MODEL TASK TEAM WORKSHOP REPORT

Final Report of the International Workshop to Develop a Prototype Lower Trophic Level Ecosystem Model for Comparison of Different Marine Ecosystems in the North Pacific

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Summary

The NEMURO workshop made several significant achievements:

1. Assembled an international team of marine biologists and physical oceanographers who collectively achieved a consensus on the structure and function of a PICES CCCC prototype lower trophic level ecosystem model for the North Pacific Ocean, and named it "*NEMURO*";
2. Developed executable computer simulation models and preliminary outputs. Models developed included:
   a) *NEMURO*/FORTRAN Box Model
   b) *NEMURO*/1-D Yamanaka Model
   c) *NEMURO*/1-D Kishi Model
   d) *NEMURO*/MATLAB Box Model;
3. Constructed physical forcing data files and parameter sets for three locations in the North Pacific, station A7 on the A-line off southeast of Hokkaido (41.5ºN, 145.5°E), Ocean Station P (50°N, 145°W), and the Eastern Bering Sea (57.5°N, 175°W);
4. Through an extensive dialog between modelers and plankton biologists, conducted a comprehensive review of NEMURO process equations and their parameter values for the three distinct geographic regions;
5. Developed post-processing software to analyze model output in tabular and graphic formats;
6. Carefully considered the benefit including a microbial food web loop in NEMURO and designed a preliminary strategy for conducting comparative model experiments;
7. Identified leaders and members of model experiment teams, a subgroup of the Model Task Team members and meeting participants, who will be active in conducting future model experiments;
8. Initiated development of comparison protocols;
9. Made recommendations for future lower trophic level modeling activities.

The significance of these achievements will ultimately be evaluated by how well the CCCC Program effectively utilizes and embraces these models as a basis of future modeling activity.

1.0 Introduction

The North Pacific Marine Science Organization (PICES) organizes and promotes an international science program on Climate Change and Carrying Capacity (CCCC) in the temperate and subarctic regions of the North Pacific Ocean. Ecosystem modeling is one of five key research activities defined by the CCCC Implementation Panel. The PICES CCCC MODEL Task Team is given the role to encourage, facilitate and coordinate modeling activities within the member nations with respect to the goals and objectives of the PICES-CCCC Program. At the 1996 Nemuro Workshop on Modeling there was no support for efforts to standardize models or model approaches within the CCCC Program, believing that diversity in assumptions and techniques lead to faster advances in the North Pacific region. However, at the Lower Trophic Level Model Workshop, held in Fairbanks, October 1998, the participants agreed that: i) Models with different state variables and mathematical formulations would be impossible to compare, and ii) comparison protocols are necessary to tackle the problem. Thus, the MODEL Task Team recommended to the CCCC Implementation Panel to convene a workshop on the development of a prototype model and comparison protocols. The recommendation was approved by the CCCC-IP, Science Board, and finally by Governing Council.

2.0 Goals and Objectives of the Workshop

The goals of the workshop were to:

1. Select a lower trophic level model of the marine ecosystem as a PICES prototype;

2. Select a suite of model comparison protocols with which to examine differences and similarities in model dynamics;

3. Demonstrate the applicability of the prototype model by comparing lower trophic ecosystem dynamics among different regional study sites in the CCCC Program;

4. Compare the prototype model with other models;

5. Identify information gaps and the necessary process studies and monitoring activities to fill the gaps;

6. Discuss how to best link lower trophic level (LTL) marine ecosystem models to higher trophic level (HTL) marine ecosystem models, regional circulation models, and how to best incorporate these unified models into JGOFS models and the PICES CCCC Program.

3.0 Organizing Committee, Sponsors, Venue and Participants

Drs. Michio J. Kishi, Makoto B. Kashiwai, Bernard A. Megrey and Daniel M. Ware organized the meeting. Dr. Bernard Megrey served as workshop chairman. The Japan International Science and Technology Exchange Center (JISTEC), PICES, and the city of Nemuro provided financial support and access to excellent meeting rooms in the City Hall. The Nemuro Support Committee supplied local logistical support.

The venue was set at the Multi Purpose Hall, a large octagon shaped room, in the Nemuro City Cultural Center. The hall had four personal computers forming a local network which included a server workstation, laser and color printers, and another one personal computer connected to the Internet. These computers were allocated to four work areas for use by individual workgroups. A classroom style table was arranged in the center of the room for the plenary

session. A set of LCD projectors and screens and AC power outlets for participants' laptop computers were available. These were arranged in each work area to make group work more effective.

Twenty-nine scientists from China, Korea, Russia, Japan, Canada, and the United States (Fig. 1) met in Nemuro, Japan, between January 30-February 4, 2000, to participate in a modeling workshop focused on developing a lower trophic level model of the marine ecosystem. Out of the total, 15 scientists arrived with their own laptop computers, ready to get down to the business of building a numerical NPZ (nutrients, phytoplankton-zooplankton) model, estimate the models parameters, select a suite of model comparison protocols, compare the model to validation data sets, and to perform regional comparisons.

Participants (Appendix 1) consisted of plankton scientists, modelers, and individuals with knowledge about key data sets about each selected region and lower trophic level modeling activity in that region.

4.0 Workshop Schedule

January 30

1830-1930 **Opening Ceremony**

January 31

0930-1730 **1st Session**: Opening Plenary Session
- Opening of Workshop
- General introduction
- Model Comparison Protocols
- Linking LTL model to HTL model
- Introduction of Prototype Model
- Inventory of available data and selection of Study Sites
- Discussion on Prototype Model
- Discussion on Microbial Loop
- Model Comparison Protocols
- Workplan for development of Prototype Model

1900-2030 **Welcome Reception** (Hosted by Nemuro Supporting Committee)

February 1

0930-1230 **2nd Session**: Work Group Session

1330-1730 **3rd Session**: Plenary Session
- Introduction of 1-D Yamanaka Model
- Introduction of FORTRAN Box Model
- Review of Forcing File Preparation
- Alternative Formulations for Primary Production

February 2

0930-1730 **4th Session**: Work Group Session

February 3

0930-1200 **5th Session**: Summary Plenary Session
- Reports from Working Groups
- Workplan for remaining tasks
- Discussion of Workshop Report
- Discussion of Workshop Recommendations

1200-1230 **Closing Plenary Session**
- Closing remarks by conveners
- Speech by Vice-Chairman of Nemuro Supporting Committee

1330- **Workshop Excursion**
(Draft report writing by conveners)

1500-1700 **Nemuro Public Session** for citizens of Nemuro

1830-2000 **Farewell Party** (Co-sponsored by JISTEC and Nemuro)

5.0 Workshop Activity

After an opening ceremony and a welcome party held the day before, the participants convened at the venue to start the four day workshop.

1st Session

On the first day, the workshop officially opened with a welcome to all who had endured a long journey, cold weather, and a powerful snow storm to come to Nemuro.

In the morning session, Dr. Megrey began by providing a general introduction to the activities of the PICES CCCC MODEL Task Team and some background information on decisions made at past Task Team meetings. Since many in the audience had not been involved in the deliberations of the MODEL Task Team, the introduction was designed to give the participants a better sense of how we got to the Nemuro workshop.

This was followed by a presentation by Dr. Makoto Kashiwai on model comparison protocols. Starting from a brief review of reasons for comparison, Dr. Kashiwai discussed the requirements of the model. In order for model results to be comparable, the basic underlying model should have the following items in common:

- The currency of the model and its units of measurement
- The time step
- Spatial dimensions and size segmentation
- Time series of driving factors
- Functional ecological groups (i.e. state variables)
- Mathematical description of biological processes and a definition of parameters and starting values

A model imitating observed phenomena is nothing but a scientific toy. A model can be a scientific tool only when it can output necessary comparison factors and indexes of ecosystem structure and performance. After pointing out these views, Dr. Kashiwai reviewed basic analyses resulting in graphic, diagrammatic, and/or index representation of the structure and performance of an ecosystem:

- Methods to graphically or schematically represent the structure and function of an ecosystem model
- Seasonal patterns of biomass for ecosystem components
- Seasonal patterns of production for ecosystem components
- Annual biomass balance and its seasonal pattern
- Production and its allocation to primary production, or 'ecological efficiency'
- Representation of the dynamic performance of an ecosystem model through sensitivity analysis
- Methods of performing a sensitivity analysis
- Carrying capacity dynamics described by P/B to B relationships
- Dynamic response to ecosystem interactions by interaction coefficient matrices based on ecological niche theory.

Dr. Francisco Werner presented logistical, practical, and theoretical issues related to linking lower trophic marine ecosystem models to higher trophic level models. Based on the modeling and field activities presently underway in the Northwest Atlantic (Georges Bank) Program, Dr. Werner discussed various approaches to linking lower trophic models with higher trophic levels. It was pointed out that the approaches in the NW Atlantic program have not included a detailed description of the population dynamics of the nutrient-phytoplankton-zooplankton (NPZ) system. Rather, the approach has been one where climatological maps of existing decade-long observations of the lower trophic levels have been used as a baseline for setting quantitative levels of these components of the food web. Coupled with realistic 3-D circulation fields and individual-based models of zooplankton, successful studies establishing spatial and temporal links between the zooplanktonic populations in waters neighboring Georges Bank

and their (behaviorally modified) transport onto the Bank were described. Similarly, using adjoint methods (for mathematical inversion), studies were discussed that enabled the inference of the spatial dependence of certain vital rates (e.g., mortality) that would otherwise be difficult to determine in the field. In turn, these results have been coupled with individual-based models of larval fish to determine the (vertically integrated, seasonal and monthly) optimum growth zones of cod and haddock early life stages on Georges Bank. This has allowed the examination of fundamental ecological theories of match-mismatch versus member-vagrant in the regulation of marine populations. Finally, with the recent completion of the 5-year intensive field program, data of unprecedented detail in space, time and species will be coupled to circulation models to determine the links between the larval fish and the NPZ system on shorter time scales (weekly) and in full three-dimensional space.

Dr. Megrey then had a discussion on what models, data sets, parameters, and validation data were brought to the meeting by participants. The core parts of his presentation can be found in the Introduction, Goals, and Objectives sections of this report.

The afternoon session focused primarily on a presentation by Dr. Michio J. Kishi and the current status of the prototype model as originally developed by Dr. Kishi. The state variables, process equations representing system fluxes, parameter needs and outputs were discussed in detail. A long discussion developed regarding whether the model correctly represented the marine ecosystem and could reproduce the dynamic features of lower trophic level production in the selected study areas. Consequently, one more state variable representing predatory zooplankton and the connecting process equations were added to the proposed prototype. After considerable discussion, the group of 29 scientists collectively agreed to accept this model as the PICES prototype lower trophic level marine ecosystem model (Fig. 2).

This significant occasion was followed by a presentation by Dr. Dan Ware on the importance of including a microbial food web in the marine ecosystem lower trophic level model. Details of his presentation are partly reproduced in the Microbial Food Web Team Report (below).

The afternoon ended with a selection of model comparison locations. Regions selected for comparison included station A7 on the A-line off the east side of Hokkaido (41.30°N, 145.30°E), Ocean Station P (50°N, 145°W), and the Eastern Bering Sea (57.5°N, 175°W) (Fig. 3).

A summary of changes needed to complete the prototype model was discussed, the development of a flow diagram for data processing was presented (Fig. 4), and followed by a discussion of potential topics for breakout groups. This list included

- Biological review of the model parameters
- Microbial food web formulation
- Forcing file preparation and coding of new model segments
- Post-processing and plotting programming

2nd Session

The second day was taken up primarily with the teams beginning to deal with their specific tasks. The workshop split into four teams, each addressing a specific task (Appendix 2).

The first team concerned itself with the preparation of the forcing files for the three geographic locations as well as coding of the test models. The second team had the responsibility of reviewing the appropriateness of all biological process equations and reviewing the suitability of individual parameter values. This team also generated a list of parameter values for each geographic location and supplied, where possible, a reference and a plausible possible range of values (Table 4). The third team prepared the software for post-processing the model output (reformatting of output data files and defining standardized figures for

graphical presentation of model output). The fourth team concerned itself with the development of a microbial food web formulation and a strategy to incorporate the microbial food web submodel into the existing prototype model.

Fig. 1 Nemuro Workshop participants. Left to right, bottom row: *Tomonori Azumaya, Yukimasa Ishida, Kosei Komatsu, Makoto B. Kashiwai, Michio J. Kishi, Yuri I. Zuenko, Daji Huang, Hiroaki Saito, Katsumi Yokouchi*. Top row: *Hyun-chul Kim, Hitoshi Iizumi, Gennady A. Kantakov, Francisco E. Werner, Sukyung Kang, Vladim V. Navrotsky, Atsushi Tsuda, Daniel M. Ware, Bernard A. Megrey, David L. Eslinger, Vladimir I. Zvalinsky, Jing Zhang, Naoki Yoshie, Yasuhiro Yamanaka, Masahiko Fujii, Maki Noguchi, Lan S. Smith*.

3rd Session

On the afternoon of the second day, there was a presentation by Dr. Yasuhiro Yamanaka on the structure of the 1-D bio-physical coupled model and by Mr. Naoki Yoshie and Mr. Masahiko Fujii on the status of the Box Model. Also on the afternoon of the second day, we reviewed preparation of the forcing files for stations A7, Station P and Bering Sea and Dr. Vladimir Zvalinsky gave a presentation on alternative formulations for the primary production process.

4th Session

On the morning of the third day the teams continued their deliberations. In the afternoon of the third day, the output from model comparisons were generated for the three regional areas and some provisional analysis were begun.

5th Session

At the last session on the fourth day we had a summary plenary session where we heard reports from each team, discussed the work plan for

remaining tasks, then discussed the workshop report and workshop recommendations. The results of these discussions are in the Recommendations section.

Closing Plenary Session

The participants received closing remarks from the vice-chairman of the Nemuro Supporting Committee where appreciation was extended to have helped bring into being such a productive workshop. These feelings were amplified during the Sayonara Party, which was full of warm hospitality by the people of Nemuro city.

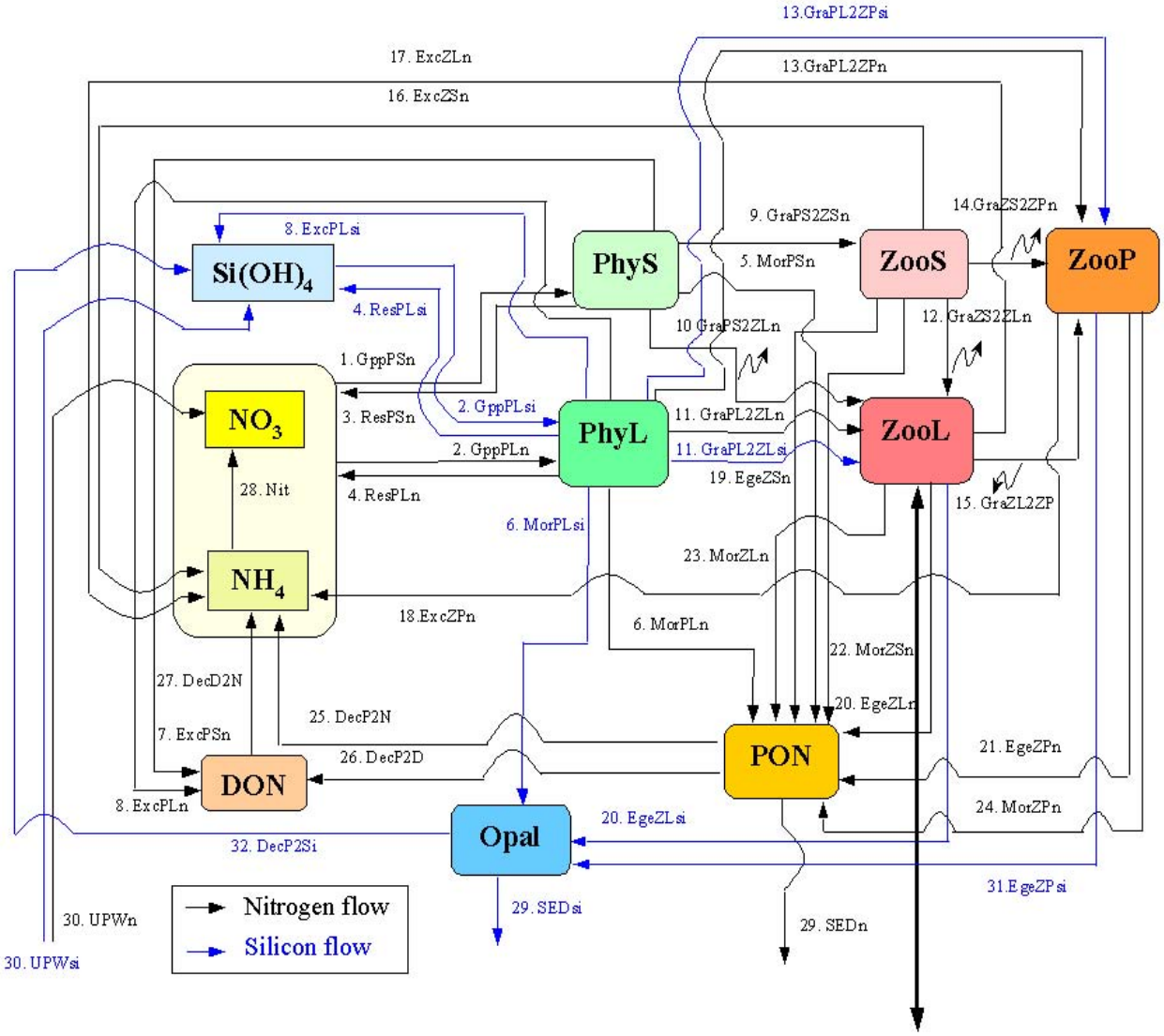

Fig. 2 *NEMURO*, a PICES CCCC prototype lower trophic level marine ecosystem model of the North Pacific Ocean. The dark arrow indicates diel vertical migration by large Zooplankton (ZooL).

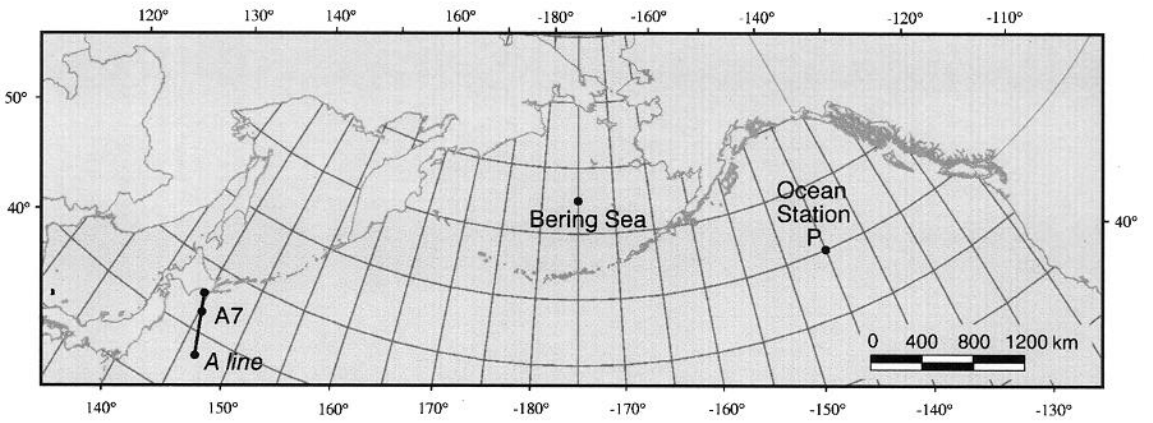

Fig. 3 Map of the North Pacific showing areas where model comparisons were performed.

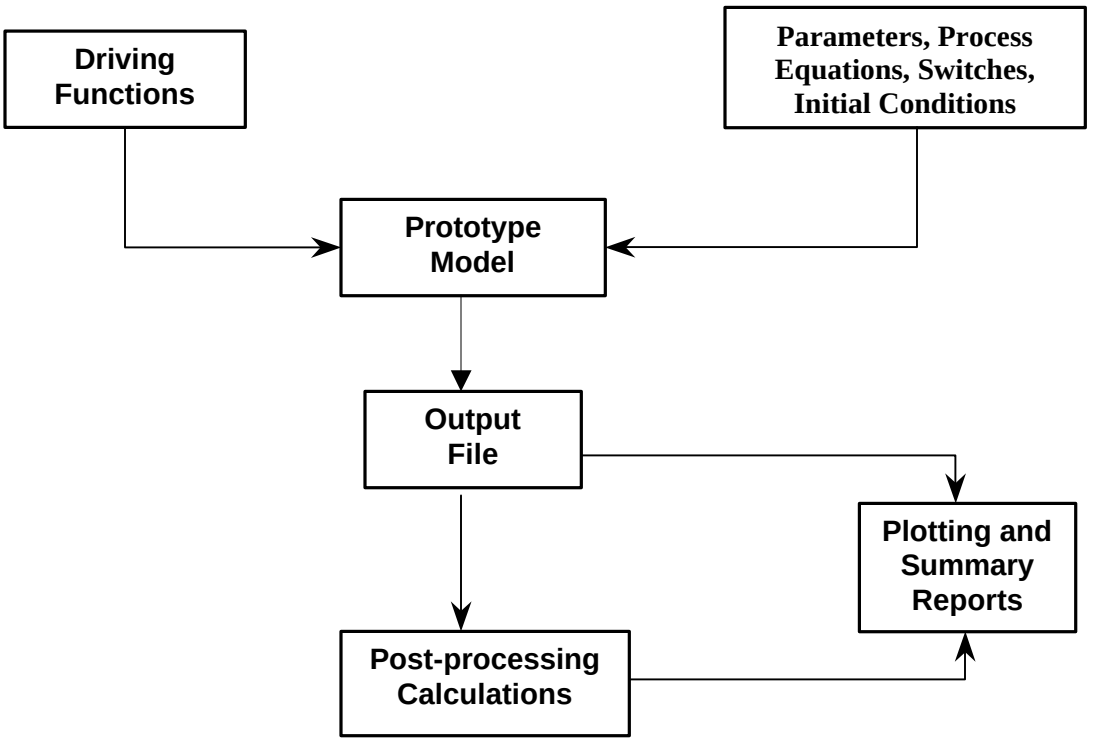

Fig. 4 Flow diagram of data processing steps used at the Modeling Workshop.

