Supplementary material

Merging bio-optical data from Biogeochemical-Argo floats and models in marine biogeochemistry

by Terzić E., et al.

Submitted to Biogeosciences Discussions

contacting author Lazzari P. (plazzari@inogs.it)

June 27, 2018

	LOV NAME	WMO CODE
1	lovbio001i	6901032
2	lovbio015c	6901513
3	lovbio016c	6901510
4	lovbio016d	6902700
5	lovbio017b	6901512
6	lovbio018c	6901528
7	lovbio035b	6901511
8	lovbio039b	6901483
9	lovbio042c	6901490
10	lovbio053b	6901529
11	lovbio058c	6901491
12	lovbio063c	6901653
13	lovbio064b	6901496
14	lovbio064c	6901776
15	lovbio066c	6901605
16	lovbio066d	6901655
17	lovbio067c	6901649
18	lovbio068d	6901648
19	lovbio072c	6901600
20	lovbio083d	6901764
21	lovbio085d	6901766
22	lovbio088d	6901768
23	lovbio089d	6901769
24	lovbio090d	6901770
25	lovbio091d	6901771
26	lovbio093d	6901773
27	ogsbio001b	6901861
28	ogsbio002b	6901864
29	ogsbio003b	6901862
30	ogsbio004b	6901863
31	ogsbio006b	6901865

```
#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
# NAMELISTS
#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
# BFM - Biogeochemical Flux Model
#-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
#
# COPYING
#
#   Copyright (C) 2015 BFM System Team (bfm_st@lists.cmcc.it)
#
#   This program is free software; you can redistribute it and/or modify
#   it under the terms of the GNU General Public License as published by
#   the Free Software Foundation;
#   This program is distributed in the hope that it will be useful,
#   but WITHOUT ANY WARRANTY; without even the implied warranty of
#   MERCHANTEABILITY or FITNESS FOR A PARTICULAR PURPOSE.  See the
#   GNU General Public License for more details.
#
#---------------------------------------------------------------------------!



!---------------------------------------------------------------------------!
!NAMELIST bfm_nml
!---------------------------------------------------------------------------!
! Main initialisation and output specifications
! NAME           KIND    DESCRIPTION
! bio_calc       logical Switch on/off BFM (for coupled configurations)
! bfm_init       integer Initialization state
!                        0. from constant values in bfm_init_nml below
!                        1. from restart
! bfm_rstctl     logical Save initial state of bfm in the output file.
! bio_setup      integer BFM configuration:
!                        1. pelagic
!                        2. benthic
!                        3. pelagic and benthic
!                        4. sea ice
!                        5. pelagic and sea ice
! out_fname      string  Name of NetCDF output file
! out_dir        string  Path to the output file
! out_title      string  Name of the experiment in NetCDF file
! out_delta      integer Output is saved every out_delta timesteps
!                        Use -1 to store with real monthly frequency
! parallel_log   logical Set true in parallel jobs for a single log file
!---------------------------------------------------------------------------!
&bfm_nml
   bio_calc     = .TRUE.
   bfm_init     = 0
   bfm_rstctl   = .FALSE.
   bio_setup    = 1
   out_fname    = 'BFM_standalone_pelagic'
   out_dir      = '.'
   out_title    = 'BFM_STANDALONE_PELAGIC'
   in_rst_fname = 'in_bfm_restart'
   out_delta    = 300  !every 30 days
   parallel_log = .FALSE.
      filename_nml_conf = 'BFM_General.nml',
/
```

```
!-------------------------------------------------------------------------!
! NAMELIST Param_parameters
!-------------------------------------------------------------------------!
! Global Switches : turn on/off or choose model components
! NAME                          KIND    DESCRIPTION
! CalcPelagicFlag               logical Pelagic System
! CalcBenthicFlag               numeric Benthic system
!                                       0 = No Benthic System
!                                       The following are Not Yet Activated
!                                       1 = Simple Benthic Return
!                                       2 = Benthic organisms and intermediate
!                                           complexity nutrient regeneration
!                                       3 = Benthic organisms and full nutrient
!                                           regeneration (early diagenesis)
! CalcTransportFlag             logical Compute Transport Term (when coupled
!                                       with a OGCM)
! CalcConservationFlag          logical Mass Conservation Check
! CalcPhytoPlankton             logical Pelagic Phytoplankton (vector)
! CalcPelBacteria               logical Pelagic Bacteria (vector)
! CalcMesoZooPlankton           logical Mesozooplankton (vector)
! CalcMicroZooPlankton          logical Microzooplankton (vector)
! CalcPelChemistry              logical Pelagic Hydrochemical Processes
! AssignPelBenFluxesInBFMFlag   logical Benthic-pelagic fluxes are added to the
!                                       time integration
! AssignAirPelFluxesInBFMFlag   logical Air-sea fluxes are added to the
!                                       time integration
! ChlDynamicsFlag    numeric Choose the dynamics of Chl-a
!                            1 = diagnostic, optimal light property
!                                in phytoplankton
!                                (Ebenhoeh et al 1995, ERSEM-II)
!                            2 = state variable, constituent of
!                                phytoplankton
! check_fixed_quota             numeric Check whether zooplankton have fixed
quota
!
