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### **D2.8 Submodel Ecopath with Ecosim, including user guide and interface variable list**

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## **D2.8 Submodel Ecopath with Ecosim, including user guide and interface variable list**

*Summary of Ersem to EwE 1 Dimensional model linkage using Couplerlib.*

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## 1. Introduction

Perhaps the most important and thorny problem in estimating the abundance of fish stocks and their response to fishing and environmental change, is the estimation of the recruitment of young fish to the adult stock. It is a difficult function to quantify in models because it is dependent not only on the size of the parent stock, but also on interactions of the lower trophic level components of marine ecosystems that are highly dependent on physical driving factors such as temperature, irradiation and wind (Cushing 1996). How such processes govern fish recruitment and population variability is still poorly understood (Minto and Myers, 2008), and thus most fisheries models tend to predict fish recruitment based on past trends and assumed stochasticity, rather than taking a process-oriented approach.

Similarly, process-oriented coupled physical-biological models such as GOTM-ERSEM (Berreta et al., 1997; Vichi et al. 2003) and POLCOMS-ERSEM (Lewis and Allen 2008; Blackford et al. 2004, Allen and Gilbert, 2004) that predict changes in primary production and zooplankton abundance as outcomes of hydrodynamic and biogeochemical processes, are hindered by their inability to capture top-down trophic impacts from higher grazer such as fish.

Although lower trophic level components can quite easily be incorporated into multi-species fisheries models such as Ecopath with Ecosim (Christensen et al. 2005) the representation of these species does not take into account their environmental drivers, nor the dynamics of the different nutrient components in determining the limitations of phytoplankton growth. With the knowledge that environmental changes can have drastic impacts on lower trophic level components such as phytoplankton (Richardson and Schoeman, 2004) and that fisheries have strong impacts on the abundance and structure of fish stocks (e.g. Lotze et al., 2006), investigating how ecosystems respond to combined pressures necessitates that processes at lower and higher levels are linked. This is the basis of the present fashion in end-to-end modelling, whereby the connection of physics to fish is made.

We do not prophesize to solve the fish recruitment problem nor predict with confidence how top-down forces feedback upon biochemical processes, but show how by coupling different types of models a modest step has been taken toward connecting processes in a way that facilitates improved predictions of how ecosystems respond to human and environmental change. The coupled LTL-HTL model system allows for iterative exchange of data among models, thus capturing important feedback processes within an ecosystem. It allows us to investigate for the first time ecological issues such as observations on the decline of phytoplankton that have been attributed simultaneously to physical drivers such as the increase in summer stratification of shelf seas and a reduction of predation on zooplankton by fish. Thus, it provides a framework to encompass the whole cause and consequences of changes in zooplankton density.

### 1.1 Challenges of Model Coupling

The principal challenges of coupling LTLs models with HTL models involves reconciling the differences in how the different models handle and represent important processes at different time and spatial scales (Rose et al. 2010). Whilst it is vitally important to test and understand how choices in the level of detail (one or many groups), which groups are represented (size, age, bulk biomass) and the impact of time and spatial scales of processes (e.g. capturing seasonality), there is also a need to be pragmatic. This means making choices that enable the models to be coupled and tested, either through comparison with empirical data or by their ability to generate plausible, testable hypothesis that are consistent with understanding.

Some existing approaches that have linked lower and higher trophic levels use single species and individual based approaches (Travers et al. 2007, Rose et al. 2010). However in connecting ERSEM

to EwE we are confronted by the problem of dealing with models that are explicitly specified at runtime or by means of a user invoked compiler. In this case it is necessary to develop a coupling mechanism which uses program generated and human created metadata to specify linkage between the models and check it for semantic and numeric consistency.