6.0 Model Description

Nota bene

We use several forms of nomenclature in this document to reference model parameters, state variables, biomass concentrations, and ecological functional groups. These are summarized below.

NOMENCLATURE

Description	Functional Groups	Biomass Concentration (Nitrogen Units)	Biomass Concentration (Silicon Units)
Small Phytoplankton	PhyS, PS	PhySn	PhySi
Large Phytoplankton	PhyL, PL	PhyLn	PhyLi
Small Zooplankton	ZooS, ZS	ZooSn	ZooSi
Large Zooplankton	ZooL, ZL	ZooLn	ZooLi
Predatory Zooplankton	ZooP, ZP	ZooPn	ZooPi
Nitrate concentration	NO3		
Ammonium concentration	NH4		
Particulate Organic Nitrogen concentration	PON		
Dissolved Organic Nitrogen concentration	DON		
Silicate concentration	Si(OH)4		
Particulate Organic Silica concentration	Opal		

Five different but related models were examined at the workshop.

- The PICES CCCC prototype lower trophic level marine ecosystem model named "*NEMURO*" (see below): a conceptual model representing the minimum trophic structure and biological relationships between and among all the marine ecosystem components thought to be essential in describing ecosystem dynamics in the North Pacific (Fig. 2).
- The "*NEMURO*/FORTRAN Box" Model: a FORTRAN computer program to solve the coupled set of differential equations making up *NEMURO* and the graphing software needed to examine model output.
- The "*NEMURO*/1-D Kishi" Model: The *NEMURO* model coupled with a 1-D ocean physics model. The physical model runs prior to *NEMURO*, and provides the necessary physical forcing required by *NEMURO*.
- The "*NEMURO*/1-D Yamanaka" Model: Similar to the 1-D Kishi model except that the ocean physics model and *NEMURO* are calculated simultaneously in one FORTRAN computer program.
- The "*NEMURO*/MATLAB Box" Model: a MATLAB® version of *NEMURO*.

In a friendly competition among meeting participants, the prototype model was named *NEMURO* (North Pacific Ecosystem Model for Understanding Regional Oceanography). The winning name was a joint effort with contributions coming from Drs. Vadim V. Navrotsky (Russia), Bernard A. Megrey (U.S.A.), and Lan S. Smith (Japan).

6.1 NEMURO Prototype Model

The *NEMURO* NPZ marine ecosystem model consists of the conceptual model, a set of coupled differential equations and process equations, and a table of parameter values and initial starting conditions. *NEMURO,* which is made up of 11 state variables each represented by a box compartment, is shown schematically in Figure 2. The state variables (and state variable names) are Nitrate (NO_3), Ammonium (NH_4), Small Phytoplankton Biomass (PhyS), Large Phytoplankton Biomass (PhyL), Small Zooplankton Biomass (ZooS), Large Zooplankton Biomass (ZooL), Predatory Zooplankton Biomass (ZooP), Particulate Organic Nitrogen (PON),

Dissolved Organic Nitrogen (DON), Particulate Organic Silicate (Opal), and Silicate Concentration ($Si(OH)_4$). Fluxes between and among the state variables (represented in Fig 2 with arrows) represent the fluxes between the model compartments in both nitrogen (black arrows) and silicon (blue arrows) units. The unit of currency for the model is expressed in units of nitrogen.

The formulation of the fluxes between the model compartments is given by a set of 14 coupled ordinary differential equations (Table 2).

Although parameter tuning is an important task for the future work, *NEMURO* is useful for use in regional comparisons of the eastern and western North Pacific by comparing results to changing the values of parameters. It is important to realize that regional comparisons cannot be made if the model is different with respect to:

- the physical model in which the ecological model is embedded,
- the number of ecological compartments,
- the equations representing each physiological process, and
- the parameter values.

During the drafting of this report, the conveners found that there were differences in the definition of important parameters used in traditional stand-alone lower trophic and higher trophic and/or population dynamics models. One is the relation-ship between assimilation coefficient (a), growth efficiency (b), egestion, and excretion. The traditional stand-alone lower trophic level models, including *NEMURO* use the following formulations:

Excretion: $ExcZ = (a - b) * GraPZ$,
Egestion: $EgeZ = (1.0 - a) * GraPZ$

where GraPZ is the grazing rate of zooplankton on phytoplankton. While the usual ecology textbook definitions of the above equations are:

Excretion: $ExcZ = (a\ (1.0 - b)) * GraPZ$,
Egestion: $EgeZ = (1.0 - a) * GraPZ$.

Another is the mortality coefficient (MorZ) which is related to biomass or the square of biomass:

$MorZ = Mor*\exp(K*Temp)*Z^2$
(traditional stand-alone LTL model), or
$MorZ = Mor*\exp(K*Temp)*Z$,

where, Mor is the mortality rate, K is the temperature coefficient, and Z is the biomass of zooplankton.

Without predation by carnivores, the model needs mortality related to biomass squared to avoid burst increases of zooplankton biomass and to stabilize the model dynamics. However, this is a mathematical trick that has nothing to do with biological theory. This may cause the linking of the lower trophic level model to higher trophic level models. This subject should be considered at the next workshop when discussing the linkage between lower trophic level ecosystem models and higher trophic level ecosystem models.

6.2 NEMURO/FORTRAN Box Model

This model is a FORTRAN computer program built to solve the coupled set of differential equations making up *NEMURO* and the graphing software needed to examine model output.

The process equations, which describe individual submodel processes (i.e. photosynthesis, grazing), are be presented in Table 2, parameter values for the three geographic areas are given in Table 1 and further details of the *NEMURO*/FORTRAN Box Model can be found in Appendix 3.3.

In Figure 5 the time-dependent features of each compartment solved by the *NEMURO*/ FORTRAN Box Model are shown. Panel A shows model dynamics for station A7 and Panel B shows dynamics for Station P (see Table 1 for simulation parameters). These results, however, are only preliminary because the parameters used are based on experiments, and are not yet tuned. Tuning of the parameters should be continued.

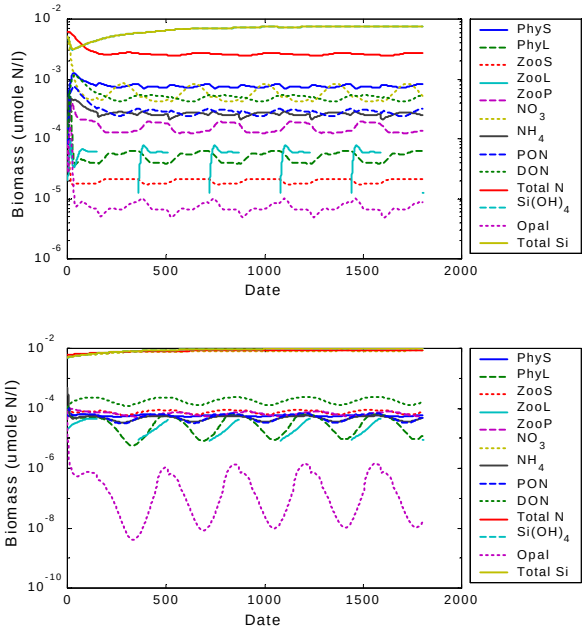

Fig. 5 *NEMURO*/FORTRAN Box model output showing the time-dependent dynamics of the state variables for two locations, station A7 (top panel) and Station P (lower panel). See Table 1 for simulation parameters and Table 2 for model equations.

6.3 NEMURO/1-D Kishi Model

The *NEMURO*/1-D Kishi Model is the *NEMURO* model coupled with a 1-D ocean physics model. The physical model runs prior to *NEMURO*, and provides the necessary physical forcing required by *NEMURO*.

Instructions for downloading the 1-D Kishi Model are given in Appendix 4, and further details about the model can be found in Appendix 3.2.

6.4. NEMURO/1-D Yamanaka Model

The *NEMURO*/1-D Yamanaka Model is similar to the 1-D Kishi model except that the ocean physics model and *NEMURO* are calculated simultaneously in one FORTRAN computer program. Biological process equations used are given in Table 2, parameter values for the three regions are described in Table 1, and further details about the model can be found in Appendix 3.

In the physical model, the water column is split into 50 layers with 20 layers above 100 m. The mixed layer process is the Mellor-Yamada level 2. Outputs from the physical model are temperature, salinity, diffusion coefficient for tracers, diffusion coefficient for momentum and turbulent energy through time and by depth.

Biological and physical results of applying the 1-D Yamanaka model to the three regions, presented as time-depth plots, are given for station A7 (Fig. 6), station P (Fig. 7), and the eastern Bering Sea station (Fig. 8). Note that the vertical axis is described by log scale and 0 of horizontal axis starts on September 1st.

It can be seen that large zooplankton immigrate into the domain of the model (i.e., shallow euphotic zone) from the zone deeper than 300 m. After large zooplankton increases, ZooLn (biomass of large zooplankton described by nitrogen) increases dramatically from large zooplankton grazing on large phytoplankton and small zooplankton. Large phytoplankton and small zooplankton decrease when large zooplankton abundance is high. Predatory zooplankton increases from grazing large zooplankton when large zooplankton densities are adequate for feding. The fluctuation of large phytoplankton follows one month after that of small phytoplankton. As to the biomass of plankton, the largest one is small phytoplankton, followed by predatory zooplankton and small zooplankton. This box model was run under the constant temperature and light without annual oscillation.

6.5. NEMURO/MATLAB

NEMURO/MATLAB is a MATLAB® version of *NEMURO*. The *MATLAB* scripts making up *NEMURO*/MATLAB are a convenient modeling framework in that MATLAB includes numerical integration routines as well as integrated plotting functions. The MATLAB scripts can be found in Appendix 5 and 6, the differential and process

equations are described in Table 3, parameter values for the base run are found in Table 4, and instructions for running the scripts are in Appendix 7.

It is important to note that the parameters and units in the *NEMURO*/MATLAB model are in different units compared to the *NEMURO*/ FORTAN Box model. For example, concentrations are in units of millimoles/m^3, lengths are in meters, time values (i.e. rates) are in units of days. Concentrations in the *NEMURO*/FORTRAN Box model are in moles/m^3. Therefore, close attention must be paid to the decimal place when converting constants, rates or comparing parameter values in Tables 1 and 4.

In preparing *NEMURO*/MATLAB changes were made to *NEMURO*, which required adding an additional 4 state variables. Thus *NEMURO* is an 11 state variable model and *NEMURO*/MATLAB is a 15 state variable model. The change was done primarily to conserve mass in *NEMURO* and does not alter system dynamics. Changes relative to 11 state variable *NEMURO*/ FORTRAN Box model are listed below.

- Large phytoplankton may be grazed by small zooplankton. Therefore terms needed to be added to the *PhyLn* and *ZooSn* equations. See Process Equation 10-2 in Table 3.
- In the *NEMURO*/MATLAB simulations, natural mortality terms are first order, not second order. These change the mortality parameters in equations *PhySn*, *PhyLn*, *ZooSn*, *ZooLn*, *ZooPn* and the related detritus (*PON*) term. Second order terms are retained in the model, but are commented out. See Process Equations 4, 5 in Table 3 for formulations.
- State variables related to silicon dynamics are simplified. Most of the 11-state variable model silicon equations either have rates equal to zero (as they should) or are simply the nitrogen dynamics with all terms multiplied by the Silicon:Nitrogen (Si:N) ratio. These three redundant equations are eliminated to make the model run faster. The silicon uptake equation uses the nitrate growth parameters multiplied by the large phytoplankton Si:N ratio. This is the same as in the *NEMURO*/FORTRAN Box model formulation, but uses fewer parameters, again, to speed things up for running on a PC.
- Four new state variables are added for the calculation of total Nitrogen (i.e., to conserve mass): *DeepNO3, DeepPON, DeepSi*, and *DeepOpal*. These are the nitrogen and silicon pools located below the model domain. They are the source of the upwelled nitrate/silicon and the recipient for the sinking detritus. They don't affect the dynamics, but are needed to conserve mass.
- Light limitation is parameterized differently. Instead of assuming some optimum light intensity and calculating light at the model depth, in the *NEMURO*/MATLAB model, light limitation is incorporated by a simple seasonally varying efficiency. In the model it ranged between 0.2 and 0.8. A diurnal component was also be added. See Process Equation 1 in Table 3.
- The *NEMURO*/MATLAB model was run with and without remineralization of particulate silicon (opal). The runs presented have no surface remineralization, i.e. $DecSi = 0$.

Preliminary results, presented in Figures 9 and 10, are from a "base" model run using the Station P parameters given in Table 4. This parameter set produced a fairly stable model with all populations persisting throughout the twenty-year model run (Fig. 9). Phytoplankton and zooplankton populations exhibited small seasonal variations, but no very large variations. There was a brief spring bloom of large phytoplankton, which was quickly grazed down by large zooplankton. This model is fairly similar to what might be expected at Station P in the North Pacific. However, the large phytoplankton (diatom) bloom, is generally not observed. However, given that this is a box model with no vertical migration of zooplankton and no iron

limitation, it was felt that this "base case" would serve to examine the behavior of the *NEMURO*/MATLAB model. Details of the "base case" run for years 4 through 6 are shown in Figure 10 for the plankton and nitrogen and silicon fields respectively.

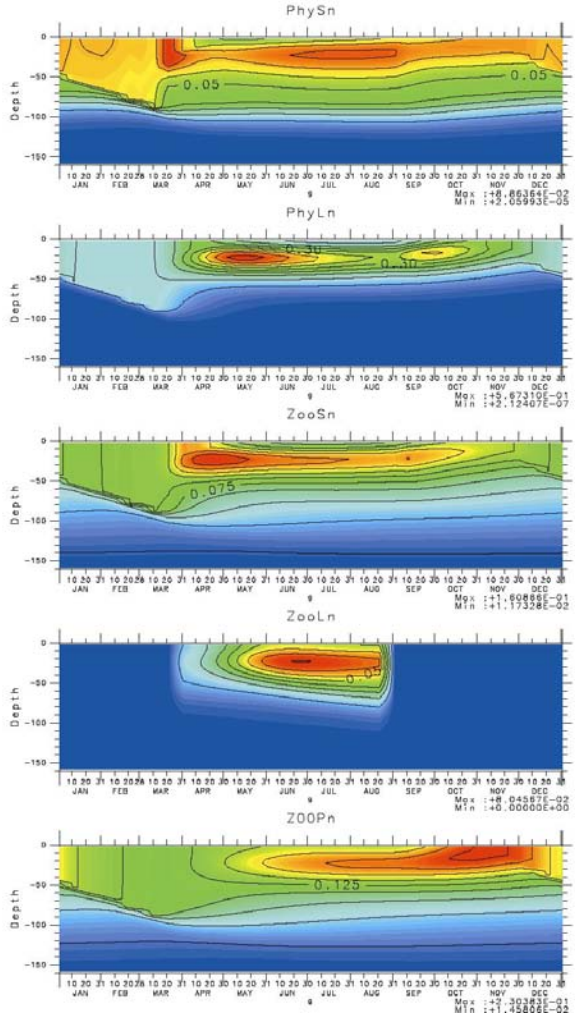

Fig. 6 Biological state variables output from applying the *NEMURO*/1-D Yamanaka model to station A7 using daily physical forcing data files and plotted against time and depth. Shown are small phytoplankton (PhySn), large phyto-plankton (PhyLn), small zooplankton (ZooSn), large zooplankton (ZooLn), and predatory zooplankton (ZooPn) biomass concentrations. All biological state variables are plotted as biomass concentration expressed in nitrogen units (*mmol*N/*l*).

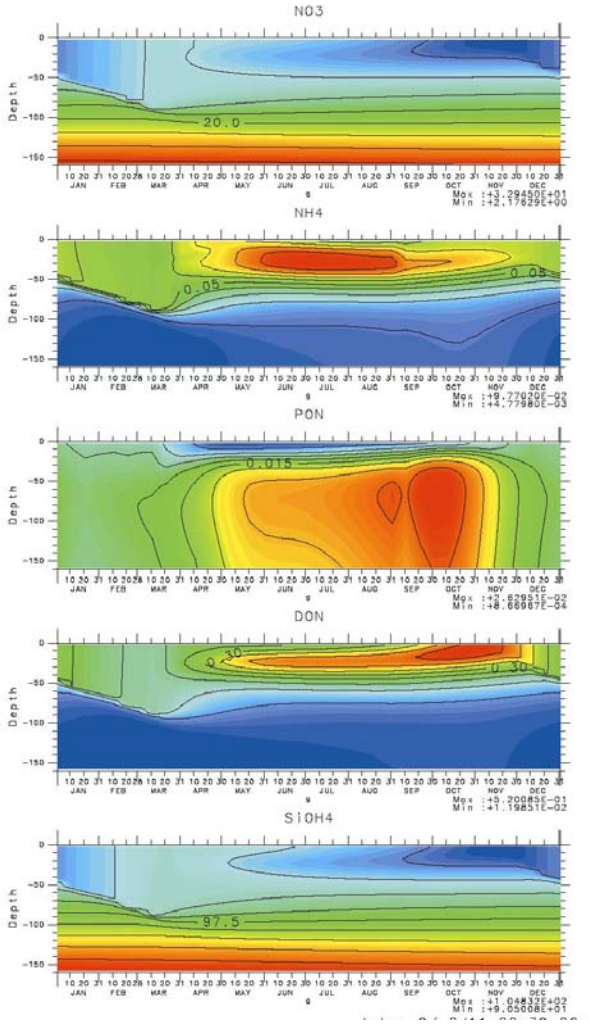

Fig. 6 (continued) Shown are nitrate (NO_3), ammonia (NH_4), particulate organic nitrogen concentration (PON), dissolved organic nitrogen concentration (DON), expressed in nitrogen units (*mmol*N/*l*) Also plotted is silicate concentration (SiOH4) in silicon units (*mmol*Si/*l*)

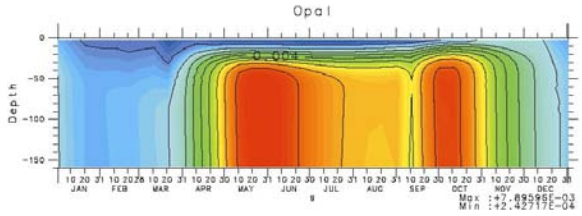

Fig. 6 (continued) Shown is Particulate Organic Silica concentration (Opal) in silicon units (*mmol*Si/*l*).

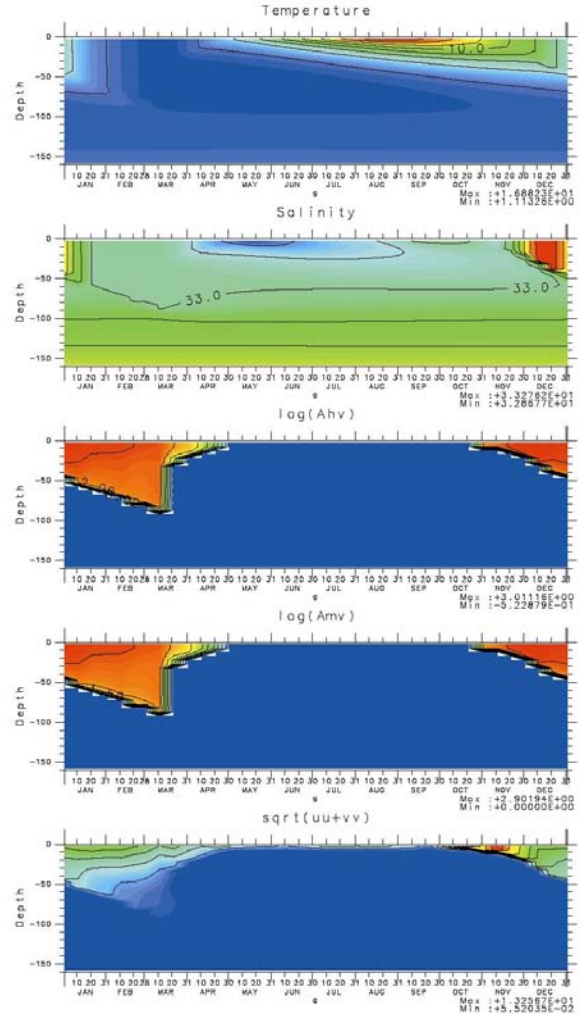

Fig. 6 (continued) Physical state variables output. Shown are temperature (°C), salinity (ppt), diffusion coefficient for tracers (log Ahv), diffusion coefficient for momentum (log Amv), and turbulent energy (sqrt(*uu*+*vv*)) plotted against time and depth.