! Global Parameters : used throughout the model and not related
!                     to a specific component
! NAME          UNIT          DESCRIPTION
! p_small      [-]           Smallest numeric value (the model "zero")
! slp0         [mbar]        Reference sea level pressure
! p_pe_R1c     [-]           Fractional content of C in cytoplasm
! p_pe_R1n     [-]           Fractional content of N in cytoplasm
! p_pe_R1p     [-]           Fractional content of P in cytoplasm
! p_qro        [mmolHS-/     Stoichiometric coefficient for
!               mmolO2]      anaerobic reactions
! p_qon_dentri [mmolO2/      Stoichiometric coefficient for
!               mmolN]       denitrification
! p_qon_nitri  [mmolO2/      Stoichiometric coefficient for
!               mmolN]       nitrification
!-------------------------------------------------------------------------!
&Param_parameters
! Switches :
            CalcPelagicFlag = .TRUE.
            CalcBenthicFlag = 0
       CalcConservationFlag = .FALSE.
          CalcTransportFlag = .FALSE.
       CalcPhytoPlankton(1) = .TRUE.
       CalcPhytoPlankton(2) = .TRUE.
       CalcPhytoPlankton(3) = .TRUE.
       CalcPhytoPlankton(4) = .TRUE.
```

```
         CalcPelBacteria(1) = .TRUE.
    CalcMicroZooPlankton(1) = .TRUE.
    CalcMicroZooPlankton(2) = .TRUE.
     CalcMesoZooPlankton(1) = .TRUE.
     CalcMesoZooPlankton(2) = .TRUE.
           CalcPelChemistry = .TRUE.
AssignPelBenFluxesInBFMFlag = .FALSE.
AssignAirPelFluxesInBFMFlag = .TRUE.
            ChlDynamicsFlag = 2
          check_fixed_quota = 0
! Parameters :
                    p_small = 1.0e-20
                       slp0 = 1013.25E0
                  p_pe_R1c = 0.60
                  p_pe_R1n = 0.72
                  p_pe_R1p = 0.832
                     p_qro = 0.5
               p_qon_dentri = 1.25
                p_qon_nitri = 2.0
     filename_nml_conf = 'BFM_General.nml',
/

!-------------------------------------------------------------------------!
! NAMELIST bfm_init_nml
!-------------------------------------------------------------------------!
!Pelagic initialisation of standard variables
!<variablename>0 = <realvalue>
!-------------------------------------------------------------------------!
&bfm_init_nml
   O2o0 = 300.0,
   N1p0 = 1.0,
   N3n0 = 5.0,
   N4n0 = 1.0,
   N5s0 = 8.0,
   N6r0 = 1.0,
   O3c0 = 27060.00,
   O3h0 = 2660.0,
   O4n0 = 200.0,
   P1c0 = 1.0,
   P2c0 = 1.0,
   P3c0 = 1.0,
   P4c0 = 1.0,
   Z3c0 = 1.0,
   Z4c0 = 1.0,
   Z5c0 = 1.0,
   Z6c0 = 1.0,
   B1c0 = 1.0,
   R1c0 = 1.0,
   R2c0 = 0.1,
   R3c0 = 1.0,
   R6c0 = 1.0,
   filename_nml_conf = 'BFM_General.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST bfm_save_nml
!-------------------------------------------------------------------------!
! Stored variables
!ave_save: average values over the output interval
!var_save: instantaneous value at the output interval
!-------------------------------------------------------------------------!
```

```
&bfm_save_nml
   var_save = ''
   ave_save = 'ETW','O2o','DIC',
          'EIR',
          'xEPS',
          'Chla',
          'N1p','N3n','N4n','N5s',
          'B1c',
          'P1c','P2c','P3c','P4c',
          'P1l','P2l','P3l','P4l',
          'P1n','P2n','P3n','P4n',
          'P1p','P2p','P3p','P4p',
          'Z3c','Z4c','Z5c','Z6c',
          'R1c','R2c','R6c',
          'R1n','R6n',
          'R1p','R6p',
          'P1s','R6s',
          'eiPPY(iiP1)','eiPPY(iiP2)','eiPPY(iiP3)','eiPPY(iiP4)',
          'sunPPY(iiP1)','sunPPY(iiP2)','sunPPY(iiP3)','sunPPY(iiP4)',
          'ruPPYc','resPBAc','resZOOc',
          'ruPPYn','ruPPYp','ruPPYs','exPPYc',
          'ruZOOc','remZOOn','remZOOp','remPBAn','remPBAp'

     filename_nml_conf = 'BFM_General.nml',
/

!-----------------------------------------------------------------------!
!NAMELIST Settling_parameters
!-----------------------------------------------------------------------!
