-library definition for the fish and macrobenthos modules.

testcases/ Paired `fabm.yaml_*` and `gotm.yaml_*` files for ECOSMO, ERGOM, and ERSEM hosts.

forcing/ Atmospheric, hydrographic, nutrient, oxygen and grid files used by the one-dimensional reference simulations.

model_output/ Archived NetCDF output for the experiments described in the manuscript, including the LTL-only, macrobenthos, fish-without-macrobenthos, control, and increased-zooplankton-mortality experiments.

ibt_survey/ International bottom trawl survey (Observational fish survey) information used in model evaluation.

The complete YAML files are intentionally not reproduced in this manual. Refer to the archived YAML files (text files) for the complete configurations.

2.2 Prerequisites

The recommended route is an isolated Conda environment. All Fortran components used in one executable—GOTM, FABM, NetCDF-Fortran, and the ECOSMO E2E v2.0 library—should be compiled with compatible compilers. Current FABM API 2.0 requires CMake 3.xx or later and a Fortran 2003 compiler.

```
conda update conda
conda create -n ecosmoe2e -c conda-forge \
    cmake ninja gfortran netcdf-fortran netcdf4 git
conda activate ecosmoe2e
```

Confirm the tools are visible:

```
gfortran --version
cmake --version
nf-config --version
git --version
```

If an existing environment is preferred, individual packages may be installed with:

```
conda install -c conda-forge \
    cmake ninja gfortran netcdf-fortran netcdf4 git
```

3 Obtaining FABM, GOTM, and ECOSMO E2E

Choose a working directory and obtain the source codes:

```
mkdir -p ~/models/ecosmoe2e
cd ~/models/ecosmoe2e

git clone https://github.com/fabm-model/fabm.git
git clone -b v6.0 --recurse-submodules \
    https://github.com/gotm-model/code.git gotm
```

Download the ECOSMO E2E v2.0 archive from Zenodo and extract it:

```
tar -xvf ecosmoe2e_gmd.tar.gz
```

In the examples below, define:

```
export FABM_SRC=$HOME/models/ecosmoe2e/fabm
export GOTM_SRC=$HOME/models/ecosmoe2e/gotm
export E2E_SRC=$HOME/models/ecosmoe2e/ecosmoe2e_gmd
```

Adapt the paths to the actual extraction location.

4 Building GOTM–FABM with the E2E modules

The ECOSMO E2E v2.0 source is registered as the FABM institute [hereon](#). Build GOTM in a clean build directory and tell CMake where the FABM and Hereon sources are located.

```
mkdir -p ~/models/ecosmoe2e/build/gotm
cd ~/models/ecosmoe2e/build/gotm

cmake "$GOTM_SRC" \
    -DFABM_BASE="$FABM_SRC" \
    -DFABM_INSTITUTES="akvaplan;au;bb;examples;gotm;jrc;nersc;msi;niva;pml;selma;hereon;bsh" \
    -DFABM_HEREON_BASE="$E2E_SRC/src" \
    -DFABM_BSH_BASE='$ERGOM/src' \
    -DCMAKE_INSTALL_PREFIX="$CONDA_PREFIX" \
    -DCMAKE_Fortran_COMPILER=gfortran

make
make install
```

DFABM_HEREON_BASE must point to the directory containing the E2E CMakeLists.txt and Fortran source files. In the archived structure described above, this is \$E2E_SRC/src. The lower-trophic-level host model must also be compiled if using a version that is not included in the FABM source code. In such cases, DFABM_ISTITUTES must point to the directory containing the LTL host model's source code. For example, \$BSH_SRC/src specifies the path to the ERGOM source code.

Verify the executable:

```
which gotm
gotm --version
```

If the executable is not found, inspect `$CONDA_PREFIX/bin` and the final CMake installation messages. For reproducibility, record the Git commit or release tag used for GOTM and FABM.

5 Configuration files

A GOTM–FABM simulation is controlled primarily by two YAML files:

- `gotm.yaml1`: physical setup, simulation period, time step, forcing, relaxation, FABM inputs, restart options, and output;
- `fabm.yaml1`: active biogeochemical model instances, parameters, initial values, and coupling links.

YAML is indentation-sensitive. Use spaces rather than tabs and preserve the hierarchy when editing.