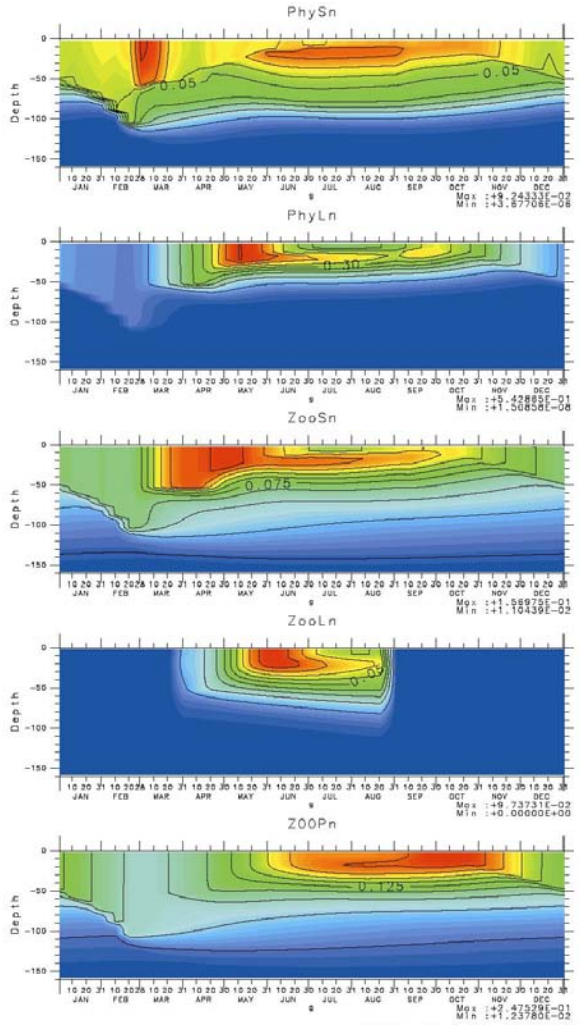

Fig. 7 Biological state variables output from applying the *NEMURO*/1-D Yamanaka model to station P using daily physical forcing data files and plotted against time and depth. Shown are small phytoplankton (PhySn), large phyto-plankton (PhyLn), small zooplankton (ZooSn), large zooplankton (ZooLn), and predatory zooplankton (ZooPn) biomass concentrations. All biological state variables are plotted as biomass concentration expressed in nitrogen units (*mmol*N/*l*).

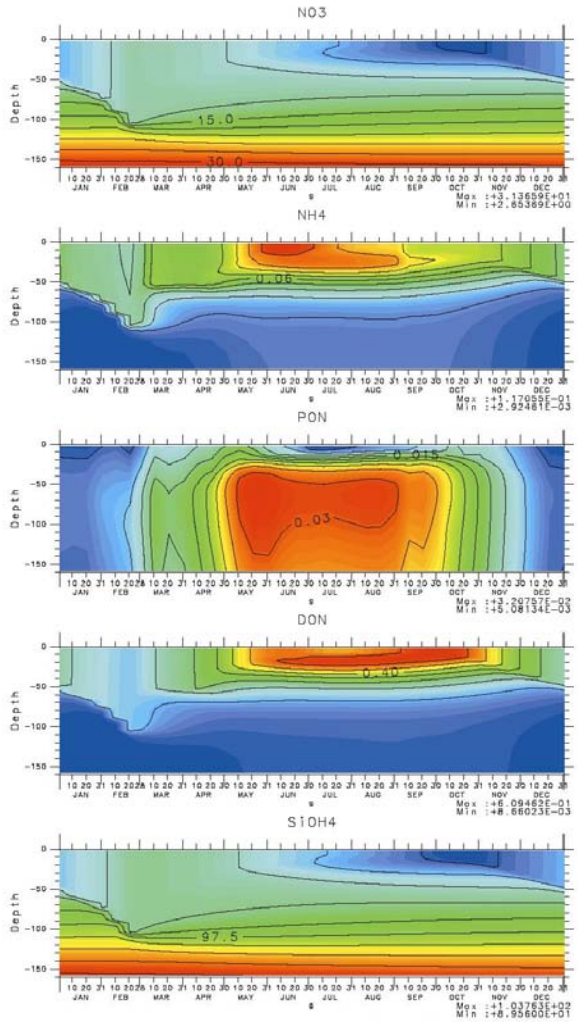

Fig. 7 (continued) Biological state variables output from applying the *NEMURO*/1-D Yamanaka model to station P using daily physical forcing data files and plotted against time and depth. Shown are nitrate (NO_3), ammonia (NH_4), particulate organic nitrogen concentration (PON), dissolved organic nitrogen concentration (DON), expressed in nitrogen units (*mmol*N/*l*). Also plotted is silicate concentration (SiOH4) in silicon units (*mmol*Si/*l*).

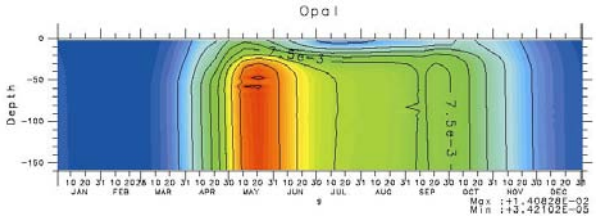

Figure 7 (continued) Shown is Particulate Organic Silica concentration (Opal) in silicon units (*mmol*Si/*l*).

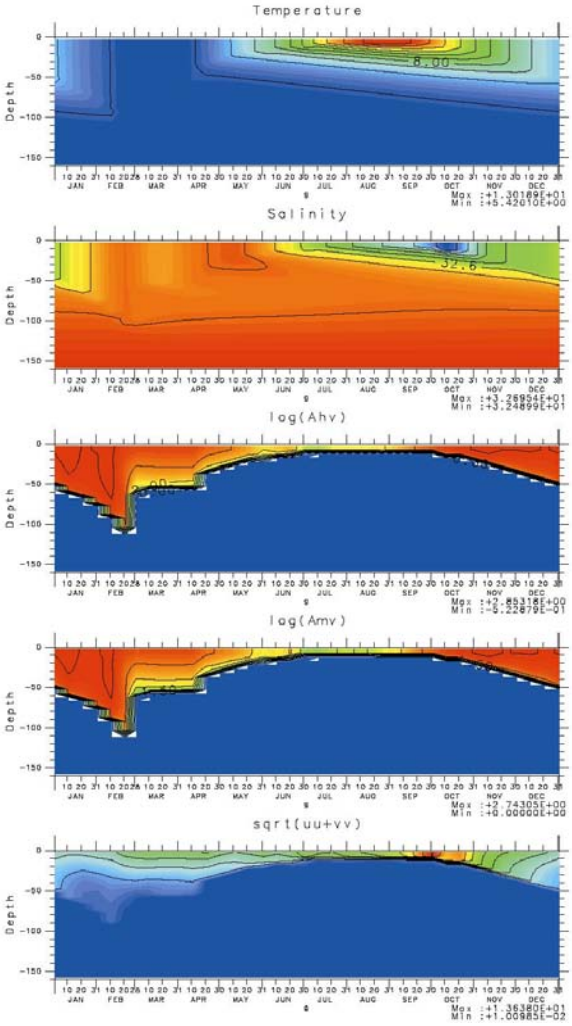

Fig. 7 (**continued**) Physical state variables output. Shown are temperature (°C), salinity (ppt), diffusion coefficient for tracers (log Ahv), diffusion coefficient for momentum (log Amv), and turbulent energy (sqrt(uu+vv)) plotted against time and depth plotted against time and depth.

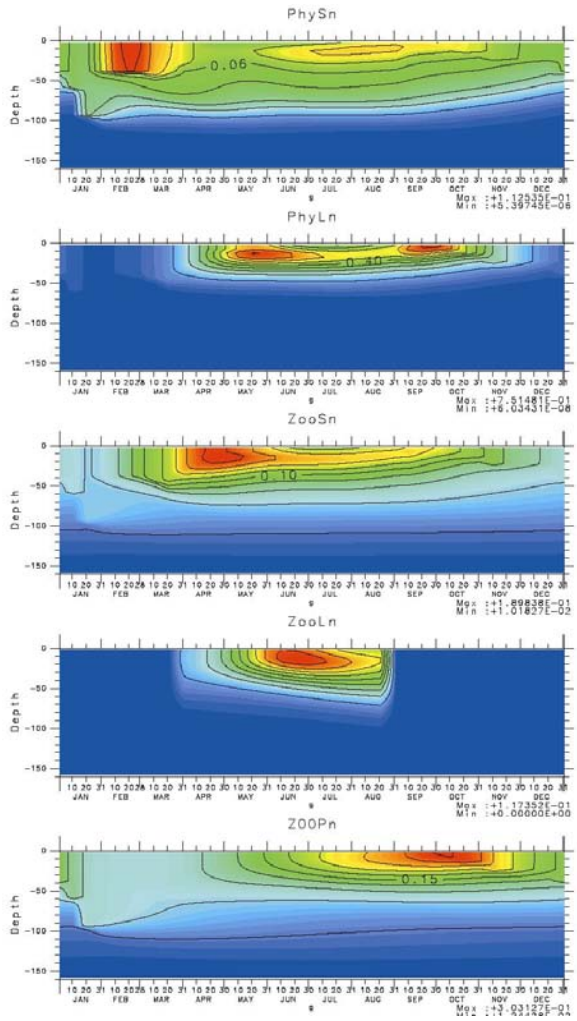

Fig. 8 Biological state variables output from applying the *NEMURO*/1-D Yamanaka model to station Bering Sea using daily physical forcing data files and plotted against time and depth. Shown are small phytoplankton (PhySn), large phytoplankton (PhyLn), small zooplankton (ZooSn), large zooplankton (ZooLn), and predatory zooplankton (ZooPn) biomass concentrations. All biological state variables are plotted as biomass concentration expressed in nitrogen units (*mmol*N/*l*).

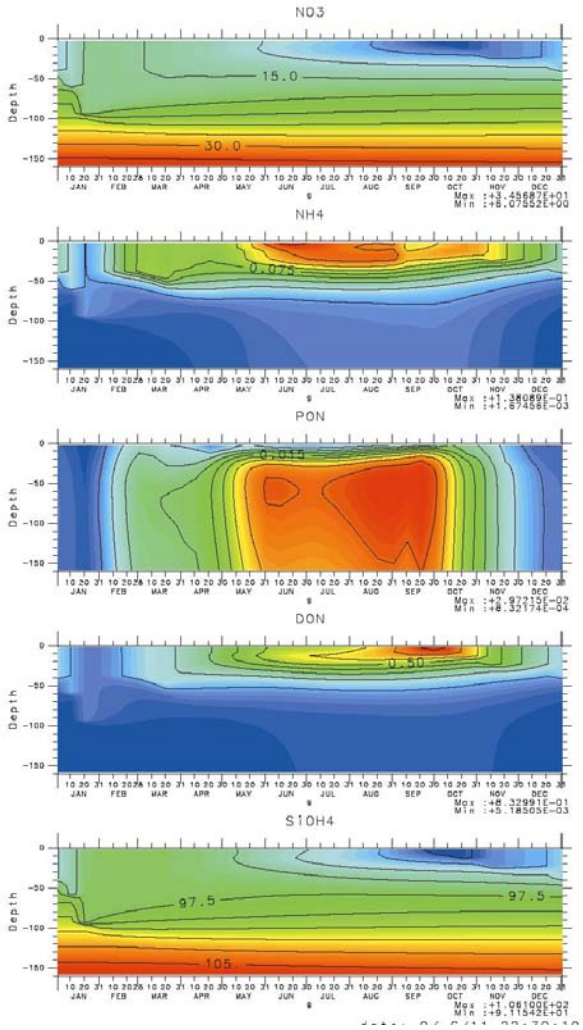

Fig. 8 (**continued**) Shown are nitrate (NO_3), ammonia (NH_4), particulate organic nitrogen concentration (PON), dissolved organic nitrogen concentration (DON), expressed in nitrogen units (*mmol*N/*l*). Also plotted is silicate concentration (SiOH4) in silicon units (*mmol*Si/*l*).

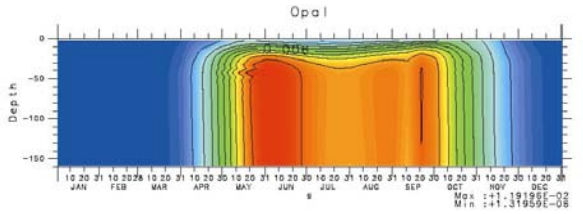

Fig. 8 (**continued**) Shown is Particulate Organic Silica concentration (Opal) in silicon units (*mmol*Si/*l*).

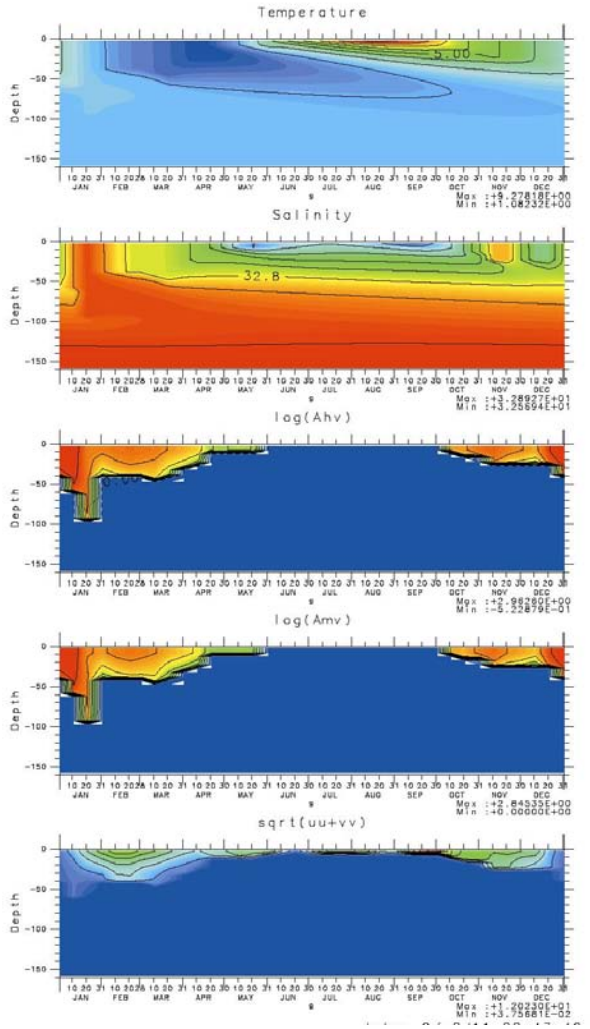

Fig. 8 (**continued**) Physical state variables output. Shown are temperature (°C), salinity (ppt), diffusion coefficient for tracers (log Ahv), diffusion coefficient for momentum (log Amv), and turbulent energy (sqrt($uu+vv$)) plotted against time and depth plotted against time and depth.

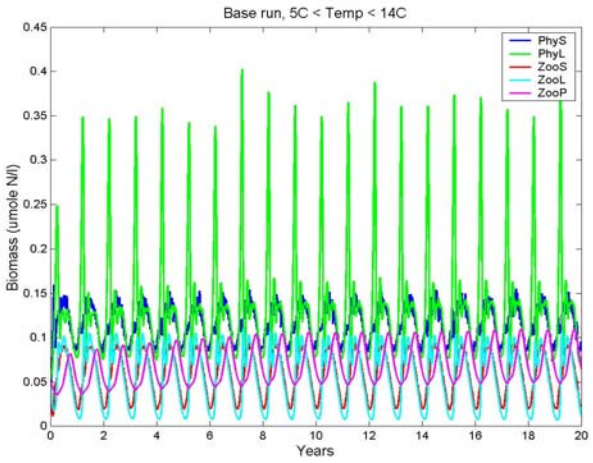

Fig. 9 Base twenty-year run of the *NEMURO*/MATLAB Box model for Station P. Shown are biomass dynamics of Small Phytoplankton (PhyS), Large Phytoplankton (PhyL), Small Zooplankton (ZooS), Large Zooplankton (ZooL), and Predatory Zooplankton (ZooP).

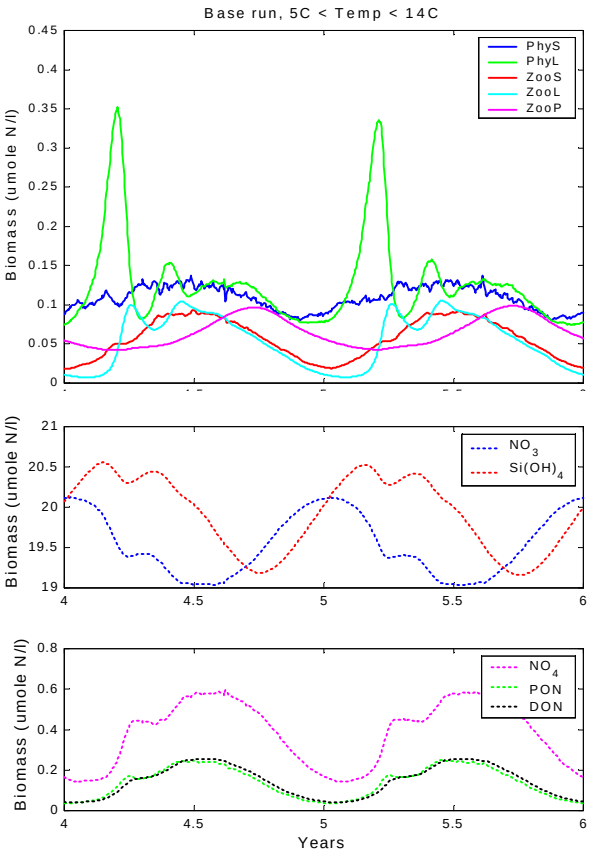

Fig. 10 Details of plankton fields for years 4 through 6 of the *NEMURO*/MATLAB Box model 20-year base run for Station P.

7.0 Model Comparison Measures

The participants discussed the possible outputs from the model. For adequate model comparison, the minimum requirements from the model are as follows:

- Time trace of state variables
- P/B ratio
- Proportion of production by trophic functional groups
- Ecotrophic coefficient (%Primary Production available to ZL & ZP)
- Total biomass (ZS+ZL+ZP) production
- Si/NO3 integrated over the whole water column
- Si production/N production integrated over the whole water column
- Evaluation of conservation of mass

However, during the workshop, there was not enough time to change the model code to add the above variables. Thus only the time-dependent features of each compartment were discussed.

8.0 Team Groups' Reports

8.1 Biological Parameter Team Report

Discussions were held over three days to review the suitability of the biological process equations formulations, determine the appropriate parameter values for three distinct physical locations, provide references and parameter ranges where possible, and to examine different formulations for several of the biological equations. The general form of the equations was endorsed, but there were a few minor changes. The most important was the suggestion to replace the Steele (1962) formulation of the photosynthesis light curve

$$P = P_{\max} \frac{I}{I_{opt}} e^{\left(1-\frac{I}{I_{opt}}\right)} \qquad (1)$$

with the Platt et al. (1980) formulation:

$$P = P_{\max}(1-e^{\left[-\frac{a*I}{P}\right]})e^{\left[-\frac{b*I}{P}\right]} \qquad (2)$$

where

P= Photosynthetic rate
P_{max} = maximum photosynthetic rate
á= light attenuation with depth
â= self shading light inhibition
I= light intensity (W/m^2)
I_{opt}= optimum light intensity (W/m^2)

This change was made because the Steele formulation uses only one parameter to describe both the increase in photosynthesis with light at low light levels and the decrease in photosynthesis with light at high light levels. Using only one parameter produces a photosynthesis light relationship with excessive light inhibition (Fig. 11).

Another major discussion and effort went into the formulation of a grazing selectivity equation for the new predatory zooplankton component. The formulation agreed upon (proposed by Dr. Kishi) used an approach similar to the ammonium inhibition formulation to account for the fact that the diet of predatory zooplankton consists of three prey groups and the grazing equation needed to take into consideration prey preferences (assumed to be proportional to abundance):

$$\begin{aligned} GrZP = \; & GR_{max}(R_{PL}\,(1-\exp^{-ëpl(P*plp-PL)})\exp^{Øplp(ZS+ZL)} \\ & + R_{ZS}\,(1-\exp^{-ëzs(P*pzs-ZS)})e^{Øzsp(ZL)} \\ & + R_{ZL}\,(1-\exp^{-ëzl(P*pzl-ZL)})\,) \end{aligned} \qquad (3)$$

A test suite of parameter values for three locations: Ocean Station P, Station 7 on the A line south of Hokkaido (A7), and a Bering Sea basin location, were compiled. Station P values were used as a base case. References, comments and appropriate ranges were provided whenever possible. Some parameters were estimated and were noted as needing additional research and

sensitivity analyses performed on them. In particular, all the parameters related to processes required to describe the dynamics of the ZP state variable were unknown.

8.2 Microbial Food Web Team Report

The PICES *NEMURO* simulation model partitions the plankton into five state variables: small phytoplankton, large phytoplankton, small zooplankton, large zooplankton, and predatory zooplankton. The task of the working group was to describe what functional groups of organisms were represented by these five components, to develop a simple parameterization of the microbial food web for inclusion in the model, and to suggest possible additions that could be included in future generations of the model.