! BURIAL VELOCITIES into the sediment
! NAME         [UNIT]/KIND            DESCRIPTION
! p_burvel_R6     [m/d]              Bottom Burial Velocity for detritus
! p_burvel_R2     [m/d]              Bottom Burial Velocity for dissolved
! p_burvel_PI     [m/d]              Bottom Burial Velocity for plankton
!-----------------------------------------------------------------------!
&Settling_parameters
  p_burvel_R6 = 1.5,
  p_burvel_R2 = 0.0,
  p_burvel_PI = 0.0
     filename_nml_conf = 'Benthic_Environment.nml',
/



!-----------------------------------------------------------------------!
!NAMELIST CO2_parameters
!-----------------------------------------------------------------------!
! CARBONATE SYSYEM SETTING
! NAME           [UNIT]/KIND             DESCRIPTION
! AtmCO20        [ppmv]           Initial atmospheric concentration of CO2
! calcAtmpCO2    logical          Compute the partial pressure of Atmospheric
CO2
! pCO2Method     integer          pCO2 computation method: 1=MixRatio*slp0,
2=Magnus formula
! phstart        [pH]             Initial pH value
! K1K2           integer          Switch for the acidity constants
parameterization
!                                 1 : Roy et al. (1993); DOE (1994); pH on total
scale
!                                 2 : Default. OCMIP STANDARD; pH on Sea Water
Scale
```

```
!                                   Mehrbach et al (1973) refit by Dickson &
Millero (1987)
!                                3 : Mehrbach et al (1973) refit by Lueker et
al. (2000)
!                                   pH on total scale
!                                4 : Hansson (1973b) data as refitted by
Dickson and
!                                   Millero (1987);  pH on Sea Water Scale
! MethodCalcCO2  numeric         Switch for the choice of [H+] numerical
computation
!                                1 : Approximate static solution
!                                2 : Default. Standard OCMIP iteration
!                                3 : Follows et al., Ocean Modelling 2006
! CalcBioAlkFlag logical         Compute biological processes corrections on
total alkalinity
!              ---------  Parameters for MethodCalcCO2=2 -----------
! M2XACC         real            Accuracy of the iterative scheme for OCMIP
(default 1.E-10)
! M2PHDELT       [pH]            Delta of pH for the root search (realized
pH+/-DELT)
!                                in the OCMIP scheme (default 0.5)
! M2MAXIT        integer         Maximum number of iterations for OCMIP
(default 100 )
!              ---------  Parameters for calcium and calcite ---------
! Caconc0        [mol/m3]        Calcium ion concentration
!                                ["Seawater : Its composition, properties and
behaviour"
!                                (2nd Edition), Open University Course Team,
1995]
!                                Seawater concentration   = 412 mg / l
!                                                       -> atomic weight =
40.078 g / mol
!                                therefore, concentration = 10.279 mmol / l =
10.279 mol / m3
! Canorm          logical        Normalize Calcium ion concentration by sea
water salinity
!              ---------  EXTERNAL DATA INPUT STRUCTURES -----------
! AtmCO2_N       structure       Read external data for atmospheric CO2 values
! AtmSLP_N       structure       Read external data for atmospheric sea level
pressure
! AtmTDP_N       structure       Read external data for atmospheric dew-point
temperature
! Example of general input structure for the data structure:
!          ! Read  !   File                                ! NetCDF  !  Var    !
!          ! Input !   name                                ! Logical !  name   !
!AtmCO2_N  =    0  , 'CMIP5_Historical_GHG_1765_2005.dat' , .FALSE.  , 'CO2'  ,
!          !  RefTime          ! Input      !   Time   !
!          !  yyyymmdd         ! Frequency  !  interp  !
!           '1764-07-01 00:00' ,  'yearly'  ,  .TRUE.
!
! Convention for Input reading : 0 = use constant value (default if structure is
not initialized)
!                                2 = read timeseries file ( e.g. CO2 mixing
ratios)
!                                4 = field from a coupled model (e.g. atmospheric
SLP from OGCM)
! NOTE: The file "CMIP5_Historical_GHG_1765_2005.dat" is located in
"$BFMDIR/tools" folder
!-------------------------------------------------------------------------------
----!
&CO2_parameters
```

```
   AtmCO20       = 370.0E0
   calcAtmpCO2   = .FALSE.
   pCO2Method    = 1
   AtmCO2_N  =    0  , 'CMIP5_Historical_GHG_1765_2005.dat' , .FALSE.  , 'CO2'
, '1764-07-01 00:00' ,  'yearly'  ,  .TRUE.
   AtmSLP_N  =    0  , 'AtmSLP.nc' , .TRUE.  ,'AtmSLP' , '1764-07-01 00:00'  ,
'dummy' ,  .TRUE.
   AtmTDP_N  =    0  , 'AtmTDP.nc' , .TRUE.  ,'AtmTDP' , '1764-07-01 00:00'  ,
'dummy' ,  .TRUE.
   phstart       = 8.10E0
   K1K2          = 2
   MethodCalcCO2 = 2
  CalcBioAlkFlag = .FALSE.