5.1 Structure of `fabm.yaml1`

The following shortened example illustrates the essential pattern:

```
instances:
  LTL:
    model: nersc_ecosmo
    parameters:
      # lower-trophic-level parameters
    initialization:
      # lower-trophic-level initial conditions, if it is not defined in gotm.yaml
  MB:
    model: ecosmoe2e_mb
    parameters:
      nprey: 4
      mMB1: 0.001
      excMB1: 0.025
      # other MB parameters
    initialization:
      c: 0.01
    coupling:
      prey1: LTL/fla
      prey2: LTL/dia
      prey3: LTL/microzoo
      prey4: LTL/mesozoo
      det: LTL/det
      dom: LTL/dom
      sed1: LTL/sed1
      nh4: LTL/nh4
      pho: LTL/pho
      oxy: LTL/oxy
  FISH1:
    model: ecosmoe2e_fish
    parameters:
      nprey: 2
      mF1: 0.001
      excF1: 0.001
      # other MB parameters
      Gr1      : 0.033    # Grazingrate fish1 on prey1 (1/day)
      Gr2      : 0.033    # Grazingrate fish1 on prey2 (1/day)
      pref1    : 0.40     # Grazing preference fish1 on prey1
      pref2    : 0.40     # Grazing preference fish1 on prey2
      GrF1MB1  : 0.005    # Grazingrate fish1 on macrobenthos (1/day)
      prefF1MB1 : 0.10    # Grazing preference fish1 on MB1
    initialization:
      c: 1.0
    coupling:
      prey1: LTL/mesozoo
      prey2: LTL/microzoo
      mb: MB/c
      det: LTL/det
      dom: LTL/dom
      nh4: LTL/nh4
      pho: LTL/pho
      oxy: LTL/oxy
```

Each top-level name (for example, LTL or FISH1, here) below `instances` is user-defined and becomes part of

the output variable name. The **model** entry selects the compiled FABM component. The other blocks have the following meanings:

- parameters** Rate constants, preferences, half-saturation constants, efficiencies, conversion factors, switches, and number of prey types.
- initialization** Initial values of the state variables owned by that model instance. The HTL carbon state is named **c** and is expressed in the units registered by the module.
- coupling** Runtime links from dependencies required by the HTL module to variables supplied by another model instance. The syntax is **instance/variable**.

5.2 Fish functional-group instances

The same fish source module can be iterated repeatedly to generate more than one functional group of fish. For example FISH2 can be configured as follows.

```
instances:
  LTL:
    model: nersc_ecosmo
    parameters:
      # lower-trophic-level parameters
    initialization:
      # lower-trophic-level initial conditions, if it is not defined in gotm.yaml
  MB:
    model: ecosmoe2e_mb
    parameters:
      # MB parameters
    initialization:
      c: 0.01
    coupling:
      # MB coupling relations
  FISH1:
    model: ecosmoe2e_fish
    parameters:
      # FISH1 parameters
    initialization:
      c: 1.0
    coupling:
      # FISH1 coupling relations
  FISH2:
    model: ecosmoe2e_fish
    parameters:
      nprey: 2
      mF1: 0.0005
      excF1: 0.001
      # other MB parameters
      Gr1      : 0.001    # Grazingrate fish1 on prey1 (1/day)
      Gr2      : 0.0045   # Grazingrate fish1 on prey2 (1/day)
      pref1    : 0.40     # Grazing preference fish1 on prey1
      pref2    : 0.10     # Grazing preference fish1 on prey2
      GrF1MB1  : 0.0045   # Grazingrate fish1 on macrobenthos (1/day)
      prefF1MB1 : 0.40    # Grazing preference fish1 on MB1
    initialization:
      c: 1.0
    coupling:
      prey1: FISH1/c
      prey2: LTL/mesozoo
      mb: MB/c
      # other coupling relations
```

In the reference configurations:

- FISH1 represents a mainly planktivorous functional group;
- FISH2 represents a benthic-piscivorous group and may consume FISH1/c and MB/C.

The functional definition of the group is therefore determined by the prey list, grazing parameters, and preferences.

5.3 Prey lists and consistency rules

For a model with `nprey: N`, provide `Gr1–GrN`, `pref1–prefN`, the required scaling terms, and `prey1–preyN` coupling links. Before running, check that:

1. every coupled target exists in the selected LTL host;
2. prey and receiving HTL modules use compatible dimensions after applying scale factors;
3. no coupling points to a misspelled instance or variable.

The archived ECOSMO, ERGOM, and ERSEM configurations use different LTL variable names and, in some cases, conversion factors because the hosts use different elemental currencies or concentration conventions. These factors must not be copied blindly between hosts.