Here, an example application is developed using the North Sea 1991 EwE model (Mackinson and Daskalov 2007) coupled to GOTM-ERSEM, and 1D model parameterised for a stratified site representing the Oyster Ground (54°24' N, 4°3' E). A step-by-step approach is taken, starting with a coupling between 2 functional groups, a single feedback loop and with a model 1-D representation of GOTM-ERSEM and spatially averaged representation in EwE. Omnivorous and carnivorous zooplankton (Z4 and Z3 in ERSEM) are chosen as the coupling groups since in the open ocean these form the principal pathway that connects the energy from the lower trophic food web with the higher trophic level consumers. The 1-D version of GOTM-ERSEM, captures the biogeochemical processes occurring in the water column. The spatially averaged EwE model assumes that the biomass of all functional groups is distributed evenly throughout the model domain. Full spatial representations of both models are available and future plans are to couple them.

To facilitate a clear understanding and promote further development of the methodological approaches, we describe the technical process of linking EwE to GOTM-ERSEM, in words, annotated diagrams and pseudo-code. Specific problems and solutions to overcoming them are discussed.

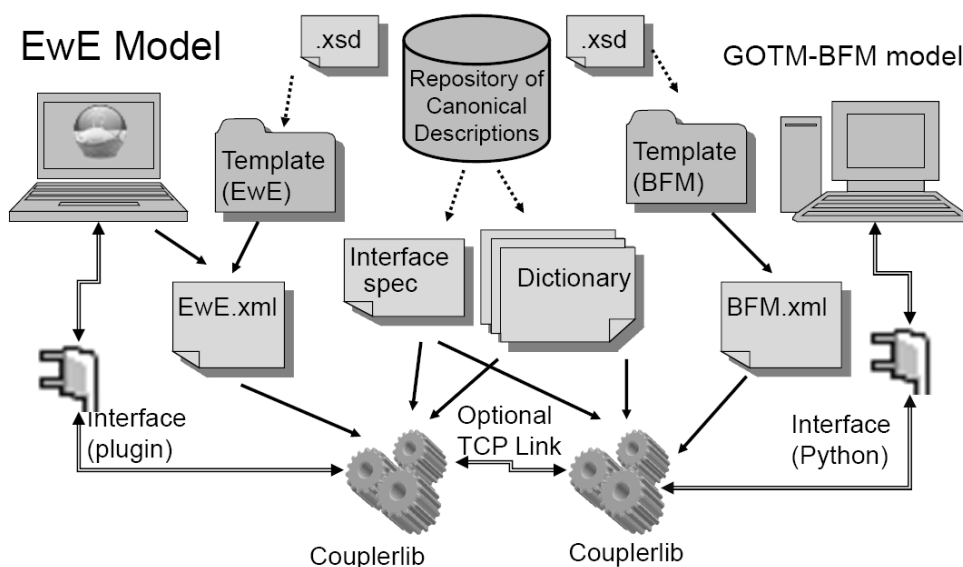


Figure 1. Outline of the information sources in the form of xml files and model components between two models running in network mode with twin copies of couplerlib.