          M2XACC = 1.0E-10
        M2PHDELT = 0.3
         M2MAXIT = 100
         Caconc0 = 10.279E0
         Canorm  = .TRUE.
     filename_nml_conf = 'Carbonate_Dynamics.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST PelBac_parameters
!-------------------------------------------------------------------------!
!  PELAGIC BACTERIA
!
! NAME         [UNIT]/KIND            DESCRIPTION
! p_version   integer         Switch for bacteria parameterization
!                              1 : Baretta-Bekker et al. 1995;
!                                  Vichi et al., 2007
!                              2 : Vichi et al., 2004
!                              3 : Polimene et al., 2006
! p_q10       [-]              Q10-value (temperature dependency)
! p_chdo      [mmol/m3]        Half-saturation constant for O2 limitation
! p_sd        [1/d]            Specific mortality rate
! p_sd2       [1/d]            Density dependent specific mortality rate
! p_suhR1     [1/d]            Specific potential uptake for nutrient-rich DOM
! p_sulR1     [1/d]            Specific potential uptake for nutrient-poor DOM
! p_suR2      [1/d]            Specific potential uptake for semi-labile DOC
! p_suR3      [1/d]            Specific potential uptake for semi-refractory DOC
! p_suR6      [1/d]            Specific potential uptake for POM (1/d)
! p_sum       [1/d]            Potential specific growth rate
! p_pu_ra     [-]              Activity respiration fraction
! p_pu_ra_o   [-]              Additional respiration fraction at low O2 conc
! p_srs       [1/d]            Specific rest respiration
! p_qncPBA    [mmolN/mgC]      Optimal N/C ratio
! p_qpcPBA    [mmolP/mgC]      Optimal P/C ratio
! p_qlnc      [mmolN/mgC]      Minimal N/C ratio
! p_qlpc      [mmolP/mgC]      Minimal P/C ratio
! p_qun       [mmolN/mgC/day]  Membrane affinity for N
! p_qup       [mmolP/mgC/day]  Membrane affinity for N
! p_chn       [mmolN/m3]       Half saturation ammonium conc. for uptake
! p_chp       [mmolP/m3]       Half saturation phosphate conc. for uptake
! p_ruen      [1/d]            Relaxation timescale for N uptake/remin.
! p_ruep      [1/d]            Relaxation timescale for P uptake/remin.
! p_rec       [1/d]            Relaxation timescale for semi-labile excretion
! p_pu_ea_R3  [-]              Excretion of semi-refractory DOC
!-------------------------------------------------------------------------!
&PelBacteria_parameters
!               B1
     p_version = 2
```

```
         p_q10 = 2.95
        p_chdo = 30.0
          p_sd = 0.0
         p_sd2 = 0.0
       p_suhR1 = 0.5
       p_sulR1 = 0.0
        p_suR2 = 0.25
        p_suR3 = 0.0
        p_suR6 = 0.1
         p_sum = 8.38
       p_pu_ra = 0.6
     p_pu_ra_o = 0.2
         p_srs = 0.01
      p_qncPBA = 0.017
      p_qpcPBA = 0.0019
        p_qlnc = 0.0085
        p_qlpc = 0.00095
         p_qun = 0.05
         p_qup = 0.005
         p_chn = 0.05
         p_chp = 1.00
         p_rec = 1.0
       p_ruen = 1.0
       p_ruep = 1.0
    p_pu_ea_R3 = 0.0
     filename_nml_conf = 'Pelagic_Ecology.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST Phyto_parameters, Phyto_parameters_iron
!-------------------------------------------------------------------------!
!  PELAGIC PHYTOPLANKTON
! NAME          [UNIT]/KIND            DESCRIPTION
!        :     --------- Physiological parameters -----------------
!  p_q10       [-]             Characteristic Q10 coefficient
!  p_qtemp     [-]             Cut-off threshold for temperature factor
!  p_sum       [1/d]           Maximal productivity at 10 degrees C
!  p_srs       [1/d]           Respiration rate at 10 degrees C
!  p_sdmo      [1/d]           Max.specific nutrient-stress lysis rate
!  p_thdo      [-]             Half saturation constant for nutrient stress lysis
!  p_seo       [1/d]           Extra lysis rate (biomass density-dependent)
!  p_sheo      [mgC/3]         Half saturation constant for extra lysis
!  p_pu_ea     [-]             Excreted fraction of primary production
!  p_pu_ra     [-]             Activity respiration fraction
!  p_switchDOC [1-3]           Switch for the type of DOC excretion
!                              This choice must be consistent with bacteria
!                              1. All DOC is released as R1c (Vichi et al., 2007)
!                              2. Activity DOC is released as R2c (Vichi et al.,
2004)
!                                 (there is no nutrient-stress excretion)
!                              3. All DOC is released as R2c (Polimene et al.,
2006)
!