Why is the Microbial Food-web Important?

The classical food web concept that many of us were taught assumed that the primary production in marine ecosystems was grazed primarily by herbivorous mesozooplankton, which in turn supported a food-web of higher trophic level predators. However, studies over the last decade have revealed the importance of the microbial food-web in aquatic ecosytems, and have shown that it can have a significant impact on the amount of primary production that is actually available to the mesozooplankton, and hence to higher trophic levels (Moloney and Field, 1991). For example, in low nutrient ecosystems, or during periods of low nutrient availability, a relatively high percentage of the gross primary production ends up as dissolved organic matter that is utilized by bacteria. The bacteria in turn are grazed by heterotrophic nanoflagellates, which in turn are eaten by ciliates and other microzooplankton. Since the microzooplankton are an important food source for the mesozooplankton, this group of organisms links the microbial food web to the classical food-web. Cushing (1989) noted that the classical food-web transfers most energy during the spring and autumn blooms in temperate waters (under weakly stratified conditions), but that the microbial food-web dominates the strongly stratified (oligotrophic) waters of the temperate summer. Permanently well-mixed coastal zones in the temperate seas presumably could be dominated by either the classical food web or the microbial food web, depending on the trophic status of the area.

It has been estimated that 10 to 50% of the primary production passes through the bacterioplankton (McManus and Peterson 1988), and that very little of the resulting bacterial production is available to the mesozooplankton. For example, in the NE subactic Pacific Ocean, Rivkin et al. (1999) estimate that only about 3% to 12% of the bacterial carbon production is transferred to copepods. Consequently, in this ecosystem a large proportion of the primary production is respired by the microbial food web in the surface layer, rather than being exported to higher trophic level predators, or the deep-sea.

Structure of the Plankton Community

It is imperative that the model user has a clear understanding of the components of the plankton which are represented by each state variable, and the "hidden" interactions that can occur between the components within some state variables. Figure 12 indicates that the small phytoplankton (PS) group implicitly contains the autotrophic picoplankton (0.2-2 microns equivalent spherical diameter (ESD) in size), and autotrophic nanoflagellates (2-20 microns ESD). The large phytoplankton group (PL) contains the netphytoplankton (20-200 microns ESD), which are primarily diatoms. The small zooplankton (ZS) group contains the heterotrophic flagellates (2-20 microns ESD), and the microzooplankton (20-200 microns ESD). The large zooplankton (ZL) group consists of copepods and euphausiids, which are primarily (but not exclusively) herbivores. The predatory zooplankton, like amphipods and chaetognaths, are represented by the state variable, ZP. The predatory zooplankton and large herbivorous zooplankton form the interface between the lower trophic levels and the higher trophic levels, which will be added to future generations of the model.

Trophic Interactions

Figure 12 indicates that picophytoplankton are primarily eaten by heterotrophic flagellates, while the microzooplankton are assumed to graze primarily on nanophytoplankton. An important "hidden" feeding interaction occurs within the ZS compartment, since microzooplankton will also consume heterotrophic flagellates. Similarly, within the ZL compartment euphausiids will consume copepods, under some circumstances.

Note that the functional importance of bacteria is captured implicitly in *NEMURO* in the decomposition process, which is assumed to occur "instantaneously". Bacteria do not appear explicitly in the model, because very little bacterial production passes through the microbial loop to the large herbivorous and predatory zooplankton, which form the link to the higher trophic levels.

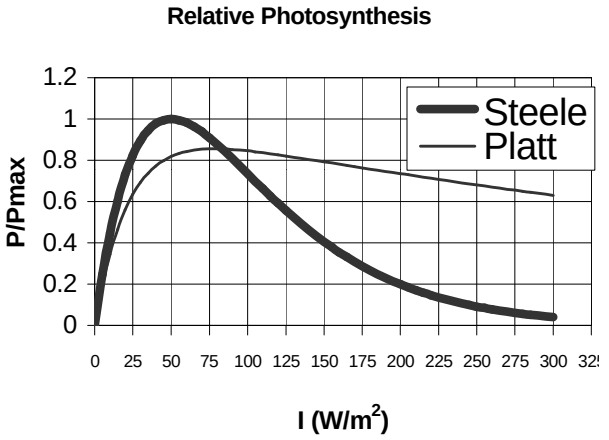

Fig. 11 Comparison of the light-photosynthesis relationship using the Platt (1980) two parameter and the one parameter Steel (1962) formulation.

To anticipate future requirements, the model has a switch, which allows the user to enable microzooplankton to consume netphytoplankton. Normally this switch will not be activated, because it is not a primary pathway of energy flow.

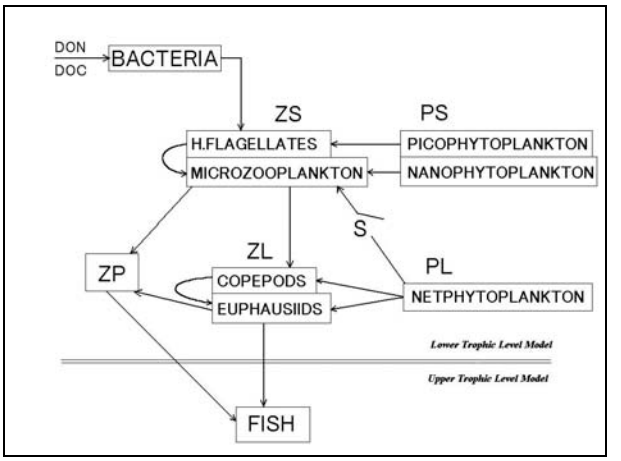

Fig. 12 Proposed microbial food web submodel with a suggestion for linking lower trophic level (LTL) models to higher trophic level (HTL) models. Compartments above the double line belong to the LTL model while the fish compartment, falling below the doubel line, belongs to the HTL model.

Representing the Microbial Food Web

In natural communities, diatoms and dinoflagellates are able to take rapid advantage of nitrate availability, whereas the smaller phytoplankton are more adapted to survive in nutrient poor, oligotrophic environments. Diatoms and dinoflagellates tend to be the main contributors to new production, while cyanobacteria, prochlorophytes and small autotrophic flagellates are believed to be most likely involved in systems dominated by regenerated production. In oligotrophic regions of the oceans and in some coastal upwelling regions, picophytoplankton can contribute up to 80% of the total autotrophic biomass and primary production.

In response to changes in nitrate availability, temperature and grazing pressure, there is an implicit shift in the size structure of the microbes within the small phytoplankton and small zooplankton compartments in the model, which has important energetic implications. For example, when nanoplankton dominate the small phytoplankton (PS) component it requires one

trophic step to convert nanoplankton production into microzooplankton production, with a growth efficiency of 0.3 (Fig. 12). At the other extreme, when picoplankton dominate the PS, then two trophic steps are required to convert picoplankton production into microzooplankton production, with an efficiency of 0.3^2 (or 0.09). The resulting growth efficiency is much lower in this case because picophytoplankton are primarily consumed by heterotrophic flagellates, which in turn, are eaten by microzooplankton. Accordingly, the length of the microbial food chain will vary dynamically between a value of 1 and a maximum of 2, in response to changes in physical forcing, nutrient availability, and grazing mortality. The working group discussed how these "hidden" changes in the length of the microbial food chain and, their impact on the growth efficiency of the ZS could be parameterized with a minimal increase in model complexity.

Field studies have shown that the large phytoplankton are dominant when there is an abundant supply of silicate and nitrate (a high f-ratio). Conversely, the smaller phytoplankton become dominant when the concentrations of nitrite and silicate are depleted, and the ammonium concentration increases. Accordingly, when the proportion of small phytoplankton (i.e. PS/[PS+PL]) changes in the model, we assume that a similar change occurs in the relative proportion of picoplankton in the PS compartment (i.e. pico/[pico + nano]). The resulting change this causes in the length of the microbial food chain (m = fractional number of trophic steps between PS and ZS), and in the PZ growth efficiency ($\hat{a}_{ZS}$) can be represented by:

$$m = \left[1 + a\left(\frac{PS}{PS + PL}\right)\right]$$

$$b_{ZS} = 0.3^{[1+m]} \qquad (4)$$

where, α = maximum ratio of picoplankton/total phytoplankton biomass in the study area. Observed values of α vary between 0.2 to 0.8; lower values are typical in coastal ecosystems and larger values in oceanic systems. The simple formulation summarized in equation 4 causes the growth efficiency to vary between 0.11 when picophytoplankton dominate the PS biomass, and 0.3 when nanophytoplankton dominate. In *NEMURO*, changes in the growth efficiency affect the excretion rate, and hence the productivity of the small zooplankton.

Future Steps

The sensitivity of the model output to "the band-aid solution" proposed in equation 4 needs to be fully tested. If the productivity of the large zooplankton is particularly sensitive to equation 4, then a better formulation of the ZS growth efficiency equation should be developed and tested. Clearly, it is important that the model estimate the production of large zooplankton, as accurately as possible because this functional group of organisms often forms the primary link to higher trophic levels, which will eventually be added to the model. In ecosystems where autotrophic picoplankton are particularly important, the microbial food web could be simulated better by creating separate picoplankton, nanophytoplankton, heterotrophic flagellates and microzooplankton groups. However, this increase in realism comes at an expense, since it would increase the model complexity by two state variables and several process equations.

In the current formulation of the model the team noted that the production of large zooplankton will be somewhat overestimated because euphausiids can also eat copepods (Fig. 12). Hence the ZL growth efficiency will be somewhat less than the fixed value of 0.3 assumed in the model. If this interaction is considered to be important, the ZL growth efficiency should also be transformed into a variable.

8.3 Post Processing & Plotting Software Team

The post-processing team's efforts focused on taking the output of Yamanaka's preliminary 1-D

coupled physics and foodweb model and post-processing it for display by MATLAB. Four cases were processed:

1. Station P Climatological Conditions
2. Bering Sea Climatological Conditions
3. Station A7 Climatological Conditions
4. Station A7 for 1990

and presented at the workshop. *It should be stressed that all these cases are preliminary and should be considered only representative of the type of analyses and inter-comparisons that could be possible once the Yamanaka model is fully tested.*

All files generated by the team are available via the web at ***http://www.OPNML.unc.edu/Personnel/few/Nemuro.html***. Web-postings for each of the 4 cases above have 14 files associated with them. We list below only the names of the files related to the A7 1990 case; the remaining 3 cases have identical formats, with only the file names changing slightly:

1. *YThist.dat*: 1-D Yamanaka Model Foodweb Output (ASCII text format)

2. *ztlabel.f*: Order of output foodweb variables from Yamanaka Model (ASCII text format)

3. *Bio2mat.f*: Fortran code for translation of foodweb model output into MATLAB format (ASCII text format) (Appendix 8)
   Input file: *YThist.dat* (ASCII text format)
   NOTE: The example code in Appendix 8 uses the Bering Sea data set as the input data set.
   Output file:*YThist_mat.dat* (ASCII text format)

4. *YThist_mat.dat*: output from *Bio2mat.f* formatted for input to MATLAB (ASCII text format)

5. *matlab.A7bio*: MATLAB code for generating plots of model foodweb results (ASCII text format) (Appendix 9)
   Input file: YThist_mat.dat

6. *YPhist.dat*: 1-D Yamanaka Model Physics Output (ASCII text format)

7. *zplabel.f*: Order of output physical variables from Yamanaka Model (ASCII text format)

8. *Phys2mat.f*: Fortran code for translation of physics model output into MATLAB format (ASCII text format) (Appendix 10)
   Input file: *YPhist.dat* (ASCII text format)
   NOTE: The example code in Appendix 10 uses the Bering Sea data set as the input data set.
   Output file: *YPhist_mat.dat* (ASCII text format)

9. *YPhist_mat.dat*: output from *Phys2mat.f* formatted for input to MATLAB (ASCII text format)

10. *matlab.A7phys*: MATLAB code for model (physics) plotting (text format) (Appendix 11)
    Input file: *YPhist_mat.dat*

11. *A7phys.jpg*: Plot of physical variables - T, S, Vertical Eddy Viscosity (jpeg format)

12. *A7bio1.jpg*: Plot of foodweb variables - PSn, ZSn, PLn, ZLn (jpeg format)

13. *A7bio2.jpg*: Plot of foodweb variables - ZPn, PLs, ZLs, ZPs (jpeg format)

14. *A7bio3.jpg*: Plot of foodweb variables - NO3, NH4, PON, DON, SiO (jpeg format)

8.4. Model Coding & Forcing File Team Report

The model coding team consisted of four subgroups. The first was lead by Prof. Yamanaka. They worked on coding the *NEMURO*/1-D Yamanaka Model. The second, lead by Dr. Kishi, worked on coding the *NEMURO*/1-D Kishi Model. The third, lead by Dr. Fujii, worked on coding the *NEMURO*/ FORTRAN Box Model. The fourth, lead by Dr. Dave Eslinger, engaged in coding of *NEMURO*/MATLAB Box Model.

The specifications of these models are described in the section on Model Descriptions and in Appendix 3.

The following forcing files were assembled;

1. Climatological forcing file (monthly averages) for Station A7;
2. Climatological forcing file (monthly averages) for Station P;
3. Climatological forcing file (monthly averages) for Eastern Bering Sea; and
4. Daily forcing file (daily averages) for Station A7 for the year 1990.

9.0 Model Experiments and Model Comparisons

Several model comparison experiments were designed during the workshop. For those planned experiments, three factors were varied: which model was used, which geographical location and corresponding set of biological parameters were used, and which physical forcing scenario was used. The details of the experiments and their objectives are described below.

Experiment 1

Objective: To compare the *NEMURO*/FORTRAN Box model with simpler physical forcing (biology but minimal physics) to the fully forced *NEMURO*/1-D Yamanaka NPZ bio-physical model. Both models used the same biological state variables, parameters and process equations.

Configuration: The *NEMURO*/FORTRAN Box Model configured to station A7 was compared to the *NEMURO*/1-D Yamanaka model configured to station A7. The *NEMURO*/FORTRAN Box model was forced with sea surface temperature and solar radiation, while the *NEMURO*/1-D Yamanaka model was forced with daily average values from station A7.

Experiment 2

Objective: To observe differences in model behavior due to differences in temporal resolution of the physical forcing data while holding the biological model information set constant.

Configuration: The *NEMURO*/1-D Yamanaka model with the biological model configured for station A7. This model was run with A7 physical forcing data on two temporal scales, daily averages and monthly averages.

Experiment 3

Objective: To compare the same bio-physical marine ecosystem model to two widely separated locations in the North Pacific using separate biological data and physical forcing data. This run provided an west (A7)-east (Station P) North Pacific comparison in model dynamics.

Configuration: The *NEMURO*/1-D Yamanaka model configured for specific geographic locations. This model was run with biological data and climatological physical forcing data (monthly averages) from station A7 and compared to a *NEMURO*/1-D Yamanaka model run with the Ocean Station P biological and climatological physical forcing data (monthly averages).

Experiment 4

Objective: To compare the same bio-physical marine ecosystem model to two widely separated locations in the North Pacific using separate biological data and physical forcing data. This run provided model dynamics for a western Pacific open ocean station (A7) to an enclosed sea North Pacific station (Bering Sea).

Configuration: The *NEMURO*/1-D Yamanaka model configured for specific geographic

locations. This model was run with biological data and climatological physical forcing data (monthly averages) from station A7 and compared to a *NEMURO*/1-D Yamanaka model run with the Bering Sea biological and climatological physical forcing data (monthly averages).

Experiment 5

Objective: To compare the same bio-physical marine ecosystem model to two widely separated locations in the North Pacific using separate biological data and physical forcing data. This run provided model dynamics for an eastern Pacific open ocean station (Ocean Station P) to an enclosed sea North Pacific station (Bering Sea).

Configuration: The *NEMURO*/1-D Yamanaka model configured for specific geographic locations. This model was run with biological data and climatological physical forcing data (monthly averages) from Ocean Station P and compared to a *NEMURO*/1-D Yamanaka model run with the Bering Sea biological and climatological physical forcing data (monthly averages).

Experiment 6

Objective: To compare the sensitivity of the biological processes equations to different physical forcing scenarios.

Configuration: The *NEMURO*/1-D Yamanaka model configured for station A7. This experiment was run with biological data from station A7 and climatological physical forcing data from station A7 and Ocean Station P.

Experiment 7

Objective: To compare the sensitivity of model's biological parameters to the same physical forcing scenario.

Configuration: The *NEMURO*/1-D Yamanaka model configured for station A7. This experiment was run with biological data from station A7 and Ocean Station P and climatological physical forcing data from station A7.

10.0 Recommendations

Results of the MODEL TASK TEAM work accomplished at the workshop results in several recommendations:

- Perform a sensitivity/stability analysis on *NEMURO*, and proceed to compare the structure and performance, and dynamic characteristics of the model.

- Test the sensitivity of production of small and large zooplankton, P/B ratio, and ecological efficiency to inclusion of the "Band-Aid" microbial food web. If model output is sensitive then implement a more complete description of the microbial food web.

- Develop a way to measure when a change in model output is "significant". The metric should consider time, space, and some absolute values of parameters.

- Future work should be coordinated by the MODEL Task Team Co-Chairmen and encouraged to present results at next annual meeting of PICES. Cooperation and coordination with other CCCC Task Teams is very important.

- Issues related to model management need to be addressed so as to better control the increasing number of different versions of a model, including process equations, parameter files, physical forcing data files, and post-processing programs. We propose to examine the ICES/GLOBEC experience to obtain guidance as to how best to proceed.

- Develop "*NEMURO*/Stella" Box Model using the Stella software package.
- Make progress on making an executable version of the prototype model available on the WWW.
- Develop a means of staying in contact to continue unfinished work.
- Develop a project home page.

11.0 Achievements and Future Steps

The achievements of the Workshop can be listed as follows:

1. Developed the prototype model, *NEMURO*
2. Developed executable models and preliminary outputs for
   2-1. *NEMURO*/FORTRAN Box Model
   2-2. *NEMURO*/1-D Yamanaka Model
   2-3. *NEMURO*/1-D Kishi Model
   2-4. *NEMURO*/MATLAB Model
3. Assembled forcing data files and parameter sets
   3-1. Daily Forcing/Sta. A/Sta. P
   3-2. Climatological Forcing/Sta. A/Sta. P /Bering Sea
   3-3. Parameter Sets/Sta. A/Sta. P/Bering Sea
4. Reviewed biological parameters and process equations
5. Developed tools for post analysis viewing of model output
6. Considered the microbial food web model and developed an implementation plan
7. Identified model experiment teams
   Compared to the goals and objectives of the workshop, the following activities must be undertaken:
   - Link with high trophic level model
     The model needs to include fishes, marine mammal, marine birds, and also micro-nekton.
   - Perform basic model validation studies
     Develop model validation protocols.
     Compare physical factors with direct observations.
     Compare model biomass predictions with direct observations.
   - Identify scientific questions for comparison
     Communication and cooperation with the REX and BASS Task Teams is needed
   - Perform listed experiments.
     It is important to identify a leader for each experiment and to encourage team activities. Dr. Kishi will contact participants of the Nemuro workshop by e-mail and will give a concrete task to each participant. The results of each team should be presented at the MODEL workshop at PICES IX in Hakodate.

12.0 Acknowledgements

This workshop was proposed and convened by PICES, more precisely the PICES/CCCC-IP/MODEL Task Team. On behalf of the workshop participants, the co-conveners would like to express sincere thanks for giving us a timely and valuable opportunity to participate in the development of a lower trophic level marine ecosystem model common among component programs of PICES GLOBEC Program. The Japan International Science and Technology Exchange Center, charged by Japan Science and Technology Agency for execution of the international workshop by Japan Science and Technology Promotion and Coordination Fund,

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Table 1 *NEMURO*/FORTRAN Box Model parameters for three regions of the North Pacific. Columns 1 (Simulation parameter set A7) and 2 (Station P) were used to generate Figure 5.
Small-Phytoplankton: PhyS, Large-Phytoplankton: PhyL, Small-Zooplankton: ZooS, Large-Zooplankton: ZooL, Predatory Zooplankton: ZooP

Parameter	*Description*	Simulation Parameter set A7	Station P	A7	Bering
alpha1	Light extinction coefficient of sea water	3.500E-04	4.000E-04	Same as P	Same as A7
alpha2	Light extinction coefficient of Phytoplankton self shading	2.810E+02	6.000E+02	Same as P	Same as A7
Int0	Light intensity of sea surface	8.000E-02	Same as Sim	Same as P	Same as A7
IoptS	Light intensity of optimum phytosynthesis by PhyS	7.000E-02	Same as Sim	Same as P	?
IoptL	Light intensity of optimum phytosynthesis by PhyL	7.000E-02	Same as Sim	Same as P	?
VmaxS	Maximum rate of photoshynthesis at 0 °C by PhyS	1.000E+00	5.000E-01	6.000E-01	7.200E-01
KNO3S	Half saturation constant for NO3 by PhyS	3.000E-06	Same as Sim	Same as P	6.000E-07
KNH4S	Half saturation constant for NH4 by PhyS	1.000E-06	1.000E-07	Same as P	6.000E-07
PusaiS	Ammonium inhibition coefficient by PhyS	1.500E+06	1.300E+06	Same as P	1.400E+06
KGppS	Temperature coefficient for photosynthesis by PhyS	6.930E-02	Same as Sim	Same as P	Same as A7
VmaxL	Maximum rate of photoshynthesis at 0 °C by PhyL	1.000E+00	2.000E-01	8.500E-01	1.100E+00
KNO3L	Half saturation constant for NO3 by PhyL	3.000E-06	Same as Sim	Same as P	2.500E-06
KNH4L	Half saturation constant for NH4 by PhyL	1.000E-06	1.300E-06	Same as P	2.500E-06
KSiL	Half saturation constant for Si(OH)4 by PhyL	3.000E-06	Same as Sim	Same as P	Same as A7
PusaiL	Ammonium inhibition coefficient by PhyL	1.500E+06	2.700E+06	Same as P	1.400E+06
KGppL	Temperature coefficient for photosynthesis by PhyL	6.930E-02	Same as Sim	Same as P	Same as A7
ResPS0	Respiration rate at 0 °C by PhyS	3.000E-02	Same as Sim	Same as P	Same as A7
KResPS	Temperature coefficient for respiration by PhyS	5.190E-02	6.930E-02	Same as P	Same as A7
ResPL0	Respiration rate at 0 °C by PhyL	3.000E-02	4.250E-02	Same as P	5.000E-02
KResPL	Temperature coefficient for respiration by PhyL	5.190E-02	6.930E-02	Same as P	Same as A7

Table 1 (Continued) *NEMURO*/FORTRAN Box Model parameters for three regions of the North Pacific. Columns 1 (Simulation parameter set A7) and 2 (Station P) were used to generate Figure 5.