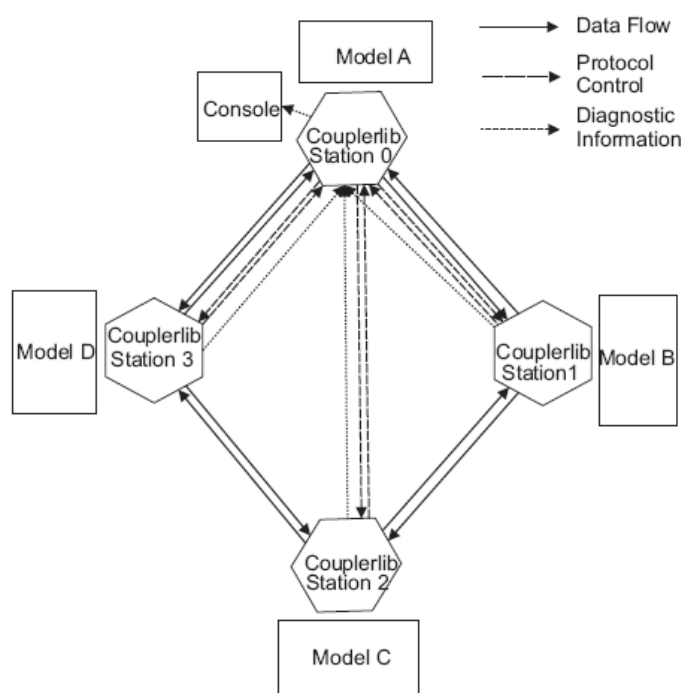
## 2. Implementation

### 2.1 Outline of coupling mechanism

Exchange of information between the LTL and HTL models is achieved via Couplerlib (Figure 1), which is a library of routines for checking data consistency between models, carrying out data conversions and providing network protocols. It is not a universal coupler, which would be very difficult to achieve given the potentially enormous range of languages and calling conventions that

models may use. Instead, the user is required to provide a compatible interface for use with couplerlib, this being the 'front end' used to input required information to setup and perform a model run. In this case the EwE front end serves as the primary interface, through which the front end of GOTM-ERSEM is called for specification of the LTL model run.

Couplerlib can operate in two different modes: managed and networked. In managed mode the coupled models operate on the same process so that they can share memory and call each other's routines. Typically however, they will operate on separate threads of execution within the same program, with couplerlib being used as a data bridge between them. The data store in couplerlib is global and persistent, and is referenced by an enumeration of model and interface. In principle a single couplerlib can be used to link multiple models with multiple connections for different types of data between them. However, care must be taken to ensure that a frame of data (data for single model and interface combination) is only read after it is completely written; otherwise the data may be corrupted. Because programming libraries for multithreaded systems have various ways to signal events and suspend program execution on a thread, these mechanisms need to be provided by the program interface.



*Figure 2. Data transfers between a network of four linked models running in network mode, with transfers of control messages, data and diagnostic information, using a mixed point to point and central client model.*

When models reside on different processes, systems and machines, couplerlib will operate in networked mode. In this case, each process or machine is required to have its own couplerlib. The networked couplerlibs are initially synchronised by reading metadata descriptions of all the models being linked from files that will be available on all machines as a Uniform Resource Identifier (Berners-Lee et al. 2005). At run time the networked couplerlibs are partially synchronised on a just-in-time, need-to-know, object request basis. Data from a model is written to the local copy of couplerlib and the remote copy synchronises its own copy when an instruction is received to fetch data. In addition to transferring data, the networked couplerlib exchanges diagnostics and model output to be displayed remotely and controls the synchronisation of data (Figure 2).

To ensure that coupled models are synchronised, Couplerlib uses the Berkeley Sockets Mechanism, specifically blocking sockets. By assigning each a station number, multiple models can connect using networked couplerlibs –. One station (station zero) is the controller, to which all diagnostic information is given, and which instigates requests to start and stop models, and instigate data transfer etc. The remaining stations typically operate as model servers operating on request from the controller. However data transfer is point to point so that models that required large volumes of data to be transferred between them do not need to exchange this via the central server. This is different to the Atlantis model which transfers all data via a central point.

## 2.2 Metadata information exchange and Specification

Both EwE and GOTM-ERSEM are reconfigurable modelling frameworks which can emit metadata to describe their composition. In the case of GOTM-ERSEM the output data to be emitted is partly specified by user configured components which are then mapped into the main data array (known internally as the CC array) at source level, with parameter values being loaded from a FORTRAN namelist. The front end of GOTM has a system editor and so model specification can be adjusted during the data editing phase of the front end program running before the core GOTM program starts up. There is a related array which describes the data in terms of full name, abbreviated name and unit dimensions, which is created for each instantiation of the source code at the same time as the CC array. The Ecopath, Ecosim and Ecospace programs also have a main data array where metadata is stored, although dimensional information is specified for all data items together. This data array can be changed at runtime by means of the Ecopath editor.