!               --------- Nutrient parameters in phytoplankton -----------------
!  p_netgrowth [T or F]        Logical switch for nutrient-limited growth
!                              .T. nutrient-balanced growth (Vichi et al.2004)
!                              .F. nutrient-stress carbon excretion
!                                (Baretta-Bekker et al.1995 and Vichi et al.2007)
!  p_limnut    [1-3]           Switch for N-P co-limitation
!                              0. Geometric mean
!                              1. Threshold (Liebig-like)
```

```
!                              2. Combined
!                    ---- N limitation control ----
!  p_qun        [m3/mgC/d]     Membrane affinity for N
!  p_lN4        [mmolN/m3]     Half saturation constant for NH4 uptake preference
over NO3
!  p_qnlc       [mmolN/mgC]    Minimum quotum Si:C
!  p_qncPPY     [mmolN/mgC]    Reference quotum Si:C
!  p_xqn        [-]            Multiplication factor for luxury storage
!                    ---- P limitation control ----
!  p_qup        [m3/mgC/d]     Membrane affinity for P
!  p_qplc       [mmolP/mgC]    Minimum quotum Si:C
!  p_qpcPPY     [mmolP/mgC]    Reference quotum Si:C
!  p_xqp        [-]            Multiplication factor for luxury storage
!                    ---- Si limitation control ----
!  p_switchSi   [1-2]          Switch for Silica limitation
!                              1. Si limitation is controlled by external Si
conc.
!                              2. Si limitation is controlled by internal quota
!  p_chPs       [mmolSi/m3]    Half saturation conc. for dissolved Si limitation
!  p_Contois    [>=0]          If >0, use Contois formulation
!  p_qus        [m3/mgC/d]     Membrane affinity for Si
!  p_qslc       [mmolSi/mgC]   Minimum quotum Si:C
!  p_qscPPY     [mmolSi/mgC]   Reference quotum Si:C
!                              Brzezinski (1985) 0.13 mol/mol
!                    ---- nutrient stressed sinking ----
!  p_esNI       [-]            Nutrient stress threshold for sinking
!  p_res        [m/d]          Maximum Sinking vel city (m/d)
!                 --------- Chlorophyll parameters -----------
!  p_switchChl  [1-4]          Switch for Chla-a synthesis
!  p_sdchl      [1/d]          Specific turnover rate for Chla
!  p_alpha_chl  [mgC s m2/     Initial slope of the P-E curve
!                mgChl/uE]
!  p_qlcPPY     [mgChla/mgC]   Reference quotum Chla:C
!  p_epsChla    [m2/mgChla]    Chla-specific extinction coefficient
!  p_tochl_relt  [1/d]         Relaxation rate towards maximum Chla:C
!  p_EpEk_or    [-]            Optimal value of E_PAR/E_K
!                 --------- Iron parameters -----------
!  p_quf        [m3/mgC/d]     Membrane affinity for Fe
!  p_qflc       [umolFe/mgC]   Minimum quotum Fe:C derived from 3 umol Fe/mol C
!                              Sunda & Huntsman (1997), Nature, 390, p 389-392
!  p_qfcPPY     [umolFe/mgC]   Reference quotum Fe:C
!  p_xqf        [-]            Multiplication factor for luxury storage
!                 --------- Light parameters ERSEM-II -----------
!  p_iswLtyp    [0-6]          Shape of the productivity function
!  p_chELiPPY   [W/m2]         Maximum Iopt
!  p_clELiPPY   [W/m2]         Minimum Iopt
!  p_ruELiPPY   [1/d]          Maximum daily shift in Iopt (1/d)
!  p_addepth    [m]            Adaptation depth. Meaningless with high-res models
!                 --------- Sinking parameters -----------
!  p_rPIm       [m/d]          Phytoplankton background sinking rate
!-------------------------------------------------------------------------!
&Phyto_parameters
!                 P1       P2       P3       P4
        p_q10 = 2.0,     2.0,     2.0,     2.0
       p_temp = 0.0,     0.0,     0.75,     0.0
        p_sum = 2.5,     3.0,     3.5,     1.5
        p_srs = 0.1,    0.05,    0.1,     0.1
       p_sdmo = 0.0,    0.0,    0.0,    0.0
       p_thdo = 0.0,     0.0,     0.0,     0.0
        p_seo = 0.0,     0.0,     0.0,     0.0
       p_sheo = 0.0,     0.0,     0.0,     100.0
```

```
      p_pu_ea = 0.05,   0.1,    0.1,    0.15
      p_pu_ra = 0.1,    0.1,    0.2,   0.1
  p_switchDOC = 2,      2,      2,      2
  p_netgrowth = .TRUE.,.TRUE.,.TRUE.,.TRUE.