Parameter	*Description*	Simulation Parameter set A7	Station P	A7	Bering
MorPS0	Mortality rate of PhyS at 0 °C	5.850E+04	5.000E+04	Same as P	Same as A7
KMorPS	Temperature coefficient for PhyS Mortality	6.930E-02	Same as Sim	Same as P	Same as A7
MorPL0	Mortality rate of PhyL at 0 °C	5.850E+04	5.000E+04	Same as P	Same as A7
KMorPL	Temperature coefficient for PhyL Mortality	6.930E-02	Same as Sim	Same as P	Same as A7
GammaS	Ratio of extracellular excretion to photosynthesis of PhyS	1.350E-01	Same as Sim	Same as P	Same as A7
GammaL	Ratio of extracellular excretion to photosynthesis of PhyL	1.350E-01	Same as Sim	Same as P	Same as A7
GRmaxSps	Maximum rate of grazing at 0 °C by PhyS to ZooS	4.000E-01	4.000E+00	1.000E+00	3.120E-01
GRmaxSpl	Maximum rate of grazing at 0 °C by PhyL to ZooS	0.000E+00	Same as Sim	2.000E-01	1.200E-01
KGraS	Temperature coefficient for grazing by ZooS	6.930E-02	Same as Sim	Same as P	Same as A7
LamS	ZooS Ivlev constant	1.400E+06	1.500E+06	Same as P	Same as A7
PS2ZSstar	Threshold value for grazing by ZooS	4.300E-08	4.000E-08	Same as P	Same as A7
GRmaxLps	Maximum rate of grazing at 0 °C by PhyS to ZooL	4.000E-01	1.000E-01	5.000E-02	2.160E-01
GRmaxLpl	Maximum rate of grazing at 0 °C by PhyL to ZooL	4.000E-01	2.000E-01	4.000E-01	2.160E-01
GRmaxLzs	Maximum rate of predation at 0 °C by ZooS to ZooL	4.000E-01	2.000E-01	1.000E-01	0.000E+00
KGraL	Temperature coefficient for grazing by ZooL	6.930E-02	Same as Sim	Same as P	Same as A7
LamL	ZooL Ivlev constant	1.400E+06	1.500E+06	Same as P	Same as A7
PL2ZLstar	Threshold value for grazing PhyL to ZooL	1.433E-08	4.000E-08	Same as P	Same as A7
PS2ZLstar	Threshold value for grazing PhyS to ZooL	1.433E-08	4.000E-08	Same as P	Same as A7
ZS2ZLstar	Threshold value for predation ZooS to ZooL	1.433E-08	4.000E-08	Same as P	Same as A7

Table 1 (continued) *NEMURO*/FORTRAN Box Model parameters for three regions of the North Pacific. Columns 1 (Simulation parameter set A7) and 2 (Station P) were used to generate Figure 5.

Parameter	*Description*	Simulation Parameter set A7	Station P	A7	Bering
GRmaxPpl	Maximum rate of grazing at 0 °C by PhyL to ZooP	4.000E-01	1.000E-01	Same as P	Same as A7
GRmaxPzs	Maximum rate of predation at 0 °C by ZooS to ZooP	4.000E-01	2.000E-01	Same as P	Same as A7
GRmaxPzl	Maximum rate of predation at 0 °C by ZooL to ZooP	4.000E-01	2.000E-01	Same as P	Same as A7
KGraP	Temperature coefficient for predation by ZooP	6.930E-02	Same as Sim	Same as P	Same as A7
LamP	ZooP Ivlev constant	1.400E+06	1.500E+06	Same as P	Same as A7
PL2ZPstar	Threshold value for grazing PhyL to ZooP	1.433E-08	4.000E-08	Same as P	Same as A7
ZS2ZPstar	Threshold value for predation ZooS to ZooP	1.433E-08	4.000E-08	Same as P	Same as A7
ZL2ZPstar	Threshold value for predation ZooL to ZooP	1.433E-08	4.000E-08	Same as P	Same as A7
PusaiPL	Grazing inhibition coefficient PhyL to ZooP	4.605E+06	Same as Sim	Same as P	Same as A7
PusaiZS	Grazing inhibition coefficient ZooS to ZooP	3.010E+06	Same as Sim	Same as P	Same as A7
AlphaZS	Assimilation efficiency of ZooS	7.000E-01	Same as Sim	Same as P	Same as A7
BetaZS	Growth efficiency of ZooS	3.000E-01	Same as Sim	Same as P	Same as A7
AlphaZL	Assimilation efficiency of ZooL	7.000E-01	Same as Sim	Same as P	Same as A7
BetaZL	Growth efficiency of ZooL	3.000E-01	Same as Sim	Same as P	Same as A7
AlphaZP	Assimilation efficiency of ZooP	7.000E-01	Same as Sim	Same as P	Same as A7
BetaZP	Growth efficiency of ZooP	3.000E-01	Same as Sim	Same as P	Same as A7
MorZS0	Mortality rate of ZooS at 0 °C	5.850E+04	5.000E+04	Same as P	Same as A7
KMorZS	Temperature coefficient for ZooS mortality	6.930E-02	Same as Sim	Same as P	Same as A7
MorZL0	Mortality rate of ZooL at 0 °C	5.850E+04	5.000E+04	Same as P	Same as A7
KMorZL	Temperature coefficient for ZooL mortality	6.930E-02	Same as Sim	Same as P	Same as A7
MorZP0	Mortality rate of ZooP at 0 °C	5.850E+04	5.000E+04	Same as P	Same as A7
KMorZP	Temperature coefficient for ZooP mortality	6.930E-02	Same as Sim	Same as P	Same as A7

Table 1 (continued) *NEMURO*/FORTRAN Box Model parameters for three regions of the North Pacific. Columns 1 (Simulation parameter set A7) and 2 (Station P) were used to generate Figure 5.

Parameter	*Description*	Simulation Parameter set A7	Station P	A7	Bering
VP2N0	Remineralization rate at 0 °C (PON-NH4)	5.000E-02	2.200E-02	Same as P	Same as A7
KP2N	Temp. coefficient for Remineralization (PON-NH4)	6.930E-02	3.000E-02	Same as P	Same as A7
VP2D0	Decomposition rate at 0 °C (PON-DON)	5.000E-02	2.200E-02	Same as P	Same as A7
KP2D	Temp. coefficient for decomposition (PON-DON)	6.930E-02	3.000E-02	Same as P	Same as A7
VD2N0	Remineralization rate at 0 °C (DON-NH4)	5.000E-02	2.200E-02	Same as P	Same as A7
KD2N	Temp. coefficient for Remineralization (DON-NH4)	6.930E-02	3.000E-02	Same as P	Same as A7
VO2S0	Remineralization rate at 0 °C (Opal-Si(OH)4)	5.000E-03	5.000E-03	Same as P	Same as A7
KO2S	Temp. coefficient for Remineralization (Opal-Si(OH)4)	6.930E-02	6.930E-02	Same as P	Same as A7
Nit0	Nitrification rate at 0 °C	3.000E-02	1.000E-01	Same as P	Same as A7
Knit	Temp. coefficient for Nitrification	6.930E-02	Same as Sim	Same as P	Same as A7
RSiNPL	Si/N Ratio of PhyL	1.000E+00	Same as Sim	Same as P	Same as A7
RCN	C/N Ratio	6.625E+00	Same as Sim	Same as P	Same as A7
setVP	Sinking rate of PON	5.000E+01	Same as Sim	Same as P	Same as A7
setVO	Sinking rate of Opal	1.000E+02	Same as Sim	Same as P	Same as A7
setVC	Sinking rate of CaCO3	1.000E+02	Same as Sim	Same as P	Same as A7

Table 1 (continued) *NEMURO*/FORTRAN Box Model parameters for three regions of the North Pacific. Columns 1 (Simulation parameter set A7) and 2 (Station P) were used to generate Figure 5.

Parameter	*Description*	Simulation Parameter set A7	Station P	A7	Bering
Box, model parameters					
Vsedn	Sinking rate of PON	1.000E+03	Same as Sim		
Vsedsi	Sinking rate of Opal	1.000E+04	Same as Sim		
TMP	Water temperature	1.300E+01	Same as Sim		
Lzmax	Depth of euphotic layer	1.000E+04	Same as Sim		
ExUP	Exchange coefficient	3.000E-03	Same as Sim		
NO3D	Conc. of Nitrate at under euphotic layer	1.000E-05	Same as Sim		
SiOH4D	Conc. of Silicate at under euphotic layer	1.000E-05	Same as Sim		

Table 2 *NEMURO*/FORTRAN Box Model Equations for an 11 state variable model differential equations. Process equations are indexed to flux arrows in Figure 2.

Nitrogen

$$\frac{dPhySn}{dt} = GppPSn - ResPSn - MorPSn - ExcPSn - GraPS2ZSn - GraPS2ZLn$$

$$\frac{dPhyLn}{dt} = GppPLn - ResPLn - MorPLn - ExcPLn - GraPL2ZLn - GraPL2ZPn$$

$$\frac{dZooSn}{dt} = GraPS2ZSn - GraZS2ZLn - GraZS2ZPn - MorZSn - ExcZSn - EgeZSn$$

$$\frac{dZooLn}{dt} = GraPS2ZLn + GraPL2ZLn + GraZS2ZLn - GraZL2ZPn - MorZLn - ExcZLn - EgeZLn$$

$$\frac{dZooPn}{dt} = GraPL2ZPn + GraZS2ZPn + GraZL2ZPn - MorZPn - ExcZPn - EgeZPn$$

$$\frac{dNO_3}{dt} = -(GppPSn - ResPSn)RnewS - (GppPLn - ResPLn)RnewL + Nit + UPWn$$

$$\frac{dNH_4}{dt} = -(GppPSn - ResPSn)(1 - RnewS) - (GppPLn - ResPLn)(1 - RnewL) - Nit + DecP2Nn + DecD2Nn + ExcZSn + ExcZLn + ExcZPn$$

$$\frac{dPON}{dt} = MorPSn + MorPLn + MorZSn + MorZLn + MorZPn + EgeZSn + EgeZLn + EgeZPn - DecP2Nn - DecP2Dn - SEDn$$

$$\frac{dDON}{dt} = ExcPSn + ExcPLn + DecP2Dn - DecD2Nn$$

Silicon

$$\frac{dPhyLsi}{dt} = GppPLsi - ResPLsi - MorPLsi - ExcPLi - GraPL2ZLsi - GraPL2ZPsi$$

$$\frac{dZooLsi}{dt} = GraPL2ZLsi - EgeZLsi$$

$$\frac{dZooPsi}{dt} = GraPL2ZPsi - EgeZPsi$$

$$\frac{dSi(OH)_4}{dt} = -GppPLsi + ResPLsi + ExcPLsi + UPWsi + DecP2Si$$

$$\frac{dOpal}{dt} = MorPLsi + EgeZLsi + EgeZPsi - SEDsi - DecP2Si$$

$$\frac{dOpal}{dt} = MorPLsi + EgeZLsi + EgeZPsi - SEDsi - DecP2Si$$

PhySn:	Small-Phytoplankton Biomass	(ìmolN/l)
PhyLn:	Large-Phytoplankton Biomass	(ìmolN/l)
ZooSn:	Small-Zooplankton Biomass	(ìmolN/l)
ZooLn:	Large-Zooplankton Biomass	(ìmolN/l)
ZooPn:	Predator-Zooplankton Biomass	(ìmolN/l)
NO3:	Nitrate concentration	(ìmolN/l)
NH4:	Ammonium concentration	(ìmolN/l)
PON:	Particulate Organic Nitrogen concentration	(ìmolN/l)
DON:	Dissolved Organic Nitrogen concentration	(ìmolN/l)
PhyLsi:	Large-Phytoplankton Biomass	(ìmolSi/l)
ZooLsi:	Large-Zooplankton Biomass	(ìmolSi/l)=0
ZooPsi:	Predator-Zooplankton Biomass	(ìmolSi/l)=0
Si(OH)4:	Silicate concentration	(ìmolSi/l)
Opal:	Particulate Organic Silica concentration	(ìmolSi/l)

Process Equations

Nitrogen

1. ***GppPSn*:** Gross Primary Production rate of Small-Phytoplankton (ìmolN/l/day)

$$GppPSn = V\max S * \left(\frac{NO_3}{NO_3 + K_{NO3S}} \exp(-Ø_S * NH_4) + \frac{NH_4}{NH_4 + K_{NH4S}} \right) * \exp(kGpp_S * TMP) * \int_{-H}^{0} \frac{I}{I_{optS}} \exp\left(1 - \frac{I}{I_{optS}}\right) dz * PhySn$$

$$I = I_0 \exp(-k|Z|)$$

$$k = a_1 + a_2(PhySn + PhyLn)$$

***RnewS*:** f-ratio of Small-Phytoplankton (No dimension)

$$RnewS = \frac{\frac{NO_3}{NO_3 + K_{NO3S}} \exp(-Ø_S * NH_4)}{\frac{NO_3}{NO_3 + K_{NO3S}} \exp(-Ø_S * NH_4) + \frac{NH_4}{NH_4 + K_{NH4S}}}$$

2. ***GppPLn*:** Gross Primary Production rate of Large-Phytoplankton (ìmolN/l/day)

$$GppPLn = V\max L * \min\ \frac{NO_3}{NO_3 + K_{NO3L}}\exp(-\ _L * NH_4) + \frac{NH_4}{NH_4 + K_{NH4L}}, \frac{Si(OH)_4}{Si(OH)_4 + K_{SiL}} / (Si/N)_{pl}$$

$$* \exp(kGpp_L * TMP) * \int_{-H}^{0} \frac{I}{I_{optL}} \exp\left(1 - \frac{I}{I_{optL}}\right) dz * PhyLn$$

$$I = I_0 \exp(-k|Z|)$$

$$k = a_1 + a_2(PhySn + PhyLn)$$

RnewL: f-ratio of Large-Phytoplankton (No dimension)

$$RnewL = \frac{\frac{NO_3}{NO_3 + K_{NO3L}}\exp(-\Psi_L * NH_4)}{\frac{NO_3}{NO_3 + K_{NO3L}}\exp(-\Psi_L * NH_4) + \frac{NH_4}{NH_4 + K_{NH4L}}}$$

3. ***ResPSn*:** Respiration rate of small-phytoplankton (ìmolN/l/day)
   ResPSn = Res_{PS0} * exp(K_{ResPS} * TMP) * PhySn

4. ***ResPLn*:** Respiration rate of large-phytoplankton (ìmolN/l/day)
   $ResPLn = Res_{PL0} * exp(K_{ResPL} * TMP) * PhyLn$

5. ***MorPSn*:** Mortality rate of small-phytoplankton (ìmolN/l/day)
   $MorPSn = Mor_{PS0} * exp(K_{MorPS} * TMP) * PhySn^2$

6. ***MorPLn*:** Mortality rate of large-phytoplankton (ìmolN/l/day)
   $MorPLn = Mor_{PL0} * exp(K_{MorPL} * TMP) * PhyLn^2$

7. ***ExcPSn*:** Extracellular Excretion rate of small-phytoplankton (ìmolN/l/day)
   ExcPSn = GammaS * GppPSn

8. ***ExcPLn*:** Extracellular Excretion rate of large-phytoplankton (ìmolN/l/day)
   ExcPLn = GammaL * GppPLn

9. ***GraPS2ZSn*:** Grazing rate of small-phytoplankton to small-zooplankton (ìmolN/l/day)

$$GraPS2ZSn = \text{Max}\left[0, GR\max S * \exp(k_{GraS} * TMP) * \left\{1 - \exp(\ _S * (PS2ZS^* - PhySn))\right\} * ZooSn\right]$$

$$GraPS2ZLn = \text{Max}\left[0, GR\max L_{ps} * \exp(k_{GraL} * TMP) * \left\{1 - \exp(\ _L * (PS2ZL^* - PhySn))\right\} * ZooLn\right]$$

10. ***GraPS2ZLn*:** Grazing rate of small-phytoplankton to large-zooplankton (ìmolN/l/day)

11. ***GraPL2ZLn*:** Grazing rate of large-phytoplankton to large-zooplankton (ìmolN/l/day)

$$GraPL2ZLn = \text{Max}\left[0, GR\max L_{pl} * \exp(k_{GraL}T) * \left\{1 - \exp(\ _L(PL2ZL^* - PhyLn))\right\} * ZooLn\right]$$

12. ***GraZS2ZLn*:** Grazing rate of small-zooplankton to large-zooplankton (ìmolN/l/day)

$$GraZS2ZLn = \text{Max}\left[0, GR\max L_{zs} * \exp(k_{GraL}T) * \left\{1 - \exp(\ _L(ZS2ZL^* - ZooSn))\right\} * ZooLn\right]$$

13. ***GraPL2ZPn*:** Grazing rate of large-phytoplankton to predator-zooplankton (ìmolN/l/day)

$$GraPL2ZPn = \mathrm{Max}\begin{bmatrix} 0, GR\max P_{pl} * \exp(k_{GraP} * TMP) * \{1 - \exp(\ddot{e}_P * (PL2ZP^* - PhyLn))\} \\ * \exp(-Ø_{PL} * (ZooLn + ZooSn)) * ZooPn \end{bmatrix}$$

14. ***GraZS2ZPn*:** Grazing rate of small-zooplankton to predator-zooplankton (ìmolN/l/day)

$$GraZS2ZPn = \mathrm{Max}\begin{bmatrix} 0, GR\max P_{zs} * \exp(k_{GraP} * TMP) * \{1 - \exp(\ddot{e}_P (ZS2ZP^* - ZooSn))\} \\ * \exp(-Ø_{ZS} * ZooLn) * ZooPn \end{bmatrix}$$

15. ***GraZL2ZPn*:** Grazing rate of large-zooplankton to predator-zooplankton (ìmolN/l/day)

$$GraZL2ZPn = \mathrm{Max}\left[0, GR\max P_{zl} * \exp(k_{GraP} * TMP) * \{1 - \exp(\ _P(ZL2ZP^* - ZooLn))\} * ZooPn\right]$$

***BetaZS* :** Growth efficiency of small-zooplankton (No dimension)

$Beta_{ZS} = 0.3 \wedge (1 + PhySn / (PhySn + PhyLn))$

16. ***ExcZSn*:** Excretion rate of small-zooplankton (ìmolN/l/day)

$ExcZSn = (Alpha_{ZS} - Beta_{ZS}) * GraPS2ZSn$

17. ***ExcZLn*:** Excretion rate of large-zooplankton (ìmolN/l/day)

$ExcZLn = (Alpha_{ZL} - Beta_{ZL}) * (GraPL2ZLn + GraZS2ZLn + GraPS2ZLn)$

18. ***ExcZPn*:** Excretion rate of predator-zooplankton (ìmolN/l/day)

$ExcZPn = (Alpha_{ZP} - Beta_{ZP}) * (GraPL2ZPn + GraZS2ZPn + GraZL2ZPn)$

19. ***EgeZSn*:** Egestion rate of small-zooplankton (ìmolN/l/day)

$EgeZSn = (1.0 - Alpha_{ZS}) * GraPS2ZSn$

20. ***EgeZLn*:** Egestion rate of large-zooplankton (ìmolN/l/day)

$EgeZLn = (1.0 - Alpha_{ZL}) * (GraPL2ZLn + GraZS2ZLn + GraPS2ZLn)$

21. ***EgeZPn*:** Egestion rate of predator-zooplankton (ìmolN/l/day)

$EgeZPn = (1.0 - Alpha_{ZP}) * (GraPL2ZPn + GraZS2ZPn + GraZL2ZPn)$

22. ***MorZSn*:** Mortality rate of small-zooplankton (ìmolN/l/day)