Consequently the location of the data needed for linkage is not fixed at runtime. Indeed there is no guarantee that the necessary data for a linked model run will even be available, once the simulation starts. The first stage of model coupling is for each model to provide a specification of the data which it provides between model loading / editing and the start of the run. Each model provides this information in xml format. The data is supplied in a hierarchical manner, suitable for reading with the Document Object Model library (Le Hégarret et al., 2009) with the following hierarchy:

```
<Model>
  <Description> Author, System, Languages
  <Interface>
    <Time Information> Periodicity, Start and Stop Times
    <Grid Information> Dimensions, Start and end, Resolution
    <Dataitems> of type Phytoplankton, Zooplankton, Consumers, Resources
      <Name>
      <Symbol>
      <Chemical Consituent> Carbon, Nitrogen, Silicate, Phosphorous
      <Flux Direction> Concentration, Intake, Offtake, Mortality, Production
      <Units>
    </Dataitems>
  </Interface>
</Model>
```

ERSEM produces separate concentration data for Carbon, Nitrogen, Phosphorous and (for some functional groups) Silicon. However Ecosim and Ecospace are biomass only models. Consequently data transferred from EwE models back to GOTM-ERSEM must estimate the proportions of the model components using predefined ratios or the ratio of incoming constituents. The model specification is produced from a template file, which is an xml file describing the basics of each model (such as language and system), and the metadata output by the model after loading /editing.

The Specifications for the coupled models are combined by use of a coupler specification which is also an xml file; this species the models to be linked as a number of interfaces. The coupler cross

checks for each interface in turn to see whether the connection is permissible. Permissible interfaces occur when: The model and system information are permissible (specified as a range of allowable version numbers for the component models), the spatial and temporal dimensions are in range for the data, and there is a registered correspondence between all functional groups specified in the interface. These functional groups are only those which are specified as actually needing to be linked in the interface specification.

However, it will often be the case that there is a disparity between the metadata produced by the two models to be coupled. The simplest is the use of different names by the two models, other situations arise where there is an inexact match of the functional group definitions between the two models: For example ERSEM has 6 different phytoplankton groups whereas the EwE North sea model has a single phytoplankton class. It is acceptable to model offtake of all the phytoplankton groups as a single value in the case where predation by groups whose predation is represented in the EwE model is assumed to be the same amongst all phytoplankton groups, but the fluxes within GOTM –ERSEM vary between groups. The final case of disparity is where units of measurement vary between models, which occurs in this case as ERSEM expresses plankton concentrations in molar concentration units and the EwE North Sea model in terms of tonnes per square kilometre. The final xml file is the dictionary file. This specifies mappings between groups and units, unit conversions and synonyms. Furthermore items in the dictionary can be specified in terms of their context (models, interface and organism name). This is useful for exceptions to normal rules, such as greater wet-mass to dry mass ratios for jellyfish compared to most organisms. The dictionary is searched when an exception is found between organism names, or unit names, during the coupling process.

### **2.3 GUI – model front ends**

Both the EwE models and GOTM and hence ERSEM through GOTM, have GUIs. In the case of EwE the interface is written in the .net programming environment for windows, and whilst programmed in Visual Basic uses an object structure which is fully accessible using Visual C++ and C Sharp. The EwE system is runtime extendable using plugins which use the .net interface system to extend the object model of the underlying EwE system. Plugins are dynamically loaded as dlls (executable code program extensions, which must be called from another executable). The GOTM interface, however, is written in Python which is an interpreted language. In order to launch the python scripts for the front end an interpreter is embedded within the plugin dll together with python.net which is a .net compatible api for the python interpreter.

The coupler plugin has a visual interface to select the directory where the coupler description information is contained, which launches the Python interpreter to run the scripts which collectively make up the GOTM-ERSEM front end. These scripts enable the GOTM and ERSEM data files to be manipulated at run time and also for output data to be visualised and manipulated. The front end links to the FORTRAN parts of GOTM and ERSEM via a C wrapper layer – F2Py (Peterson 2007) , which also includes calls to manipulate the FORTRAN data objects, in particular the master 2D and 3D arrays). Couplerlib is available to parse metadata and carry out the kind of managed data conversion described in the previous section. The net result of these various conversion and API layers is that meaningful data objects in GOTM-ERSEM are available from within EwE and vice versa.