     p_limnut = 1,      1,      1,      1
        p_qun = 0.025,  0.025,  0.25,  0.025
        p_lN4 = 1.0,    0.5,    0.1,    1.0
       p_qnlc = 0.00687, 0.00687, 0.00687, 0.00687
     p_qncPPY = 1.26e-2,1.26e-2,1.26e-2,1.26e-2
        p_xqn = 2.0,    2.0,    2.0,    2.0
        p_qup = 0.0025,  0.0025,  0.0025,  0.0025
       p_qplc = 0.0004288,0.0004288,0.0004288,0.0004288
     p_qpcPPY = 7.86e-4,7.86e-4,7.86e-4,7.86e-4
        p_xqp = 2.0,    2.0,    2.0,    2.0
   p_switchSi = 2,      0,      0,      0
      p_chPs = 0.3,    0.0,    0.0,    0.0
    p_Contois = 0.0,    0.0,    0.0,    0.0
        p_qus = 0.0025,    0.0,    0.0,    0.0
       p_qslc = 0.007,    0.0,    0.0,    0.0
     p_qscPPY = 0.01,   0.0,    0.0,    0.0
       p_esNI = 0.7,    0.75,   0.75,   0.75
       p_res  = 5.0,    0.0,    0.0,    2.5
  p_switchChl = 2,      2,      2,      2
      p_sdchl = 0.2,    0.2,    0.2,    0.2
  p_alpha_chl = 2.50e-5, 1.70e-5, 2.75e-5, 0.68e-5
     p_qlcPPY = 0.02,  0.02,  0.02,   0.02
    p_epsChla = 0.03,   0.03,   0.03,   0.03
    p_EpEk_or = 0.0,    0.0,    0.0,    0.0
 p_tochl_relt = 0.0,    0.0,    0.0,    0.0
    p_iswLtyp = 5,      5,      5,      5
    p_addepth = 50.0,   50.0,   50.0,   50.0
  p_chELiPPY  = 100.0,  100.0,  100.0,  100.0
  p_clELiPPY  = 8.0,    10.0,   6.0,    12.0
  p_ruELiPPY  = 0.2,    0.25,   0.3,    0.15
       p_rPIm = 0.0,    0.0,    0.0,    0.0
     filename_nml_conf = 'Pelagic_Ecology.nml',
/

&Phyto_parameters_iron
     filename_nml_conf = 'Pelagic_Ecology.nml',
/

!------------------------------------------------------------------------!
!NAMELIST PAR_parameters
!------------------------------------------------------------------------!
! LightPeriodFlag    numeric Choose the light averaging period
!                            1 = Instantanous irradiance
!                            2 = Daily average
!                            3 = Daylight average with explicit
!                                photoperiod
! LightLocationFlag  numeric Choose the parameterization of light
!                            location in the discrete grid
!                            1 = Light at the top of the cell
!                            2 = Light in the middle of the cell
!                            3 = Average Light in the cell
! ChlAttenFlag        numeric Choose the PAR attenuation due to Chl
!                            1 = broadband linear attenuation
!                            2 = 3-band tabulated attenuation coefficients
!                                (Morel, 1988; Lengaigne et al, 2007)
! p_PAR        [-]           Fraction of Photosynthetically Available Radiation
! p_eps0       [1/m]         Background extinction coefficient
```

```
! p_epsIR      [1/m]         Infrared extinction coefficient
!                            (to use with ChlAttenFlag=2)
! p_epsESS     [m2/g]        Specific attenuation coefficient of
!                            suspended sediments
! p_epsR6      [m2/mgC]      Specific attenuation coefficient of particulate
!                            detritus
!-------------------------------------------------------------------------!
&PAR_parameters
  LightPeriodFlag    =  1
  LightLocationFlag  =  2
  ChlAttenFlag       =  1
  p_PAR        =  0.40
  p_eps0       =  0.0435
  p_epsIR      =  2.857
  p_epsESS     =  0.04d-3
  p_epsR6      =  0.1d-3
      filename_nml_conf = 'Pelagic_Environment.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST MicroZoo_parameters
!-------------------------------------------------------------------------!
!  MICRO-ZOOPLANKTON
!
! NAME         [UNIT]/KIND           DESCRIPTION
! p_q10        [-]             Q10 value for physiological rates
! p_srs        [1/d]           Respiration rate at 10 degrees Celsius
! p_sum        [1/d]           Potential growth rate
! p_sdo        [1/d]           Mortality rate due to oxygen limitation
! p_sd         [1/d]           Temperature independent mortality rate
! p_pu         [-]             Assimilation efficiency
! p_pu_ea      [-]             Fraction of activity excretion
! p_chro       [mmolO2/m3]     Half-saturation oxygen concentration
! p_chuc       [mgC/m3]        Half-saturation Food concentration for Type II
! p_minfood    [mgC/m3]        Half-saturation food concentration for
!                              preference factor
! p_qncMIZ     [mmolN/mgC]     Maximum quotum P:C
! p_qpcMIZ     [mmolN/mgC]     Maximum quotum N:C
! p_paPBA(z,b) [-]             Availability of pelagic Bacteria group b
!                              to Zooplankton group z
! p_paPPY(z,p) [-]             Availability of PhytoPlankton group p
!                              to Zooplankton group z
! p_paMIZ(z,m) [-]             Availability of MicroZooplankton group m
!                              to Zooplankton group z
!-------------------------------------------------------------------------!