$MorZSn = Mor_{ZS0} * exp(K_{MorZS} * TMP) * ZooSn^2$

23. ***MorZLn*:** Mortality rate of large-zooplankton (ìmolN/l/day)

$MorZLn = Mor_{ZL0} * \exp(K_{MorZL} * TMP) * ZooLn^2$

24. ***MorZPn*:** Mortality rate of predator -zooplankton (ìmolN/l/day)

$MorZPn = Mor_{ZP0} * \exp(K_{MorZP} * TMP) * ZooPn^2$

25. ***DecP2N*:** Decomposition rate from PON to NH_4 (ìmolN/l/day)

$DecP2N = VP2N_0 * exp(K_{P2N} * TMP) * PON$

26. ***DecP2D*:** Decomposition rate from PON to DON (ìmolN/l/day)

$DecP2D = VP2D_0 * exp(K_{P2D} * TMP) * PON$

27. ***DecD2N*:** Decomposition rate from DON to NH_4 (ìmolN/l/day)
    $DecD2N = VD2N_0 * exp(K_{D2N} * TMP) * DON$

28. ***Nit:*** Nitrification rate (ìmolN/l/day)
    $Nit = Nit_0 * exp(K_{Nit} * TMP) * NH4$

29. ***SEDn:*** Sedimentation rate of PON (ìmolN/l/day)
    SEDn = Vsedn / H * PON

30. ***UPWn:*** Upwelling rate of NO_3 (ìmolN/l/day)
    *UPWn = ExUP * (NO3D - NO3)*

Silicon

2. ***GppPLsi:*** Gross Primary Production rate of large-phytoplankton (ìmolSi/l/day)
    *GppPLsi = GppPLn * RSiNPL*

4. ***ResPLsi:*** Respiration rate of large-phytoplankton (ìmolSi/l/day)
    *ResPLsi = ResPLn * RSiNPL*

6. ***MorPLsi:*** Mortality rate of large-phytoplankton (ìmolSi/l/day)
    *MorPLsi = MorPLn * RSiNPL*

8. ***ExcPLsi:*** Extracellular Excretion rate of large-phytoplankton (ìmolSi/l/day)
    *ExcPLsi = ExcPLn * RSiNPL*

11. ***GraPL2Zlsi:*** Grazing rate of large-phytoplankton to large-zooplankton (ìmolSi/l/day)
    *GraPL2ZLsi = GraPL2ZLn * RSiNPL*

13. ***GraPL2ZPsi:*** Grazing rate of large-phytoplankton to predator-zooplankton (ìmolSi/l/day)
    *GraPL2ZLsi = GraPL2ZLn * RSiNPL*

20. ***EgeZLsi:*** Egestion rate of large-zooplankton (ìmolSi/l/day)
    EgeZLsi = GraPL2ZLsi

29. ***SEDsi:*** Sedimentation rate of Opal (ìmolSi/l/day)
    *SEDsi = Vsedsi / H * Opal*

30. ***UPWsi:*** Upwelling rate of Si(OH)4 (ìmolSi/l/day)
    *UPWsi = ExUP * (SiOH4D - SiOH4)*

31. ***EgeZPsi:*** Egestion rate of predator-zooplankton (ìmolSi/l/day)
    EgeZPsi = GraPL2Zpsi

32. ***DecP2Si*:** Decomposition rate from Opal to $Si(OH)_4$ (ìmolSi/l/day)
    $DecP2Si = VP2Si_0 * exp(K_{P2Si} * TMP) * Opal$

Table 3 NEMURO/MATLAB 15 Compartment Box model equations.

Differential Equations

Nitrogen

$$\frac{dPhySn}{dt} = GppPSn - ResPSn - MorPSn - ExcPSn - GraPS2ZSn - GraPS2ZLn$$

$$\frac{dPhyLn}{dt} = GppPLn - ResPLn - MorPLn - ExcPLn - GraPL2ZSn - GraPL2ZLn - GraPL2ZPn$$

$$\frac{dZooSn}{dt} = GraPS2ZSn + GraPL2ZSn - GraZS2ZLn - GraZS2ZPn - MorZSn - ExcZSn - EgeZSn$$

$$\frac{dZooLn}{dt} = GraPS2ZLn + GraPL2ZLn + GraZS2ZLn - GraZL2ZPn - MorZLn - ExcZLn - EgeZLn$$

$$\frac{dZooPn}{dt} = GraPL2ZPn + GraZS2ZPn + GraZL2ZPn - MorZPn - ExcZPn - EgeZPn$$

$$\frac{dNO_3}{dt} = -(GppPSn - ResPSn)RnewS - (GppPLn - ResPLn)RnewL + Nit + UPWn$$

$$\frac{dNH_4}{dt} = -(GppPSn - ResPSn)(1 - RnewS) - (GppPLn - ResPLn)(1 - RnewL) - Nit + DecP2Nn + DecD2Nn + ExcZSn + ExcZLn + ExcZPn$$

$$\frac{dPON}{dt} = MorPSn + MorPLn + MorZSn + MorZLn + EgeZSn + EgeZLn - DecP2Nn - DecP2Dn - SEDn$$

$$\frac{dDON}{dt} = ExcPSn + ExcPLn + DecP2Dn - DecD2Nn$$

$$\frac{dDeepNO_3}{dt} = -UPWn$$

$$\frac{dDeepPON}{dt} = SEDn$$

Silicon

$$\frac{dSiOH_4}{dt} = \left(-GppPLn + ResPLn + ExcPLn\right) \quad RSiNPL + UPWsi + DecP2Si$$

$$\frac{dOpal}{dt} = \left(MorPLn + EgeZLn\right) \quad RSiNPL - SEDsi - DecP2Si$$

$$\frac{dDeepSiOH_4}{dt} = -UPWsi$$

$$\frac{dDeepOpal}{dt} = SEDsi$$

PhySn:	Small-Phytoplankton Biomass	(mmolN/l)
PhyLn:	Large-Phytoplankton Biomass	(mmolN/l)
ZooSn:	Small-Zooplankton Biomass	(mmolN/l)
ZooLn:	Large-Zooplankton Biomass	(mmolN/l)
ZooPn:	Predator-Zooplankton Biomass	(mmolN/l)
NO3:	Nitrate concentration	(mmolN/l)
NH4:	Ammonium concentration	(mmolN/l)
PON:	Particulate Organic Nitrogen concentration	(mmolN/l)
DON:	Dissolved Organic Nitrogen concentration	(mmolN/l)
DeepNO3:	Nitrate concentration	(mmolN/l)
DeepPON:	Particulate Organic Nitrogen concentration	(mmolN/l)
SiOH4:	Silicate concentration	(mmolSi/l)
Opal:	Particulate Organic Silica concentration	(mmolSi/l)
DeepSiOH4:	Silicate concentration	(mmolSi/l)
DeepOpal:	Particulate Organic Silica concentration	(mmolSi/l)

Equations of Each Process

Nitrogen

1. ***GppPSn*** **:** Gross Primary Production rate of Small-Phytoplankton (mmolN/l/day)

$$GppPSn = V\max S * \frac{NO_3}{NO_3 + K_{NO3S}} \exp(-\ _S * NH_4) + \frac{NH_4}{NH_4 + K_{NH4S}} * \exp(kGpp_S * TMP) * PhySn$$

TMP: Water temperature (Celcius)

LIGHT: Relative photosynthetic efficiency (unitless). Ranges seasonally from 0.2 to 0.8, decreases due to light limitation. Use second formulation to include diurnal variability.

$$LIGHT = 0.2 + 0.6\left(0.5(1 - \cos(2pt / 365))\right)$$

For diurnal variability:

$$LIGHT = \left[0.2 + 0.6\left(0.5(1 - \cos(2pt / 365))\right)\right] \quad \max\left(0, \cos(2pt)\right)$$

RnewS**:** f-ratio of Small-Phytoplankton (Non-dimensional)

$$RnewS = \frac{\frac{NO_3}{NO_3 + K_{NO3S}} \exp(-\Psi_S * NH_4)}{\frac{NO_3}{NO_3 + K_{NO3S}} \exp(-\Psi_S * NH_4) + \frac{NH_4}{NH_4 + K_{NH4S}}}$$

2. ***GppPLn* :** Gross Primary Production rate of Large-Phytoplankton (mmolN/l/day)

$$GppPLn = V\max L * \min\left(\frac{NO_3}{NO_3 + K_{NO3L}}\exp(-\Psi_L * NH_4) + \frac{NH_4}{NH_4 + K_{NH4L}}, \frac{Si(OH)_4}{Si(OH)_4 + K_{SiL}}\right) / \left(Si/N\right)_{pl} * \exp(kGpp_L * TMP) * LIGHT$$

RnewL: f-ratio of Large-Phytoplankton (Non-dimensional

$$RnewL = \frac{\frac{NO_3}{NO_3 + K_{NO3L}}\exp(-\Psi_L * NH_4)}{\frac{NO_3}{NO_3 + K_{NO3L}}\exp(-\Psi_L * NH_4) + \frac{NH_4}{NH_4 + K_{NH4L}}}$$

3. ***ResPSn*:** Respiration rate of small-phytoplankton (mmolN/l/day)
   ResPSn = Res_{PS0} * exp(K_{ResPS} * TMP) * PhySn

4. ***ResPLn*:** Respiration rate of large-phytoplankton (mmolN/l/day)
   $ResPLn = Res_{PL0} * exp(K_{ResPL} * TMP) * PhyLn$

5. ***MorPSn*:** Mortality rate of small-phytoplankton (mmolN/l/day)
   $MorPSn = Mor_{PS0} * exp(K_{MorPS} * TMP) * PhySn^2$ First order mortality
   $MorPSn = Mor_{PS0} * exp(K_{MorPS} * TMP) * PhySn^2$ Second order mortality, **not used.**

6. ***MorPLn*:** Mortality rate of large-phytoplankton (mmolN/l/day)
   $MorPLn = Mor_{PL0} * exp(K_{MorPL} * TMP) * PhyLn$ First order mortality
   $MorPLn = Mor_{PL0} * exp(K_{MorPL} * TMP) * PhyLn^2$ Second order mortality, **not used.**

7. ***ExcPSn*:** Extracellular Excretion rate of small-phytoplankton (mmolN/l/day)
   ExcPSn = GammaS * GppPSn

8. ***ExcPLn*:** Extracellular Excretion rate of large-phytoplankton (mmolN/l/day)
   ExcPLn = GammaL * GppPLn

9. ***GraPS2ZSn*:** Grazing rate of small-phytoplankton to small-zooplankton (mmolN/l/day)

$$GraPS2ZSn = \text{Max}\left[0, GR\max S * \exp(k_{GraS} * TMP) * \left\{1 - \exp(\ _S * (PS2ZS^* - PhySn))\right\} * ZooSn\right]$$

9-2. ***GraPS2ZLn*:** Grazing rate of small-phytoplankton to large-zooplankton (mmolN/l/day)

$$GraPS2ZLn = \text{Max}\left[0, GR\max L_{ps} * \exp(k_{GraL} * TMP) * \left\{1 - \exp(\ _L * (PS2ZL^* - PhySn))\right\} * ZooLn\right]$$

$$GraPL2ZLn = \text{Max}\left[0, GR\max L_{pl} * \exp(k_{GraL} T) * \left\{1 - \exp(\ _L (PL2ZL^* - PhyLn))\right\} * ZooLn\right]$$

10. ***GraPL2ZLn*:** Grazing rate of large-phytoplankton to large-zooplankton (mmolN/l/day)

10-2. ***GraPL2ZSn*:** Grazing rate of large-phytoplankton to small-zooplankton (mmolN/l/day)

$$GraPL2ZSn = \text{Max}\left[0, GR\max S_{pl} * \exp(k_{GraS} T) * \left\{1 - \exp(\ _L (PL2ZS^* - PhyLn))\right\} * ZooSn\right]$$

11. ***GraZS2ZLn*:** Grazing rate of small-zooplankton to large-zooplankton (mmolN/l/day)

$$GraZS2ZLn = \mathrm{Max}\left[0, GR\max L_{zs} * \exp(k_{GraL}T) * \left\{1 - \exp(\ {}_{L}(ZS2ZL^{*} - ZooSn))\ \right\} * ZooLn\right]$$

11-2. ***GraPL2ZPn*:** Grazing rate of large-phytoplankton to predator-zooplankton (mmolN/l/day)

$$GraPL2ZPn = \mathrm{Max}\left[\begin{matrix} 0, GR\max P_{pl} * \exp(k_{GraP} * TMP) * \left\{1 - \exp(\ddot{e}_{P} * (PL2ZP^{*} - PhyLn))\right\} \\ * \exp(\ -\emptyset_{PL} * (ZooLn + ZooSn)\ ) * ZooPn \end{matrix}\right]$$

11-3. ***GraZS2ZPn*:** Grazing rate of small-zooplankton to predator-zooplankton (mmolN/l/day)

$$GraZS2ZPn = \mathrm{Max}\left[\begin{matrix} 0, GR\max P_{zs} * \exp(k_{GraP} * TMP) * \left\{1 - \exp(\ddot{e}_{P}(ZS2ZP^{*} - ZooSn))\right\} \\ * \exp(\ -\emptyset_{ZS} * ZooLn\ ) * ZooPn \end{matrix}\right]$$

11-4. ***GraZL2ZPn*:** Grazing rate of large-zooplankton to predator-zooplankton (mmolN/l/day)

$$GraZL2ZPn = \mathrm{Max}\left[0, GR\max P_{zl} * \exp(k_{GraP} * TMP) * \left\{1 - \exp(\ {}_{P}(ZL2ZP^{*} - ZooLn))\right\} * ZooPn\right]$$

***BetaZS* :** Growth efficiency of small-zooplankton (Nodim)
$Beta_{ZS} = 0.3\ \hat{}\ (\ 1 + PhySn\ /\ (\ PhySn + PhyLn\ )\ )$

12. ***ExcZSn*:** Excretion rate of small-zooplankton (mmolN/l/day)
ExcZSn = ($Alpha_{ZS}$ - $Beta_{ZS}$) * GraPS2ZSn

13. ***ExcZLn*:** Excretion rate of large-zooplankton (mmolN/l/day)
$ExcZLn = (\ Alpha_{ZL} - Beta_{ZL})\ *\ (\ GraPL2ZLn + GraZS2ZLn + GraPS2ZLn\ )$

13-2. ***ExcZPn*:** Excretion rate of predator-zooplankton (mmolN/l/day)
$ExcZPn = (\ Alpha_{ZP} - Beta_{ZP}\ )\ *\ (\ GraPL2ZPn + GraZS2ZPn + GraZL2ZPn\ )$

14. ***EgeZSn*:** Egestion rate of small-zooplankton (mmolN/l/day)
EgeZSn = (1.0 - $Alpha_{ZS}$) * GraPS2ZSn

15. ***EgeZLn*:** Egestion rate of large-zooplankton (mmolN/l/day)
$EgeZLn = (\ 1.0 - Alpha_{ZL})\ *\ (\ GraPL2ZLn + GraZS2ZLn + GraPS2ZLn\ )$

15-2. ***EgeZPn*:** Egestion rate of predator-zooplankton (mmolN/l/day)
$EgeZPn = (\ 1.0 - Alpha_{ZP}\ )\ *\ (\ GraPL2ZPn + GraZS2ZPn + GraZL2ZPn\ )$

16. ***MorZSn*:** Mortality rate of small-zooplankton (mmolN/l/day)
$MorZSn = Mor_{ZS0} * exp(\ K_{MorZS} * TMP\ ) * ZooSn^{2}$

17. ***MorZLn*:** Mortality rate of large-zooplankton (mmolN/l/day)
MorZLn = Mor_{ZL0} * exp(K_{MorZL} * TMP) * $ZooLn^{2}$

17-2. ***MorZPn*:** Mortality rate of predator -zooplankton (mmolN/l/day)
MorZPn = Mor_{ZP0} * exp(K_{MorZP} * TMP) *$ZooPn^{2}$

18. ***DecP2N*:** Decomposition rate from PON to NH_4 (mmolN/l/day)
$DecP2N = VP2N_{0} * exp(\ K_{P2N} * TMP\ ) * PON$

19. ***DecP2D*:** Decomposition rate from PON to DON (mmolN/l/day)
    $DecP2D = VP2D_0 * exp(K_{P2D} * TMP) * PON$

20. ***DecD2N*:** Decomposition rate from DON to NH_4 (mmolN/l/day)
    $DecD2N = VD2N_0 * exp(K_{D2N} * TMP) * DON$

21. ***Nit:*** Nitrification rate (mmolN/l/day)
    $Nit = Nit_0 * exp(K_{Nit} * TMP) * NH4$

22. ***SEDn:*** Sedimentation rate of PON (mmolN/l/day)
    SEDn = Vsedn / H * PON

23. ***UPWn:*** Upwelling rate of NO_3 (mmolN/l/day)
    *UPWn = ExUP * (NO3D - NO3)*

Silicon

22. ***SEDSi:*** Sedimentation rate of Opal (mmolSi/l/day)
    *SEDSi = Vsedsi / H * Opal*

23. ***UPWSi:*** Upwelling rate of Si(OH)4 (mmolSi/l/day)
    *UPWSi = ExUP * (SiOH4D - SiOH4)*

25. ***DecP2Si*:** Decomposition rate from Opal to $Si(OH)_4$ (mmolSi/l/day)
    $DecP2Si = VP2Si_0 * exp(K_{P2Si} * TMP) * Opal$

Table 4 *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			A(7)			Bering		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
V_{maxS}	Small Phytoplankton Maximum Photosynthetic Rate at 0 ºC	1/day	1.000		0.3 - 1	0.6	0.6 Vmax*e^(ksT)<2.0 0.85 (Eppely's 1977)	0.3 - 0.85	0.72	Epply, 77	
Ψ_S	Small Phytoplankton Ammonium Inhibition Coefficient	l/ìmol	1.300	1.3 Lomas&Gilbert, 1996; 1.4 Wroblewski, 1977		Same as P			1.4	Wroblewski	
K_{no3S}	Small Phytoplankton Half Saturation Constant for nitrate	ìmol/l	3.000	4.21 Parsons et al., 1984	1-5?	Same as P			0.6	PROBES data	
K_{nh4S}	Small Phytoplankton Half Saturation Constant for ammonium	ìmol/l	0.100	1.3 Parsons et al. 1984 0.05 ref Saito?	0.05 - 1.3	Same as P			0.6	PROBES data	
K_{SiS}	Small Phytoplankton Half Saturation Constant for silicate	ìmol/l	0.000	No Si uptake		Same as P			Same as A(7)		
κ_S	Small Phytoplankton Temperature Coefficient for Photosynthetic Rate	1/deg. C	0.069	Q10 = 2.0	1.5<Q10<2.5 ?	Same as P			Same as A(7)		
I_{optS}	Small Phytoplankton Optimum Light Intensity	ly/min	0.070	20-500 uE/m2/s Ref Saito?		Same as P			?	3.25 with Platt et all formulation	
V_{maxL}	Large Phytoplankton Maximum Photosynthetic Rate at 0 ºC	1/day	1.000		0.3 - 1	0.85	0.6 Vmax*e^(ksT)<2.0 0.85 (Eppely's 1977); 0.5 @ ?T, MF,1989	0.3 - 0.85	1.1	PROBES data	
Ψ_L	Large Phytoplankton Ammonium Inhibition Coefficient	l/ìmol	2.700	2.7 Lomas&Gilbert, 1996; 1.4 Wroblewski, 1977		Same as P			1.4	Wroblewski	

Table 4 (continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			A(7)			Bering		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
K_{no3L}	Large Phytoplankton Half Saturation Constant for nitrate	ìmol/l	3.000	3.8 MF, 1991, 0.4 - 5.1 Parsons et al.	.4 - 5.1	Same as P			2.5	Epply et al., 1969	
K_{nh4L}	Large Phytoplankton Half Saturation Constant for ammonium	ìmol/l	1.300	1.3, .5-9.4, Parsons et al., 2,5 Epply et al., 1969	.5 - 9.4	Same as P			2.5	PROBES data	
K_{SiL}	Large Phytoplankton Half Saturation Constant for silicate	ìmol/l	3.000	0.8-3.7 Paasche, 1973 1.1 - 4.6 Nelson and Treguer, 1992		Same as P			Same as A(7)		
κ_L	Large Phytoplankton Temperature Coefficient for Photosynthetic Rate	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
I_{optL}	Large Phytoplankton Optimum Light Intensity	ly/min	0.070	20-500 uE/m2/s Ref Saito?		Same as P			?	3.25 with Platt et all formulation	
α_1	Light Dissipation Coefficient of Sea Water	1/m	0.040	Gives 1% light at 115m		Same as P			Same as A(7)		
α_2	Self Shading Coefficient	l/ìmolN m	0.060	0.281 ref		Same as P			Same as A(7)		
R_{0S}	Small Phytoplankton Respiration Rate at 0 °C	1/day	0.030	3% of Vmax		Same as P			Same as A(7)		
κ_{RS}	Small Phytoplankton Temperature Coefficient for Respiration	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
R_{0L}	Large Phytoplankton Respiration Rate at 0 °C	1/day	0.090	3% of Vmax		Same as P			0.05	0.07 @ ~8C, PROBES	

