

EcoGENIE:

A practical course in global ocean ecosystem modelling

Lesson 1b: Ecosystem configuration (ecological and physiological characteristics)

In the last section you ran a very simple version of the ecosystem model, and compared it to observations. In this section we are going to add a bit more ecological realism, with the aim of improving model performance. We will start by adding a zooplankton population that should bring a degree of ‘top-down’ control to the phytoplankton population.

1. Ecosystem configuration. Details of the original ecosystem are specified in the *user-config* file, BSS.NPD.SPIN. Locate this file (in `~/cgenie.muffin/genie-userconfigs/.`), and open it in your preferred text editor.

1.1. The *user-config* file can be used to configure the model to your liking. One of the most important amendments to note straight away can be seen on line 11, `bg_par_bio_prodopt="NONE"`. This effectively disables the biological pump in BIOGEM, replacing it with the explicit biology of ECOGEM. This is a necessary step whenever running ECOGEM, because we do not want the implicit and explicit biological schemes to be implemented in the same simulation.

1.2. We can also see a load of other model parameters. Any that begin with ‘`bg_`’ correspond to BIOGEM, while ‘`eg_`’ corresponds to ECOGEM. The ECOGEM parameters begin after line 71.

1.3. One of the most important parameters specifies the *ecosystem configuration* file

```
eg_par_ecogem_plankton_file = 'NPD.eco'
```

This points to a file (located in `~/cgenie.muffin/genie-ecogem/data/input/.`) that specifies every plankton population that is included at the start of the model run. If you open that file in the text editor, you will see something akin to the following...

```

01          02    03
  \         \    \
-START-OF-DATA-
Phytoplankton  10.00  1
-END-OF-DATA-

  /         /    /
01          02    03

DATA FORMAT AND ORDER
-----

COLUMN #01: plankton functional type name
COLUMN #02: plankton diameter (micrometers)
COLUMN #03: number of randomised replicates

INFO: TRACER ASSIGNMENT RULES
-----
Plankton functional type one of: Prochlorococcus
                                Synechococcus
                                Picoeukaryote
                                Diatom
                                Coccolithophore
                                Diazotroph
                                Phytoplankton
                                Zooplankton
                                Mixotroph

```

The first thing to note is that only the lines in between “-START-OF-DATA-” and “-END-OF-DATA-” are read by the computer. The rest is there solely for your guidance.

Each line that is entered in the computer-readable area tells the model to put a distinct plankton population in the model. The “plankton functional type” of this population is specified in the first column, while the plankton diameter specified in the second column. A ‘1’ must always be placed in the third column (it doesn’t do anything, but the model still needs it).

In this ‘NPD’ configuration, we only have a 10 micron generic phytoplankton. The ecological and physiological traits of this population are assigned automatically according to the size and the functional type.

Note that the only PFTs available at the moment are Phytoplankton, Zooplankton and Mixotroph. The other groups currently have no real functionality associated with them. (If you have some good ideas, we may be able to add them in later in the course).

1.4. We can increase the ecological complexity of the model by adding another plankton population. Save the *ecosystem configuration* file under a new and highly intuitive name (such as NPZD.eco), and add another line specifying a 100 micron zooplankton. It is important that the zooplankton is 10 times larger than the phytoplankton in terms of diameter. This is the optimal predator-prey length ratio in the default configuration. (You could maybe think about changing this value later on in the course.)

1.5. To run the model with this new configuration, change the name of the *ecosystem configuration file* in the *user-config* file...

```
eg_par_ecogem_plankton_file = 'NPZD.eco'
```

1.6. Save the new *user-config* file under a different name (e.g. BSS.NPZD.SPIN). You can now execute the model at the command line. Don't forget to change the name of the *user-config* file here as well...

```
qsub -j y -o cgenie_log -V -S /bin/bash
runmuffin.sh cgenie.eb_go_gs_ac_bg_eg.worjh2.BASESFeTDTL / BSS.NPZD.SPIN 10
BENW.worjh2.P04FeTDTL_HYBRID_new.SPIN
```

1.7. Once you have completed the new simulation, compare the new results to the old simulation, in terms of its ability to reproduce observations. Has the addition of zooplankton to the model improved its behaviour?

Look also at the global distributions of carbon biomass in the phytoplankton and zooplankton populations (again, a log scale might help).