&MicroZoo_parameters
!              Z5      Z6
       p_q10 =  2.0,    2.0
       p_srs =  0.02,   0.02
       p_sum =  2.0,    5.0
       p_sdo =  0.05,   0.05
        p_sd =  0.0,   0.0
        p_pu =  0.5,    0.3
     p_pu_ea =  0.5,    0.5
      p_chro =  8,    8
      p_chuc =  30.0,   100.0
   p_minfood =  50.0,   50.0
    p_qpcMIZ =  1.85d-3,1.85d-3
    p_qncMIZ =  1.67d-2,1.67d-2
! Food matrix parameters: take care of the notation
!               Z5      Z6
```

```
     p_paPBA =  0.1,    1.0
!                P1      P2      P3      P4
!       Z5
p_paPPY(1,:) =  0.7,    1.0,    0.1,    0.1
!       Z6
p_paPPY(2,:) =  0.0,    0.2,    1.0,    0.0
!                Z5      Z6
!       Z5
p_paMIZ(1,:) =  1.0,    1.0
!       Z6
p_paMIZ(2,:) =  0.0,    0.2
      filename_nml_conf = 'Pelagic_Ecology.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST MesoZoo_parameters
!-------------------------------------------------------------------------!
!  MESO-ZOOPLANKTON
! NAME          [UNIT]/KIND           DESCRIPTION
! p_q10         [-]              Q10 value for physiological rates
! p_srs         [1/d]            Respiration rate at 10 degrees C
! p_sum         [1/d]            Maximal productivity at 10 degrees C
! p_sd          [1/d]            Background natural mortality
! p_vum         [m3/mgC/d]       Specific search volume
! p_puI         [-]              Assimilation efficiency
! p_peI         [-]              Fraction of Faeces production
! p_sdo         [m3/mgC/d]       Specific density-dependent mortality
! p_sds         [-]              Exponent of density-dependent mortality
! p_qpcMEZ      [mmolP/mgC]      Maximum quotum P:C
! p_qncMEZ      [mmolN/mgC]      Maximum quotum N:C
! p_clO2o       [mmolO2/m3]      Half-saturation oxygen concentration
! p_paPPY(z,p) [-]               Availability of PhytoPlankton group p
!                                to Zooplankton group z
! p_paMIZ(z,m) [-]               Availability of MicroZooplankton group m
!                                to Zooplankton group z
! p_paMEZ(z,m) [-]               Availability of MesoZooplankton group m
!                                to Zooplankton group z
!-------------------------------------------------------------------------!
&MesoZoo_parameters
!                Z3      Z4
       p_q10 =  2.0,    2.0
       p_srs =  0.01,   0.02
       p_sum =  2.0,    2.0
       p_vum =  0.008,  0.02
       p_puI =  0.6,    0.6
       p_peI =  0.3,    0.35
       p_sdo =  0.01,   0.01
        p_sd =  0.02,   0.02
       p_sds =  2.0,    2.0
    p_qpcMEZ =  1.67d-3,1.67d-3
    p_qncMEZ =  0.015,  0.015
     p_clO2o =  30.0,   30.0
! Food matrix parameters: take care of the notation
!                P1      P2      P3      P4
!       Z3
p_paPPY(1,:) =  0.0,    0.0,    0.0,    1.0
!       Z4
p_paPPY(2,:) =  1.0,    0.75,    0.0,    1.0
!                Z5      Z6
!       Z3
p_paMIZ(1,:) =  0.0,    0.0
```

```
!       Z4
p_paMIZ(2,:)=   1.0,    0.0,
!               Z3      Z4
!       Z3
p_paMEZ(1,:)=   1.0,    1.0
!       Z4
p_paMEZ(2,:)=   0.0,    1.0
      filename_nml_conf = 'Pelagic_Ecology.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST PelChem_parameters, PelChem_parameters_iron
!-------------------------------------------------------------------------!
!  Pelagic Chemistry parameters
! NAME        [UNIT]/KIND      DESCRIPTION
! p_q10N4N3   [-]              Q10 factor for nitrification/denit
! p_sN4N3     [1/d]            Specific nitrification rate at 10 degC
! p_clO2o     [mmolO2/m3]      Half-saturation O2 concentration for
!                              nitrification and reoxidation
! p_rOS       [1/d]            Specific reoxidation rate of reduction
!                              equivalents
! p_sN3O4n    [1/d]            Specific denitrification rate
! p_clN6r     [mmolHS/m3]      Half-saturation concentration of
!                              reduction equivalents for denitrification
! p_rPAo      [mmolO2/m3/d]    Reference anoxic mineralization rate
! p_q10R6N5   [-]              Q10 factor for biogenic silica
! p_sR6N5     [1/d]            Specific remineralization rate of
!                              biogenic silica
!               --------- Iron parameters -----------
! p_q10R6N7   [-]              Q10 temperature dependence
! p_sR6N7     [1/d]            Specific remineralization rate of particulate
! p_sR1N7     [1/d]            Specific remineralization rate of dissolved
! p_scavN7f   [1/d]            Specific scavenging rate
! p_N7fsol    [umolFe/m3]      Solubility concentration
!-------------------------------------------------------------------------!