Table 4 (continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			A(7)			Bering		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
κ_{RL}	Large Phytoplankton Temperature Coefficient for Respiration	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
$G_{RmaxSps}$	Small Zooplankton Maximum Grazing Rate on PS at 0 ºC	1/day	3.000	Nanoflagellates & Ciliates, Hansen et al., 1997		1	Ciliates & Pseudocalanus, Hansen et al., 1997		0.312	Pseudocalanus	
$G_{RmaxSpl}$	Small Zooplankton Maximum Grazing Rate on PL at 0 ºC	1/day	0.000	not at Station P		0.2			0.12	Pseudocalanus	
κ_{gZS}	Small Zooplankton Temperature Coefficient for Grazing	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
λ_S	Small Zooplankton Ivlev Constant	l/ìmolN	1.500	Magley,1990		Same as P			Same as A(7)		
ZS^*	Small Zooplankton Threshold Value for Grazing	ìmolN/l	0.040	Fasham et al., 1990		Same as P			Same as A(7)		
GR_{maxLps}	Large Zooplankton Maximum Grazing Rate on PS at 0 ºC	1/day	0.200			0.05			0.216	Neocalanus/Calanus spp	
GR_{maxLpl}	Large Zooplankton Maximum Grazing Rate on PL at 0 ºC	1/day	1.000			0.4	GrmaxL*e^kgT < 0.9, @ 20C		0.216		
GR_{maxLzs}	Large Zooplankton Maximum Grazing Rate on ZS at 0 ºC	1/day	0.400			0.1			0		
k_{gZL}	Large Zooplankton Temperature Coefficient for Grazing	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		

Table 4 (continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			**A(7)**			**Bering**		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
λL	Large Zooplankton Ivlev Constant	l/ìmolN	1.500			Same as P			Same as A(7)		
ZL^*	Large Zooplankton Threshold Value for Grazing	ìmolN/l	0.040			Same as P			Same as A(7)		
M_{PS0}	Small Phytoplankton Mortality Rate at 0 ^oC	l/ìmolN day	0.005			Same as P			Same as A(7)		
κ_{MPS}	Temperature Coefficient for Small Phytoplankton Mortality	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
M_{PL0}	Large Phytoplankton Mortality Rate at 0 ^oC	l/ìmolN day	0.005			Same as P			Same as A(7)		
κ_{MPL}	Temperature Coefficient for Large Phytoplankton Mortality	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
M_{ZS0}	Small Zooplankton Mortality Rate at 0 ^oC	l/ìmolN day	0.050			Same as P			Same as A(7)		
κ_{MZS}	Temperature Coefficient for Small Zooplankton Mortality	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
M_{ZL0}	Large Zooplankton Mortality Rate at 0 ^oC	l/µmolN day	0.025			Same as P			Same as A(7)		
κ_{MZL}	Temperature Coefficient for Large Zooplankton Mortality	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
M_{ZP0}	Predatory Zooplankton Mortality Rate at 0 ^oC	l/µmolN day	0.004			Same as P			Same as A(7)		

Table 4 (continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			**A(7)**			**Bering**		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
κ_{MZP}	Temperature Coefficient for Predatory Zooplankton Mortality	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
k_{N0}	Nitrification Rate at 0 ºC	1/day	0.030			Same as P			Same as A(7)		
κ_{NT}	Temperature Coefficient for Nitrification	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
V_{PIN0}	Decomposition Rate at 0 ºC (PON=>NH4)	1/day	0.022	from Harrison, 1980 data		Same as P			Same as A(7)		
V_{PINT}	Temperature Coefficient for Decomposition (PON=>NH4)	1/deg. C	0.030	from Harrison, 1980 data		Same as P			Same as A(7)		
V_{PDN0}	Decomposition Rate at 0 ºC (PON=>DON)	0.05 /day	0.022	from Harrison, 1980 data		Same as P			Same as A(7)		
V_{PDNT}	Temperature Coefficient for Decomposition (PON DON)	1/deg. C	0.030	from Harrison, 1980 data		Same as P			Same as A(7)		
V_{DIN0}	Decomposition Rate at 0 ºC (DON=>PON)	1 /day	0.022	from Harrison, 1980 data		Same as P			Same as A(7)		
V_{DINT}	Temperature Coefficient for Decomposition (DON PON)	1/deg. C	0.030	from Harrison, 1980 data		Same as P			Same as A(7)		
V_{PISi0}	Decomposition Rate at 0 ºC (POSi=>Si(OH)4)	1 /day	0.005	Ref?		Same as P			Same as A(7)		

Table 4 (continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			**A(7)**			**Bering**		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
V_{PISiT}	Temperature Coefficient for Decomposition (POSi Si(OH)4)	1/deg. C	0.069	Q10 = 2.0		Same as P			Same as A(7)		
γ_S	Small Phytoplankton Ratio of Extracellular Excretion to Photosynthesis	fraction/day	0.010	Fasham et al., 1990		Same as P			Same as A(7)		
γ_L	Large Phytoplankton Ratio of Extracellular Excretion to Photosynthesis	fraction/day	0.010	Fasham et al., 1990		Same as P			Same as A(7)		
a_S	Assimilation Efficiency of Small Zooplankton	unitless	0.700			Same as P			Same as A(7)		
b_S	Growth Efficiency of Small Zooplankton	unitless	0.300			Same as P			Same as A(7)		
a_L	Assimilation Efficiency of Large Zooplankton	unitless	0.700			Same as P			Same as A(7)		
b_L	Growth Efficiency of Large Zooplankton	unitless	0.300			Same as P			Same as A(7)		
$(Si/N)_{PS}$	Si : N Ratio of Small Phytoplankton	mole Si/mole N	0.000			Same as P			Same as A(7)		
$(Si/N)_{PL}$	Si : N Ratio of Large Phytoplankton	mole Si/mole N	1.000			Same as P			Same as A(7)		
$(Si/N)_{ZS}$	Si : N Ratio of Small Zooplankton	mole Si/mole N	0.000			Same as P			Same as A(7)		

Table 4 (Continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			**A(7)**			**Bering**		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
$(Si/N)_{ZL}$	Si : N Ratio of Large Zooplankton	mole Si/mole N	0.000			Same as P			Same as A(7)		
λ_{PL}	Large Phytoplankton Ivlev Constant by ZP	l/ìmolN	1.500			Same as P			Same as A(7)		
P_{PL}^{*}	Large Phytoplankton Threshold Value for Grazing by ZP	ìmolN/l	0.040			Same as P			Same as A(7)		
Ψ_{PL}	Constant of ZP grazing inhibition of large phyto by ZS and ZL	l/ìmolN	4.500			Same as P			Same as A(7)		
R_{PL}	Large Phytoplankton relative Grazing by ZP	ìmolN/l	0.200			Same as P			Same as A(7)		
λ_{ZS}	Small zooplankton Ivlev Constant by ZP	l/ìmolN	1.500			Same as P			Same as A(7)		
P_{ZS}^{*}	Small zooplankton Threshold Value for Grazing by ZP	ìmolN/l	0.040			Same as P			Same as A(7)		
Ψ_{ZS}	Constant of ZP Predation inhibition of Small Zooplankton by ZL	l/ìmolN	3.000			Same as P			Same as A(7)		
R_{ZS}	Small Zooplankton relative Grazing by ZP	ìmolN/l	0.400			Same as P			Same as A(7)		
λ_{ZL}	Large zooplankton Ivlev Constant by ZP	l/ìmolN	1.500			Same as P			Same as A(7)		
P_{ZL}^{*}	Large zooplankton Threshold Value for Grazing by ZP	ìmolN/l	0.040			Same as P			Same as A(7)		

Table 4 (continued) *NEMURO*/MATLAB parameter values for 3 geographic regions of the North Pacific.

			Station P			**A(7)**			**Bering**		
		Unit	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**	**Value**	**Remark**	**Range**
R_{ZL}	Large Zooplankton relative Grazing by ZP	ìmolN/l	1.000			Same as P			Same as A(7)		
G_{RmaxZP}	Predatory Zooplankton Maximum Grazing Rate at 0 ºC	1/day	0.250			Same as P			Same as A(7)		
κ_{gZP}	Predatory Zooplankton Temperature Coefficient for Grazing	1/deg. C	0.069			Same as P			Same as A(7)		

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Appendix 2 List of breakout teams.

Team 1. ***PREPARATION OF FORCING FILES AND CODING OF TEST MODEL***

1-D Yamanaka Model
Leader: Yasuhiro Yamanaka
Members: Naoki Yoshie, Lan Smith, Maki Noguchi,

1-D Kishi Model
Leader: Michio J. Kishi
Members: Tomonori Azumaya, Kosei Komatsu

NEMURO/FORTRAN Box Model
Leader: Masahiko Fujii

NEMURO/MATLAB Model
Leader: David L. Eslinger
Members: Francisco E. Werner

Team 2. ***BIOLOGICAL REVIEW OF PARAMETERS AND PROCESS EQUATIONS***

Leader: David L. Eslinger
Members: Yukimasa Ishida, Katsumi Yokouchi, Shinji Hashimoto, Daji Huang, Yury Zuenko, Vladim Navrotsky, Atsushi Tsuda, Hiroaki Saito, Orio Yamamura, Kazuaki Tadokoro, Vladimir Zvalinsky, Masahiko Fujii, Hitoshi Iizumi

Team 3. ***POST- PROCESSING SOFTWARE PREPARATION***

Leader: Francisco E. Werner,
Members: Hyun-chul Kim, Gennady Kantakov

Team 4. ***DEVELOPMENT OF MICROBIAL FOOD WEB FORMATION***

Leader: Daniel M. Ware
Members: Jing Zhang, Sukyung Kang, Vladimir Zvalinsky, Lan Smith, Kosei Komatsu, Tomonori Azumaya, Makoto Kashiwai

Appendix 3 Model descriptions.

3.1 NEMURO/1-D Yamanaka Model

1. **Name (version):**
   NEMURO/1-D Yamanaka Model
2. **Coding Language:**
   FORTRAN
3. **Model Type:**
   1-D model
4. **Hardware/Software Requirements:**

5. **Linkage between Physical Process model and Biological Process model:**
   Simultaneous interaction between the physical model and the biological model
6. **Structure of Physical Model:**
   Water column split into 50 layers with 20 layers above 100 m.
   Mixed layer process is the Mellor-Yamada level 2.
   Upwelling process is not incorporated.
7. **Structure of Biological Model**
   NEMURO Prototype Model
   Photosynthesis light curve: after Platt *et al* (1980)
   Excretion:(á – â)
   Zooplankton Mortality: relate to biomass squared
8. **Input data**
   Climatic forcing: monthly mean wind stress, solar radiation, SST, SSS from Levitus data sets, COADs
   Daily forcing:
9. **Parameter set**
   Calibrated for:
   Validated for:
10. **Output data**
    Physical Model: temperature, salinity, and vertical eddy diffusivity through time and by depth.
    Biological model: NO3, NH4, PON, DON, SiO, PSn, PLn, ZSn, ZLn, ZPn; PLs, ZLs, ZPs
11. **Source Code**
    Available from:
    Contact: Prof. YAMANAKA, Yasuhiro, Graduate School of Environmental Earth Science, Hokkaido University, galapen@ees.hokudai.ac.jp
12. **Remarks:**
    The model links biological processes and physical process at each time step. This will be an advantage when incorporating effects of biological production upon thermal process in the surface layer. On the other hand, it will not be easy to apply the physical model to another areas.

    Instructions for obtaining the physical forcing files can be found at http://pices.ios.bc.ca/model/.

3.2 NEMURO/1-D Kishi Model

1. **Name (version):**
   NEMURO/1-D Kishi Model

2. **Coding Language:**
   FORTRAN

3. **Model Type:**
   1-D

4. **Hardware/Software Requirements:**

5. **Linkage between Physical Process model and Biological Process model:**
   Physical model gives the forcing data set for the biological model

6. **Structure of Physical Model:**
   Water column split into 50 layers with 20 layers above 100 m.
   Mixed layer process is the Mellor Yamada level 2 (reference).
   Upwelling process is not incorporated.

7. **Structure of Biological Model**
   NEMURO Prototype Model
   Photosynthesis light curve: after Platt *et al* (1980)
   Excretion:(alpha – beta)
   Zooplankton Mortality: relate to squared biomass

8. **Input data**
   date / time / SST / SSS / Wind / Solar Radiation

9. **Parameter set**
   Calibrated for:
   Validated for:

10. **Output data**

11. **Source Code**
    Instructions for obtaining the 1-D Kishi model and the physical forcing files can be found at http://pices.ios.bc.ca/model/
    Available from: ftp coast3.fish.hokudai.ac.jp (see Appendix 4)

12. **Remarks:**
    The separated physical process sub-model and biological process sub-model will be advantageous when one wants to use another physical model scheme.

3.3 NEMURO / FORTRAN Box Model

1. **Name (version):**
   NEMURO/FORTRAN Box Model

2. **Coding Language:**
   FORTRAN

3. **Model Type:**
   1-Box model for surface production layer

4. **Hardware/Software Requirements:**

5. **Linkage between Physical Process model and Biological Process model:**
   Biological Model is driven by given forcing data

6. **Structure of Physical Model:**

7. **Structure of Biological Model:**
   NEMURO Prototype Model
   Photosynthesis light curve: after Platt *et al* (1980)
   Excretion: (á – â)
   Zooplankton Mortality: relate to biomass squared

8. **Input data:**

9. **Parameter set:**
   Calibrated for:
   Validated for:

10. **Output data:**
    Physical Model: temperature, salinity, and vertical eddy diffusivity through time and by depth.
    Biological model: NO3, NH4, PON, DON, SiO, PSn, PLn, ZSn, ZLn, ZPn; PLs, ZLs, ZPs

11. **Source Code:**
    Available from:
    Contact: Mr. FUJII, Masahiko, Graduate School of Environmental Earth Science, Hokkaido University, fujii@ees.hokudai.ac.jp

12. **Remarks:**
    This model was originally developed to test biological parameters and process equations prior to incorporating these into the *NEMURO*/1-D Yamanaka Model.

3.4 NEMURO/MATLAB Model

1. **Name (version):**
   NEMURO/MATLAB Model

2. **Coding Language:**
   MATLAB

3. **Model Type:**
   1-Box model for surface production layer

4. **Hardware/Software Requirements:**

5. **Linkage between Physical Process model and Biological Process model:**
   The biological model is driven by the given forcing data

6. **Structure of Physical Model:**

7. **Structure of Biological Model:**
   NEMURO Prototype Model
   Photosynthesis light curve: after Platt *et al* (1980)
   Excretion: alpha (1 – â)
   Zooplankton Mortality: related to biomass

8. **Input data:**

9. **Parameter set:**
   Calibrated for:
   Validated for:

10. **Output data:**
    Biological model: NO3, NH4, PON, DON, SiO, PSn, PLn, ZSn, ZLn, ZPn; PLs, ZLs, ZPs

11. **Source Code:**
    A listing of the MATLAB scripts for implementing *NEMURO* can be found in Appendicies 5 and 6. Copies of the MATLAB script can be obtained via FTP from; http://www.OPNML.unc.edu/ Personnel/few/Nemuro.html

    Contact: Dr. WERNER, Francisco E, Department of Marine Science, University of North Carolina, cisco@marine.unc.edu

12. **Remarks:**
    The MATLAB version of the *NEMURO* was developed during the Nemuro workshop. Following the workshop, work continued to refine the model.

Appendix 4 Instructions for obtaining and the code and data files for the *NEMURO*/1-D Kishi physical biological coupled model.

(1) How to ftp
   0. make a directory under your home directory named “one-dim-phy” and “one-dim-bio”
   1. cd one-dim-phy
   2. ftp > coast0.fish.hokudai.ac.jp
   3. User(coast)> pices
   4. password required for pices
      Password
      ftp> cd /one-dim-phy
   5. ftp> mget *
   6. ftp> lcd ../one-dim-bio
   7. ftp> cd /one-dim-bio
   8. ftp> mget *
   9. ftp> quit

(2) How to compile
   0. run physical model
   0.1 need input file of sst,sss, tau under ~/one-dim-phy/ /kushiro
      surfn41-1+10.csv : sst and sss for A7 with 10 times of 1991 data to get steady annual cycle
      tau418-1+10.csv : wind stress for A7
   0.2 output file from physical part will be created in the same directory (Not /kushiro) named “hout.dat”
      move it to ~/one-dim-bio/kushiro/ and rename to "phyn41-1-b+10.dat"
   1. run biological model
      PS, PL, ZL, ZL, NO3, NH4, PON, DON, SI, POSI .
      with ZL migration
         kno3 = 2.0, knh4 = 0.6, ksi = 3.0, grmax = 0.3, W = 3.6 m/yr
         need input file under ~one-dim-bio/kushiro/
         "phyn41-1-b+10.dat": (this is from physical model)
      "srad420-1+10.csv": solar radiation

(3) How to add your idea
   1. If you want to change input file (i.e., physical forcing), make your file following to “surfn41-1+10”, “tau418-1+10.csv” and "srad420-1+10.csv"
   2. If you want to change ecosystem model, you have to change “bioprc.f” but also all kinds of common, arguments.
   3. If you want to change only values of biological parameters, change in “param2.f”

(4) When you use and publish your papers
   Refer to the following papers
   1. Kawamiya,M., M.J.Kishi, Y.Yamanaka and N.Suginohara (1995). An ecological-physical coupled model applied to Station Papa. Journal of Oceanography, 51.655-664.
   2. Kawamiya,M., M.J.Kishi, Y.Yamanaka and N.Suginohara (1997). Obtaining reasonable results in different oceanic regimes with the same ecological physical coupled model. Journal of Oceanography. 53, 397-402.
   3. Kishi, M.J. and H. Motono (2000). Ecological-physical coupled model with vertical migration of zooplankton in Northwestern Pacific. Submitted to Journal of Oceanography.

(5) When is this ftp available for use?
   March 1st, 2000

Appendix 5 NEMURO Model Commands for MATLAB Implementation.

```
PSn0=0.1*50*17/(12*133);  % converts mg Chl/m^3 --> mmole N/l
PLn0=0.1*50*17/(12*133);  % converts mg Chl/m^3 --> mmole N/l
%ZSn0=0.15; % mmolN/m^3
%ZLn0=0.15; % mmolN/m^3
%ZPn0=0.11; % mmolN/m^3
ZSn0=0.05; % mmolN/m^3
ZLn0=0.05; % mmolN/m^3
ZPn0=0.05; % mmolN/m^3
NO30=20;
%NO30=5;       % Kishi numbers
%NH40=1;       % =0   in initial runs
%PON0=1;       % =0   in initial runs
%DON0=1;       % =0   in initial runs
NH40=0;
PON0=0;
DON0=0;
RSiNPL=1.;
%PLsi0=PLn0*RSiNPL;
%ZLsi0=1;  % =0   in initial runs
%ZPsi0=1;  % =0   in initial runs
%ZLsi0=0;
%ZPsi0=0;
% Initial conditions for new equations
NO3deep0=0;
PONdeep0=0;
Sideep0=0;
SiOH40=20;
%SiOH40=20;
%Op0=1;    % =0   in initial runs
Op0=0;
Opdeep0=0;

Nem0=[PSn0 PLn0 ZSn0 ZLn0 ZPn0 NO30 NH40...
     PON0 DON0 NO3deep0 PONdeep0 Sideep0 SiOH40 Op0 Opdeep0];
%      PON0 DON0 PLsi0 ZLsi0 ZPsi0 SiOH40 Op0];

t0=0;
tf=365*20;  % in days
%tf=365*2;    % in days
nsteps=12;
dt=1/nsteps;      % in days, i.e., nsteps=2 => hour time step
tspan=[t0:dt:tf];

[t,Nemuro]=ode45('Nemuro_base',tspan,Nem0);

%setup for plotting one obs/day
lt=length(t);
```

```
ty=t(1:nsteps:lt)/365;     % Pick a time every nsteps increments to plot.
                           % Since dt = 1/nsteps, this give 1/day plotting

ps=Nemuro(:,1);
pl=Nemuro(:,2);
zs=Nemuro(:,3);
zl=Nemuro(:,4);
zp=Nemuro(:,5);
no3=Nemuro(:,6);
nh4=Nemuro(:,7);
pon=Nemuro(:,8);
don=Nemuro(:,9);
DeepNO3=Nemuro(:,10);
DeepPON=Nemuro(:,11);
Deepsi=Nemuro(:,12);
si=Nemuro(:,13);
opal=Nemuro(:,14);
Deepopal=Nemuro(:,15);

figure(1)
plot(ty,ps(1:nsteps:lt),'b',ty,pl(1:nsteps:lt),'g',...
   ty,zs(1:nsteps:lt),'r',ty,zl(1:nsteps:lt),'c',...
   ty,zp(1:nsteps:lt),'m');
legend('ps','pl','zs','zl','zp');
title('Base run','FontSize',12);
xlabel('Years');
ylabel('Biomass (umole N/l)');
%axis([0 400 0 .8])

figure(2);
subplot(211);
plot(ty,no3(1:nsteps:lt),'b:',ty,si(1:nsteps:lt),'g:');
legend('no3','si');
title('Base run','FontSize',12);
ylabel('Nutrient conc (umole/l)');


subplot(212);
plot(ty,nh4(1:nsteps:lt),'r:',...
    ty,pon(1:nsteps:lt),'c:',ty,don(1:nsteps:lt),'m:');
legend('nh4','pon','don');
xlabel('Years');
ylabel('Nutrient conc (umole/l)');
```