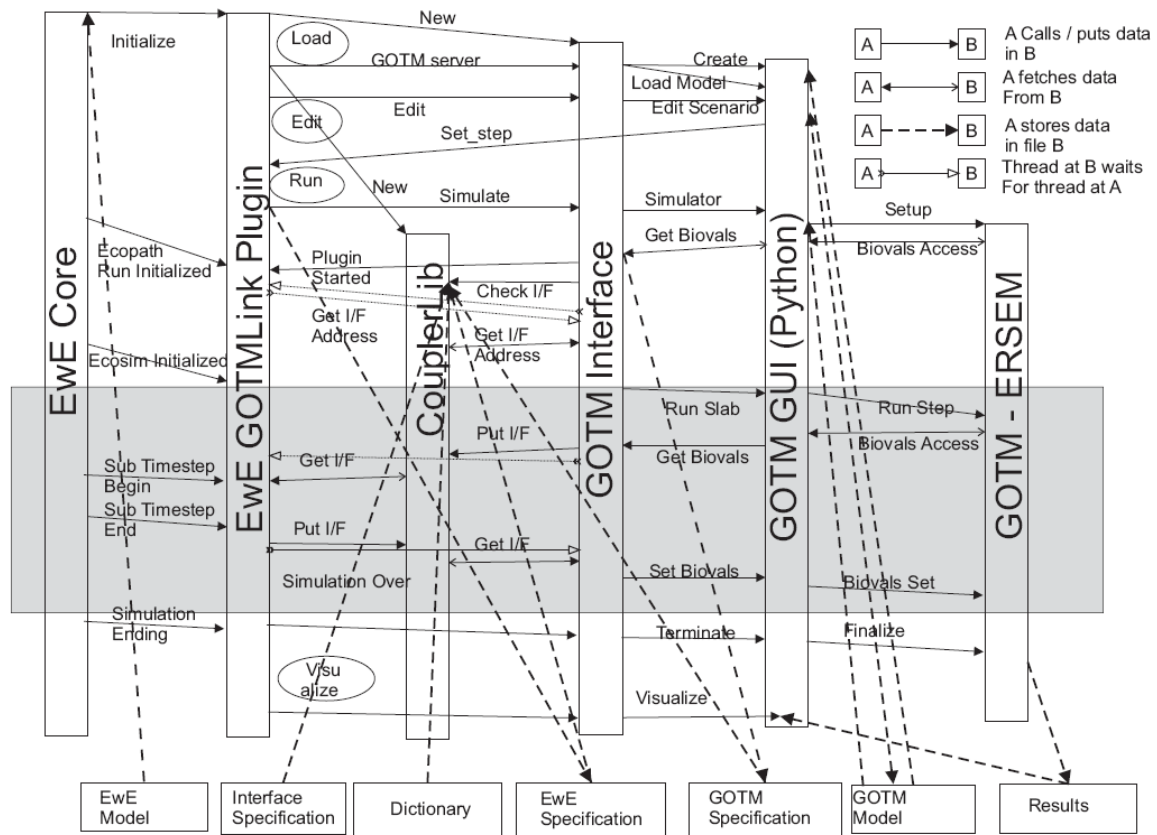


Figure 3. Sequence of operations when GOTM-ERSEM is linked with Ecopath with Ecosim (EwE) in managed model.

## 2.4 The EwE and GOTM-ERSEM models linked

The main sequence of inter model calls and data communication is illustrated in Figure 3. It can be seen that there are six model components. At the ends of the stack of components are the EwE and GOTM models themselves (ERSEM is implemented as a library extension to GOTM but is interfaced through GOTM). Furthermore there is a front end interface to GOTM, which is written in Python and uses the Qt graphical interface components (Bruggeman & Bolding 2007). Although the use of this component is optional it provides useful on line data editing, file management and visualisation facilities, so the decision was made to couple the models via the front end to keep the existing functionality.