&PelChem_parameters
  p_q10N4N3 = 2.367
    p_sN4N3 = 0.01
    p_clO2o = 10.0
      p_rOS = 0.05
   p_sN3O4n = 0.35
    p_clN6r = 1.0
     p_rPAo = 1.0
  p_q10R6N5 = 1.49
    p_sR6N5 = 0.1
      filename_nml_conf = 'Pelagic_Environment.nml',
/

&PelChem_parameters_iron
      filename_nml_conf = 'Pelagic_Environment.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST PelGlobal_parameters
!-------------------------------------------------------------------------!
! Sinking rates of Pelagic Variables
!  : for mem_PelGlobal filled by InitPelGlobal
! NAME           UNIT      DESCRIPTION
! p_rR6m         [m/d]   detritus sinking rate
! KSINK_rPPY      [m]    prescribe sinking rate for phytoplankton below this
!                        depth threshold to p_rR6m value. Use 0.0 to disable.
```

```
! AggregateSink  logic   use aggregation = true to enhance the sink rate
!                        and bypass the prescribed sinking
! depth_factor    [m]    depth factor for aggregation method
!-------------------------------------------------------------------------!
&PelGlobal_parameters
  p_rR6m         = 5.0
  KSINK_rPPY     = 150.0
  AggregateSink  = .FALSE.
  depth_factor   = 2000.0
     filename_nml_conf = 'Pelagic_Environment.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST standalone_nml
!-------------------------------------------------------------------------!
!NAME      KIND  DESCRIPTION
!nboxes    integer    Number of water volumes (boxes)
!indepth   real  Depth of each box (m)
!latitude  real  Latitude of each box
!longitude real  Longitude of each box
!maxdelt   real  Maximum timestep duration (s)
!mindelt   real  Minimum timestep duration (s)
!method    integer Integration method
!               1. Euler forward
!               2. Runge-Kutta 2nd order
!               3. Leap-frog
!-------------------------------------------------------------------------
&standalone_nml
   nboxes      = 1,
   indepth     = 5.0,
   latitude    = 45.0,
   longitude   = 13.5,
   maxdelt     = 8640.0,
   mindelt     = 1.0,
   method      = 2,
      filename_nml_conf = 'Standalone.nml',
/

!-------------------------------------------------------------------------!
!NAMELIST time_nml
!-------------------------------------------------------------------------!
!Specify time related formats and variables here.
!timefmt   integer    implicitly uses timestep=maxdelt
!               1- MaxN only - fake start time used.
!               2- start and stop - MaxN calculated.
!               3- start and MaxN - stop calculated.
!               4- simdays - fake start time used
!                  and MaxN calculated.
!MaxN      integer    do loop from n=1,MaxN
!start           string     Initial time: YYYY/MM/DD HH:MM:SS
!stop      string     Final   time: YYYY/MM/DD HH:MM:SS
!-------------------------------------------------------------------------!
 &time_nml
  timefmt=      2,
  MaxN=         144,
  simdays=      5760,
  start=        "2000-01-01 00:00:00",
  stop=         "2010-01-01 00:00:00",
     filename_nml_conf = 'Standalone.nml',
/
```

```
!-------------------------------------------------------------------------!
!NAMELIST forcings_nml
!-------------------------------------------------------------------------!
!forcing_method integer     Choice of the external forcing functions
!                1 = analytical forcings
!                2 = from file
!                3 = interactive fluxes (not yet implemented)
!
!Method 1: Analytical forcing functions
!lw         real  Sinusoidal light intensity (winter) W m^-2
!ls         real  Sinusoidal light intensity (summer) W m^-2
!sw         real  Sinusoidal salinity (winter)
!ss         real  Sinusoidal salinity (summer)
!tw         real  Sinusoidal temperature (winter) degC
!ts         real  Sinusoidal temperature (summer) degC
!tde        real  Sinusoidal temperature daily excursion degC
!ww         real  Sinusoidal wind (winter) m/s
!ws         real  Sinusoidal wind (summer) m/s
!CO2inc          real    Linear increase in CO2 air partial pressure [% per year]
!
!Method 2: data file
!forcing_file    char  Filename for external forcings
!
!use_external_data logical Read external data (user defined)
!data_file    char       Filename for external data
!
!-------------------------------------------------------------------------!
&forcings_nml
   forcing_method    = 1,
   ltype             = 1,
   lw                = 20.0,
   ls                = 300.0,
   sw                = 37.0,
   ss                = 34.0,
   tw                = 8.0,
   ts                = 28.0,
   tde               = 1.0,
   ww                = 20.0,
   ws                = 10.0,
   forcing_file      = '',
   use_external_data = .false.,
   data_file         = '',
      filename_nml_conf = 'Standalone.nml',
/

!-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
! MODEL  BFM - Biogeochemical Flux Model
!-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
```