Appendix 6 NEMURO 15 State Variable Model coded in MATLAB.

```
function xdot=Nemuro(t,x);

% Concentration are in units of millimoles/m^3
% Length are in meters
% Time values (i.e. rates)s are in units of days

RSiNPL=1;   % Si/N Ratio of Large Phytoplankton
H=100.00;   % layer depth in meters

% Light limitation parameters.  For this box model, there is a diurnal and an
%    annual light signal, calculated below.

% Small Phytoplankton Growth parameters.
VmaxS=1;
KNO3S=3.;
KNH4S=.1;
PsiS=1.3;
KGppS=0.0693;

% Large Phytoplankton Growth parameters.
VmaxL=1;
KNO3L=3;
KNH4L=1.3;
KSiL=3.;
PsiL=2.7;
KGppL=0.0693;

ResPS0=0.03;
KResPS=0.0519;
ResPL0=0.03;
KResPL=0.0519;

% Mortality parameters.
% Note bene: There are two sets of these, one for using the first-order
%   formulation and one for the sedcond order (quadratic) formulation.
%   Units and values differ.

%MorPS0=.05??;        % Second order, units are fraction biomass lost/day/unit biomass
MorPS0=.005;         % First order, units are fraction biomass lost/day.
KMorPS=0.0693;
%MorPL0=.05??;        % cond order, units are fraction biomass lost/day/unit biomass
MorPL0=.005;         % First order, units are fraction biomass lost/day.
KMorPL=0.0693;

GammaS=0.01;         % Extracellular excretion by small phyto
GammaL=0.01;         % Extracellular excretion by large phyto
```

```
%Small Zooplankton grazing parameters
GRmaxSps=3.0;        % Max grazing rate on small phytoplankton
                     % (as fraction small zoop biomass/day)
KGraSps=0.0693;
LamSps=1.5;
PS2ZSstar=4.0e-2;
GRmaxSpl=0.0;        % NEW!Max grazing rate on large phytoplankton
                     % (as fraction small zoop biomass/day)
KGraSpl=0.0693;      % NEW!
LamSpl=1.5;          % NEW!
PL2ZSstar=4.0e-2;    % NEW!

%Large Zooplankton grazing parameters
GRmaxLps=0.2;        % Max grazing rate on small phytoplankton
                     % (as fraction large zoop biomass/day)
GRmaxLpl=1.0;        % Max grazing rate on large phytoplankton
                     % (as fraction large zoop biomass/day)
GRmaxLzs=0.4;        % Max grazing rate on small zooplankton
                     % (as fraction large zoop biomass/day)
KGraL=0.0693;
LamL=1.5;
PL2ZLstar=4.e-2;
ZS2ZLstar=4.e-2;
PS2ZLstar=4.e-2;

%Predatory Zooplankton grazing parameters
GRmaxPpl=0.05;       % Max grazing rate on large phytoplankton
                     % (as fraction predatory body biomass/day)
GRmaxPzs=0.2;        % Max grazing rate on small zooplankton
                     % (as fraction predatory body biomass/day)
GRmaxPzl=0.25;       % Max grazing rate on large zooplankton
                     % (as fraction predatory body biomass/day)
KGraP=0.0693;
LamP=1.5;
PL2ZPstar=4.e-2;
ZS2ZPstar=4.e-2;
ZL2ZPstar=4.e-2;
PsiPL=4.5;
PsiZS=3.0;

AlphaZS=0.7;
BetaZS=0.3;
AlphaZL=0.7;
BetaZL=0.3;
AlphaZP=0.7;
BetaZP=0.3;

MorZS0=0.05;
KMorZS=0.0693;
MorZL0=0.025;
KMorZL=0.0693;
```

```
MorZP0=0.0035;
KMorZP=0.0693;

VP2N0=0.05;
KP2N=0.0693;
VP2D0=0.05;
KP2D=0.0693;
VD2N0=0.05;
KD2N=0.0693;
VP2Si0=0.05;          % new process
KP2Si=0.0693;         % new process

Nit0=0.03;            % Nitrification rate at 0 C.
Knit=0.0693;

Vsedn=1.0;            % PON sedimentation rate in meters/day
Vsedsi=10.0;          % Particulate Si sedimentation rate in meters/day
ExUP=0.003;           % Fraction of upper layer exchnaged per day
NO3D=20;              % Deep nitrate concentration
SiOH4D=25;            % Deep Silico concentration

xdot=zeros(15,1);

% Annual sinusoidal TEMPREATURE variation
TMP=5+(9*0.5*(1-cos(2*pi*(t-90)/365)));      % varies from 5 to 14

% Day/night and annual sinusoidal variation
annual=0.5*(1-cos(2*pi*t/365));              % varies from 0 to 1
LIGHT=0.2+0.6*annual;
daynight=max(0,cos(2*pi*t));
LIGHT=daynight*LIGHT;

% Small Phytoplankton N = x(1)

GppPSn=VmaxS*((x(6)/(x(6)+KNO3S)*exp(-PsiS*x(7))+x(7)/(x(7)+KNH4S)))
    *exp(KGppS*TMP)*LIGHT*x(1);
ResPSn=ResPS0*exp(KResPS*TMP)*x(1);
% Second order (quadratic) natural mortality
%MorPSn=MorPS0*exp(KMorPS*TMP)*x(1)*x(1);
% First order natural mortality
MorPSn=MorPS0*exp(KMorPS*TMP)*x(1);
ExcPSn=GammaS*GppPSn;
GraPS2ZSn=max(0,GRmaxSps*exp(KGraSps*TMP)*(1-exp(LamSps*(PS2ZSstar-x(1)))))*x(3);
GraPS2ZLn=max(0,GRmaxLps*exp(KGraL*TMP)*(1-exp(LamL*(PS2ZLstar-x(1)))))*x(4);
xdot(1)=GppPSn-ResPSn-MorPSn-ExcPSn-GraPS2ZSn-GraPS2ZLn;

% Large Phytoplankton N = x(2)

GppPLn=VmaxL*min(...
    (x(6)/(x(6)+KNO3L)*exp(-PsiL*x(7))+x(7)/(x(7)+KNH4L)),
    (x(13)/(x(13)+KSiL)*RSiNPL))
```

```
      *exp(KGppL*TMP)*LIGHT*x(2);
ResPLn=ResPL0*exp(KResPL*TMP)*x(2);
% Second order (quadratic) natural mortality
%MorPLn=MorPL0*exp(KMorPL*TMP)*x(2)*x(2);
% First order natural mortality
MorPLn=MorPL0*exp(KMorPL*TMP)*x(2);
ExcPLn=GammaL*GppPLn;
GraPL2ZSn=max(0,GRmaxSpl*exp(KGraSpl*TMP)*(1-exp(LamSpl*(PL2ZSstar-x(2))))*x(3));
GraPL2ZLn=max(0,GRmaxLpl*exp(KGraL*TMP)*(1-exp(LamL*(PL2ZLstar-x(2))))*x(4));
GraPL2ZPn=max(0,GRmaxPpl*exp(KGraP*TMP)*(1-exp(LamP*(PL2ZPstar-x(2))))*...
          exp(-PsiPL*(x(4)+x(3)))*x(5));
xdot(2)=GppPLn-ResPLn-MorPLn-ExcPLn-GraPL2ZSn-GraPL2ZLn-GraPL2ZPn;


% Small Zooplankton N = x(3)

GraZS2ZLn=max(0,GRmaxLzs*exp(KGraL*TMP)*(1-exp(LamL*(ZS2ZLstar-x(3))))*x(4));
GraZS2ZPn=max(0,GRmaxPzs*exp(KGraP*TMP)*(1-exp(LamP*(ZS2ZPstar-x(3))))*
          exp(-PsiZS*x(4))*x(5));
% Second order (quadratic) natural mortality
%MorZSn=MorZS0*exp(KMorZS*TMP)*x(3)*x(3);
% First order natural mortality
MorZSn=MorZS0*exp(KMorZS*TMP)*x(3);
ExcZSn=(AlphaZS*(1-BetaZS))*(GraPS2ZSn+GraPL2ZSn);
EgeZSn=(1-AlphaZP)*(GraPS2ZSn+GraPL2ZSn);
xdot(3)=GraPS2ZSn+GraPL2ZSn-GraZS2ZLn-GraZS2ZPn-MorZSn-ExcZSn-EgeZSn;

% Large Zooplankton N = x(4)

GraZL2ZPn=max(0,GRmaxPzl*exp(KGraP*TMP)*(1-exp(LamP*(ZL2ZPstar-x(4))))*x(5));
% Second order (quadratic) natural mortality
%MorZLn=MorZL0*exp(KMorZL*TMP)*x(4)*x(4);
% First order natural mortality
MorZLn=MorZL0*exp(KMorZL*TMP)*x(4);
ExcZLn=(AlphaZL*(1-BetaZL))*(GraPL2ZLn+GraZS2ZLn+GraPS2ZLn);
EgeZLn=(1-AlphaZL)*(GraPL2ZLn+GraZS2ZLn+GraPS2ZLn);
xdot(4)=GraPS2ZLn+GraPL2ZLn+GraZS2ZLn-GraZL2ZPn-MorZLn-ExcZLn-EgeZLn;

% Predatory Zooplankton N = x(5)

% Second order (quadratic) natural mortality
%MorZPn=MorZP0*exp(KMorZP*TMP)*x(5)*x(5);
% First order natural mortality
MorZPn=MorZP0*exp(KMorZP*TMP)*x(5);
ExcZPn=(AlphaZP*(1-BetaZP))*(GraPL2ZPn+GraZS2ZPn+GraZL2ZPn);
EgeZPn=(1-AlphaZP)*(GraPL2ZPn+GraZS2ZPn+GraZL2ZPn);
xdot(5)=GraPL2ZPn+GraZS2ZPn+GraZL2ZPn-MorZPn-ExcZPn-EgeZPn;

% NO3 = x(6)

RnewS=(x(6)/(x(6)+KNO3S)*exp(-PsiS*x(7)))/
```

```
    ((x(6)/(x(6)+KNO3S)*exp(-PsiS*x(7)))+x(7)/(x(7)+KNH4S));
RnewL=(x(6)/(x(6)+KNO3L)*exp(-PsiL*x(7)))/...
    ((x(6)/(x(6)+KNO3L)*exp(-PsiL*x(7)))+x(7)/(x(7)+KNH4L));
Nit=Nit0*exp(Knit*TMP)*x(7);
UPWn=ExUP*(NO3D-x(6));     % Upwelling effect
xdot(6)=-(GppPSn-ResPSn)*RnewS-(GppPLn-ResPLn)*RnewL+Nit+UPWn;

% NH4 = x(7)

DecP2Nn=VP2N0*exp(KP2N*TMP)*x(8);
DecD2Nn=VD2N0*exp(KD2N*TMP)*x(9);
xdot(7)=-(GppPSn-ResPSn)*(1-RnewS)-(GppPLn-ResPLn)*(1-RnewL)-Nit+
      DecP2Nn+DecD2Nn+ExcZSn+ExcZLn+ExcZPn;

% PON = x(8)

DecP2Dn=VP2D0*exp(KP2D*TMP)*x(8);
SEDn=Vsedn/H*x(8);
xdot(8)=MorPSn+MorPLn+MorZSn+MorZLn+MorZPn+...
      EgeZSn+EgeZLn+EgeZPn-DecP2Nn-DecP2Dn-SEDn;

% DON = x(9)

xdot(9)=ExcPSn+ExcPLn+DecP2Dn-DecD2Nn;

% Deep NO3 = x(10)

xdot(10)= -UPWn;

% Deep PON = x(11)

xdot(11)= +SEDn;

% Deep dissolved Si pool =x(12)

UPWsi=ExUP*(SiOH4D-x(13));  % Difference between deep pool and surface layer
xdot(12)= -UPWsi;  % Net loss from deep pool

% Si(OH)4 = x(13)

% with surface remineralization
%DecP2si=VP2Si0*exp(KP2Si*TMP)*x(14);
%xdot(13)=(-GppPLn+ResPLn+ExcPLn)*RSiNPL+UPWsi+DecP2si;

% WITHOUT surface remineralization
xdot(13)=(-GppPLn+ResPLn+ExcPLn)*RSiNPL+UPWsi;

% Opal  = =x(14)

SEDsi=Vsedsi/H*x(14);
%Si reimineralization
```

```
%xdot(14)=(MorPLn+GraPL2ZSn+GraPL2ZLn+GraPL2ZPn)*RSiNPL-SEDsi-DecP2si;

%No Si reimineralization
xdot(14)=(MorPLn+GraPL2ZSn+GraPL2ZLn+GraPL2ZPn)*RSiNPL-SEDsi; % No Si remin

%Deep Opal pool = x(15)
xdot(15) = +SEDsi;
```

Appendix 7 Implementation and User's Guide for the *NEMURO*/MATLAB Model.

A description of the implementation of the *NEMURO*/MATLAB model is provided below. The governing equations are described in Table 3 and model parameters are those corresponding to the "Station P base case" run as in Table 4. Two MATLAB programs are needed to run this case:

Nemuro_base.m: this is the MATLAB code containing the model equations detailed in Table 3. The full listing of the MATLAB code is provided in Appendix 6. The model parameters for the base case are included (hardwired) into the code.

Nemuro_base_commands.m: these are the commands to be issued to run the model and to generate the plots. The full listing of the MATLAB is provided in Appendix 5.

These files can also be downloaded from the PICES website http://www.pices.ios.ca/model/.

To run the model, the files should reside in a common directory. Within a MATLAB window, the simplest way to reproduce figures 5 and 6 of the report is to type "**Nemuro_base_commands**" after the MATLAB prompt. The execution of all the commands (initaliaztion, equation set-up, equation solution and plotting) will likely take several minutes on a PC with a Pentium III processor. The base case model is set up for a 20 year run with 2-hour time steps. The standard Runge-Kutta solver "ode45" is used in solving the system of equations. To get more information on the properties of the solver, type "help ode45" from within a MATLAB window.

As written, changes in initial conditions should be made in *Nemuro_base_commands.m* while changes in the form of the governing equations, or in the internal parameters should be made in the *Nemuro_base.m* file.

Appendix 8 FORTRAN code to reformat the *NEMURO*/1-D Yamanaka model biological output file into a format compatible for MATLAB plotting.

```
      parameter(nlayers=50)
      character*80 dateinfo
      real zd(nlayers+1),zl(nlayers)
      open(1,file='Ythist_Bering.dat',status='old')
      open(2,file='YThist_mat.dat',status='unknown')
c
      do il=1,nlayers
        read(1,*)jj,zd(il),zl(il)
      end do
      read(1,*)jj,zd(nlayers+1)
c
      write(*,*)' enter starting year'
      read(*,*)iy
      write(*,*)' enter starting Julian day'
      read(*,*)iday
      write(*,*)' enter interval between data in days'
      read(*,*)incd
c
      do it=1,1000000
        read(1,100,end=10)dateinfo
          do iz=1,nlayers
            read(1,*)i,p1,p2,p3,p4,p5,p6,p7,p8,p9,p10,p11
     &                          ,p12,p13,p14
            write(2,101)iy,iday,zd(iz),p1,p2,p3,p4,p5,p6,p7,p8,p9,p10,p11
     &                          ,p12,p13,p14
          end do
          iday=iday+incd
      end do
   10 continue
  100 format(a)
  101 format(2i6,15(1x,e12.5))
      stop
      end
```

Appendix 9 MATLAB script to plot the *NEMURO*/1-D Yamanaka model biological output.

```
load YThist_mat.dat;
bio=YThist_mat;

nz=50;
z=bio(1:nz,3);

nt=length(bio);

t=bio(1:nz:nt,1)+bio(1:nz:nt,2)/365.;
lt=length(t);
[t,z]=meshgrid(t,z);

%
% first page
%

%fullpage
subplot(411)
psn=reshape(bio(:,4),nz,lt);  % plots all days
colormap(jet)
axis([0 1 -300 0])
h=surface(t,z,psn);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('Climatology Bering PS_n')
set(tl,'FontSize',18)
hold on

subplot(412)
zsn=reshape(bio(:,6),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,zsn);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%set(gca,'clim',[33.2 33.7])
%colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
```

```
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('ZS_n')
set(tl,'FontSize',18)
hold on

subplot(413)
pln=reshape(bio(:,5),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,pln);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('PL_n')
set(tl,'FontSize',18)
hold on

subplot(414)
zln=reshape(bio(:,7),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,zln);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
xl=xlabel('Year')
set(xl,'FontSize',16)
%set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('ZL_n')
set(tl,'FontSize',18)
hold on

%
% second page
%

fullpage
subplot(411)
zpn=reshape(bio(:,8),nz,lt);  % plots all days
colormap(jet)
```

```
axis([0 1 -300 0])
h=surface(t,z,zpn);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('Climatology Bering ZP_n')
set(tl,'FontSize',18)
hold on

subplot(412)
pls=reshape(bio(:,13),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,pls);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%set(gca,'clim',[33.2 33.7])
%colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('PL_s')
set(tl,'FontSize',18)
hold on

subplot(413)
zls=reshape(bio(:,14),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,zls);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('ZL_s')
set(tl,'FontSize',18)
```

```
hold on

subplot(414)
zps=reshape(bio(:,15),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,zps);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
xl=xlabel('Year')
set(xl,'FontSize',16)
%set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('ZP_s')
set(tl,'FontSize',18)
hold on

%
% third page
%

fullpage
subplot(511)
no3=reshape(bio(:,9),nz,lt);  % plots all days
colormap(jet)
axis([0 1 -300 0])
h=surface(t,z,no3);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('Climatology Bering NO_3')
set(tl,'FontSize',18)
hold on

subplot(512)
nh4=reshape(bio(:,10),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,nh4);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
```

```
colorbar
%set(gca,'clim',[33.2 33.7])
%colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('NH_4')
set(tl,'FontSize',18)
hold on

subplot(513)
pon=reshape(bio(:,11),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,pon);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('PON')
set(tl,'FontSize',18)
hold on

subplot(514)
don=reshape(bio(:,12),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,don);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('DON')
set(tl,'FontSize',18)
hold on

subplot(515)
sio=reshape(bio(:,16),nz,lt);
colormap(jet)
```

```
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,sio);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
xl=xlabel('Year')
set(xl,'FontSize',16)
%set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('SiO')
set(tl,'FontSize',18)
hold on
```

Appendix 10 FORTRAN code to reformat the *NEMURO*/1-D Yamanaka model physical output file into a format compatible for MATLAB plotting.

```
      parameter(nlayers=50)
      character*80 dateinfo
      real zd(nlayers+1),zl(nlayers)
      open(1,file='Yphist_Bering.dat',status='old')
      open(2,file='YPhist_mat.dat',status='unknown')
c
      do il=1,nlayers
        read(1,*)jj,zd(il),zl(il)
      end do
      read(1,*)jj,zd(nlayers+1)
c
      write(*,*)' enter starting year'
      read(*,*)iy
      write(*,*)' enter starting Julian day'
      read(*,*)iday
      write(*,*)' enter interval between data in days'
      read(*,*)incd
c
      do it=1,1000000
        read(1,100,end=10)dateinfo
          do iz=1,nlayers
            read(1,*)i,p1,p2,p3,p4,p5,p6
            write(2,101)iy,iday,zd(iz),p1,p2,p3,p4,p5,p6
          end do
          iday=iday+incd
      end do
   10 continue
  100 format(a)
  101 format(2i6,7(1x,f12.5))
      stop
      end
```

Appendix 11 MATLAB script to plot *NEMURO*/1-D Yamanaka model physical output.

```
load YPhist_mat.dat;
TSAv=YPhist_mat;

nz=50;
z=TSAv(1:nz,3);

nt=length(TSAv);

t=TSAv(1:nz:nt,1)+TSAv(1:nz:nt,2)/365.;
lt=length(t);
[t,z]=meshgrid(t,z);

%fullpage
subplot(311)
Temp=reshape(TSAv(:,4),nz,lt);  % plots all days
colormap(jet)
axis([0 1 -300 0])
h=surface(t,z,Temp);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('Climatology Bering Temperature')
set(tl,'FontSize',18)
hold on
%clear Temp

subplot(312)
%Sal=reshape(TSAv(1:nt,5),nz,length(t));
Sal=reshape(TSAv(:,5),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,Sal);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
%set(gca,'clim',[10 25])
colorbar
%set(gca,'clim',[33.2 33.7])
%colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
set(gca,'XTick',[])
yl=ylabel('Depth (m)')
```

```
set(yl,'FontSize',16)
tl=title('Salinity')
set(tl,'FontSize',18)
hold on
%clear Sal

subplot(313)
Ahv=reshape(log10(TSAv(:,7)),nz,lt);
colormap(jet)
axis([0 1 -300 0])
%axis([10 16 -300 0])
colorbar
h=surface(t,z,Ahv);
set(h,'EdgeColor','interp','FaceColor','interp','zdata',zeros(size(t)))
colorbar
%xl=xlabel('Year')
%set(xl,'FontSize',16)
%set(gca,'XTick',[])
yl=ylabel('Depth (m)')
set(yl,'FontSize',16)
tl=title('log_{10}Ahv (cm^2/sec)')
set(tl,'FontSize',18)
hold on
```