- How have the zooplankton interacted with the phytoplankton to change the model dynamics?

2. Visualising composite data We can perhaps get a better handle on this question by looking at the ratio of phytoplankton-to-zooplankton biomass. Such ratios can, however, be difficult to assess simply by eyeballing two maps. Instead we can use Panoply to combine data arrays.

2.1. First close all your Panoply plot windows. Then open a new one for “C Biomass - Popn. 001 (10.00 micron phytoplankton)”. Next, select “C Biomass - Popn. 002 (100.00 micron zooplankton)”, and click the “Combine Plot” icon at the top of the Panoply window.

2.2. A box will open up asking you “In which existing plot should I combine the variable”. As you now only have one plot available, this should be a straightforward choice. Click “Combine”.

2.3. A new map should appear showing the total carbon biomass minus the total phosphorus biomass (see the label on the colour scale). This is not what we want. Below the map, under the “Array(s)” tab, there is a drop down menu showing the range of different ways the two arrays can be combined. We want to look at the Z:P biomass ratio, so select “Array 2 / Array 1”.

2.4. You now need to make sure that you are looking at the right year (you can time-lock the two arrays by clicking on the chain icon). You may also find it helpful to look at the data on a log scale, with a scale range of 0.1 to 10. You might also like to change the ‘Color Table:’ option to ‘GMT_polar.cpt’.

- What does this plot say about the relationship of zooplankton and phytoplankton in different regions of the ocean?
- In what regions do zooplankton or phytoplankton dominate?
- What affect does a high Z:P ratio have on the size of the phytoplankton population? (For example, in terms of the chlorophyll concentration.)

3. Iron limitation Up to this point, we have only considered phosphate as a limiting nutrient. (Iron was included in the model, but it was not limiting to phytoplankton growth.) You can switch on iron limitation by modifying two lines in the *user-config* file. Make sure that...

```
eg_useFe      =.true.
```

and

```
eg_fquota     =.true.
```

Give the *user-config* file a new name (e.g. `BSS.NPZD_Fe.SPIN`), and reevaluate the model. Again, don't forget to change the name of the *user-config* file in the command...

```
qsub -j y -o cgenie_log -V -S /bin/bash
runmuffin.sh cgenie.eb_go_gs_ac_bg_eg.worjh2.BASESFeTDTL / BSS.NPZD_Fe.SPIN 10
BENW.worjh2.P04FeTDTL_HYBRID_new.SPIN
```

3.1. Examine the effect of iron limitation in the new model. What has changed?

3.2. We can get a more exact picture of the nutrient limitation terms through “`eco2D_xGamma_Fe_001`” and “`eco2D_xGamma_P_001`”.

These two variables take values of between 0 and 1. A ‘1’ indicates that the factor is not limiting to growth. A ‘0’ indicates the factor is completely preventing growth.

- In what regions are iron and phosphorus more or less limiting to growth?
- In regions where neither is limiting, what other factors might be important?

3.3. You have seen in the lectures that the plankton stoichiometry plays a critical role in determining which nutrient is most limiting to growth. You can increase the plankton Fe:C ratio by increasing the minimum and maximum iron quotas. Look at the parameters `eg_qminFe_a` and `eg_qmaxFe_a` in the *user-config* file.

- What happens to the ecosystem if you increase these parameters by a factor of 2, 5 or 10?

Note: It can be risky to just change the parameter value in place, as you might forget what you started with. Instead copy/paste a new version of the line in question, and comment out the original by placing a ‘#’ at the beginning of the line. For example...

```
#eg_qminFe_a = 3.0e-6
eg_qminFe_a = 6.0e-6
```

How does a change in these parameters affect the model behaviour?

- What has changed in terms of the patterns of nutrient limitation?
- What has happened to the concentration of the limiting and non-limiting nutrient?

3.4. Nutrient supply ratios are also important in determining the limiting nutrient. The `bg_par_det_Fe_sol_exp` parameter determines the solubility of atmospheric iron inputs in seawater. Decreasing the value of `bg_par_det_Fe_sol_exp` will therefore decrease the iron-to-phosphorus supply ratio.

- What happens to the ecosystem if you decrease `bg_par_det_Fe_sol_exp` by 10, 20 or 50%?