The EwE model has a well developed front end, written in VB.net. Plugins are used to extend functionality or add new routines without changing the core code. The six most important points of interface between the core and the GOTMLink plugin are indicated in figure 3, but there are additional point for documentation, identification and visual interaction with the plugin. Control passes from the EwE core to the plugin at those specific points where additional functionality can be provided by the GOTMLink interface. Furthermore there is a wrapper around the GUI for GOTM. When the two models are coupled in the same process running on the same machine the two sides of the model (EwE plus its plugin and GOTM plus its GUI and Interface) operate on separate threads; that is to say there are separate sequences of operations for the EwE and GOTM models. The EwE and GOTM interfaces signal directly when a step in one model is complete and the second model should take over, with execution of the first model suspended in a wait state. Data transfer is carried out by means of



couplerlib, which provides marshalling of the data using external metadata specifications. However the two interfaces can exchange basic information about model status, time to run for and the like through shared memory.

In networked mode the GOTM and EwE sides cannot communicate directly since they do not share common memory. Instead everything goes via couplerlib. The EwE and GOTM sides will have their own copies of couplerlib. The two couplerlibs will exchange information using TCP/IP sockets so that the receiving end of a data transfer makes a copy from information requested from the sender couplerlib. Information used to synchronise the models and give information on model state such as waiting, finished and error conditions for various operation is sent via a separate pair of sockets and diagnostic information is sent to the couplerlib which is attached to the graphical console ( the EwE GOTMlink plugin in this case).

The GOTMlink plugin includes an interface to the model coupling facilities. There are four user initiated operations: GOTM model load, Edit, Run and Visualize. Only the run call operates beyond the GOTM GUI into GOTM itself. Instantiation of the EwE model is controlled through the EwE GUI itself. When the EwE and GOTM models are loaded they export their specifications to separate xml files. These are made available, together with the user provided interface specification and dictionary to couplerlib. When the models are run in managed mode data, such as the timestep, and the start and stop times are transferred read directly from GOTM to EwE sides. The bulk of the data is transferred via couplerlib. The critical call to couplerlib is the CheckIF call which loads all the metadata specifying the interface, and cross checks this against the specifications of the component models. Providing this is consistent, the GOTM and EwE threads are synchronised to ensure that the Ecosim module has been started, resulting in the EcoSimRunInitialized call being sent from the EwE core to the plugin. Both component models can then use GetIFAddress to locate the position of the data that will be transferred in the couplerlib data store.

The main loop consists of repeated calls to the GOTM library after which the CC array within GOTM is accessed and stored in couplerlib. The EwE part of the model will wait for the data to be written, continue with the EwE timestep calculations, whereup the updated EwE data is written to a different frame of the couplerlib repository and GOTM must synchronise and then read the data. Finally if EwE has finished (the Simulation Ending Interface call is made) GOTM can be made to terminate early and cleanup called to ensure are data is written to output files.

## **2.5 GOTM-ERSEM model**

The lower trophic level model was set up to represent the a site in the Oyster Grounds with appropriate water depth (40m) , tidal velocities ( $M_2$  amplitudes of  $30\text{cm s}^{-1}$ ) and meteorological forcing. Some preliminary validation was undertaken but is not reported here. The aim was to simulate the annual dynamics of a site that was to some extent representative of average behaviour over a certain portion of the North Sea rather than a fully validated simulation for a particular location. The Oyster Ground site itself is stratified but is marginal in the sense of being near to the tidal mixing front that divides summer stratified with the mixed region to the south. The model exhibited summer stratification and the lower trophic level dynamics might be expected to be reasonably representative of the central North Sea.

## **2.6 North Sea Model**

The North Sea Ecosim model (Makinson & Daskalov, 2007) consists of 67 functional groups, which are both pelagic and benthic. However, in order to be consistent with ERSEM, this 67 was extended by two new detritus groups (separating particulate organic matter (POM) into pelagic and benthic components and adding a new faecal POM group). The Lower trophic level groups used by both EwE and ERSEM for pelagic and benthic components are listed in table 1. However the benthic components of the North Sea model do not correspond well to the groups used by ERSEM. In

particular there is poor correspondence between the groups of filter feeders, deposit feeders and infaunal predators of ERSEM and the Infaunal macrobenthos, sessile epifauna and infaunal Macrofauna of the North Sea model. Consequently the decision was made only to couple the pelagic groups (phytoplankton, zooplankton and bacteria) together with a variable proportion of the detritus which is the critical linking component of a benthopelagic model.