Example (ERGOM-E2E coupling): ERGOM expresses most biogeochemical state variables in mol kg^{-1} , whereas the E2E modules use mg C m^{-3} (or mol m^{-3} for O_2). Therefore, the YAML configuration includes scaling factors to convert host model variables into the units expected by E2E. For example:

```
scalenh4 : 8.235E+07 # NH4: mol N kg-1 -> mg C m-3
scalepho : 1.317617E+09 # PO4: mol P kg-1 -> mg C m-3
scaleo2 : 1.035E+06 # O2: mol O2 kg-1 -> mol O2 m-3
scaleprey1 : 8.235E+07 # Zooplankton prey: mol N kg-1 -> mg C m-3
scaledet : 8.235E+07 # Detritus: mol N kg-1 -> mg C m-3
scaledom : 1.243E+07 # DOM: mol C kg-1 -> mg C m-3
```

5.4 Key GOTM settings

The archived `gotm.yaml_*` files define a 73-m North Sea water column, an 1800-s time step, 83 vertical layers, meteorological forcing, tidal pressure gradients, temperature and salinity profiles, nutrient relaxation, FABM activation, and NetCDF output. The most commonly edited sections are:

```
location:
  latitude: 56.0
  longitude: 3.0
  depth: 73.0

time:
  start: 2020-01-01 00:00:00
  stop: 2039-12-31 18:00:00
  dt: 1800.0

fabm:
  use: true
  repair_state: true

output:
  result:
    format: netcdf
    time_unit: day
    time_step: 1
```

Paths in `gotm.yaml` are interpreted relative to the run directory. Ensure the forcing directory name in the YAML file matches the extracted archive. The archive listing uses `forcing/`; some working configurations may refer to `forcing_data/`. Either rename the directory or update the paths consistently.

GOTM can relax the model state towards the values in a relaxation file over a user-defined relaxation timescale (`relax_tau`). In this example, the nitrate concentration is read from `nitrate.dat` and, after applying the specified `scale_factor` (for unit conversion), is used as the target profile for relaxation. The one-year relaxation timescale (3.15×10^7 s) provides weak nudging towards the prescribed profile.

```
input:
  LTL/no3:
    method: file
    constant_value: 0.0
    file: ../forcing_data/nitrate.dat
    column: 1
    scale_factor: 7.95662500E+01
    relax_tau: 3.15000000E+07
```

6 Preparing and running a reference simulation

Create a dedicated run directory. The executable expects the active files to be named `gotm.yaml` and `fabm.yaml`. The following example describes how to run the ERGOM–E2E configuration; a similar procedure can be followed for the ECOSMO–E2E and ERSEM–E2E configurations.

```
mkdir -p ~/runs/ecosmoe2e/ergom_control
cd ~/runs/ecosmoe2e/ergom_control

cp "$E2E_SRC/testcases/gotm.yaml_ergom" gotm.yaml
cp "$E2E_SRC/testcases/fabm.yaml_ergom" fabm.yaml
ln -s "$E2E_SRC/forcing" forcing
```

If the YAML files refer to `../forcing_data`, either change those paths to `forcing` or create the matching symbolic link. A simple directory layout is:

```
ergom_control/
|-- fabm.yaml
|-- gotm.yaml
'-- forcing -> /absolute/path/to/ecosmoe2e_gmd/forcing
```

Run GOTM from the setup directory:

```
gotm > gotm.log 2>&1
```

For an initial installation test, shorten `time.stop` to a few days. Inspect the end of the log and verify that the NetCDF result file was produced:

```
tail -n 50 gotm.log
ncdump -h result.nc | less
```

The exact output filename is set in the `output` block of `gotm.yaml`.

7 Reproducing model experiments

The experiments in the manuscript can be represented by enabling or removing selected HTL instances and modifying targeted parameters:

LTL only Retain only the LTL host instances and remove MB, FISH1, and FISH2.

Macrobenthos only Retain the LTL host and MB; remove fish instances.

Fish without macrobenthos Remove MB and any fish coupling that depends on MB/c; retain the desired fish groups.

Control Use the complete archived configuration with the intended LTL host, macrobenthos, and both fish groups.

Increased zooplankton mortality Change the relevant mortality parameter in the LTL host while keeping the HTL structure otherwise identical.

8 Output

The GOTM output is a NetCDF file containing physical variables, FABM state variables, and requested diagnostics. Instance names become prefixes; examples include FISH1_c, FISH2_c, and MB_c.

A compact Python check is:

```
from netCDF4 import Dataset

# Name of the GOTM output file
filename = "result.nc"

# Open the NetCDF file
with Dataset(filename, "r") as nc:
```

```
print("Variables in the file:\n")

for variable_name in nc.variables:
    print(variable_name)
```

9 Tips

Check for FABM tips and tricks <https://github.com/fabm-model/fabm/wiki/Tips-and-tricks>

The installation procedure described in this manual has been tested using a Miniconda-based Conda environment and FABM API 2.0.

10 Code availability

E2E: <https://doi.org/10.5281/zenodo.20413770>

FABM, GOTM, ECOSMO: <https://github.com/fabm-model/fabm>

ECOSMO: <https://github.com/nansencenter/nersc>

ERGOM: <https://gitlab.opencode.de/bsh/neccton/gotm-ergom>

ERSEM: <https://github.com/pmlmodelling/ersem/>

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