The coupling is by two unidirectional couplerlib interfaces. ERSEM passes to EwE the biomass of the pelagic functional groups, whereas the amount of offtake by predators as a proportion of biomass is returned to ERSEM. The version of EwE used has been specially adapted to run at a timestep of a single day, rather than a month (this is important since Productivity / Biomass ratios for Phytoplankton are of the order of 286 per year). Because there are two separate Benthic models, with coupling in the detritus and via top predators, the benthic components shadow each other, with the EwE component being affected by the temporal variability of the detritus, but not by the immediate variation of benthic conditions input experienced by the ERSEM model. Consequently the variability of the species which consume benthic components within EwE is less.

## 2.7 EwE Model re-parameterisation

The first attempt to link the two models was not successful. Pelagic groups that feed off mesozooplankton overexploited the mesozooplankton during the winter period causing the death of the plankton populations and consequent reduction in productivity of the pelagic part of the system. This was a result of the ecosim model having been calibrated primarily on summer plankton levels to set the consumption to biomass level. In practice consumption is very much lower in winter months when the plankton population is lower but also the metabolic rate of the predatory fish is very much reduced. In addition to the reduced metabolism which follows an exponential temperature to metabolism law resulting from the Arrhenius equation, there may be behavioural changes that reduce prey consumption still further. For example sand-eels, which were observed to be one of the major predators of mesozooplankton switch to being benthic between November and April (Englehard et al. 2008) and so have zero consumption of plankton in winter months. To fix these changes it was necessary to add a forcing function to reduce predation of pelagic sources in winter months. Two forcing functions were used – one a purely metabolic model using a  $Q_{10}=2.0$  rule of temperature, with maximum temperature having a multiplier based on the original EwE model of 1.0, the other fitted the observations on sand eel populations of Englehard et al. (2008). In addition metabolic costs were reduced to 0.3 for adults and 0.0 for juveniles (EwE allows only a fixed value). It was also decided to multiply by 10 the nutrient levels in ERSEM, in the first instance to examine what the productivity of the system would be under conditions of high levels of nutrients. The search area of the carnivorous zooplankton (Coepopods) was increased to 0.06 to keep both the zooplankton groups alive for the whole simulation. These parameters are often fitted and it was discovered that there was quite a narrow range of carnivorous zooplankton parameterisation that worked at all. In addition the background mortality of the zooplankton in ERSEM was reduced to a nominal value to take account of the fact that most mortality would be expected to be caused by predation which is accounted for in the EwE model. Interestingly, the level of zooplankton predicted by the ERSEM model peaked at around 0.8 of the value used to calibrate EwE, indicating that ERSEM is unable to represent very high zooplankton levels in eutrophic systems. The parameter files for EwE and ERSEM sets are located in the source code repository '[couplerlib.myversioncontrol.com](http://couplerlib.myversioncontrol.com)'

## 3. Model Code

The Source code for CouplerLib and associated source Files are hosted in a subversion (SVN) repository hosted at '[couplerlib.myversioncontrol.com](http://couplerlib.myversioncontrol.com)'

Firstly you will need to install an SVN client. For windows users the easiest client is Tortoise Subversion (Google it to find your nearest distribution). You will need administrative access to your computer to install it.

Once Installed, find a place in your file system where you want Couplerlib to be installed and right click. From the menu choose SVN Checkout.

In the URL slot type in

<https://couplerlib.myversioncontrol.com/subversion/ersemewecoupler/>

The checkout directory will come up with a path ending in ersemewecoupler.

Click OK

You will be asked for a username and password

One per institution will provided for those wanting to use couplerlib. When the system is updated, this person can then be kept informed. Please email [Jonathan.Beecham@cefas.co.uk](mailto:Jonathan.Beecham@cefas.co.uk) login details

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