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Extension of the grazing module
of the phytoplankton model BLOOM II

model report
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delft hydraulics
Extension of the grazing module
of the phytoplankton model BLOOM II

Marnix van der Vat

delft hydraulics
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1 Introduction

This report describes the implementation of a new grazing module in the stand alone version of the multi-species phytoplankton model BLOOM II (Los, 1991). Three types of application of BLOOM II can be distinguished:

- as a stand alone steady state model with growth conditions as forcing functions;
- as a semi-dynamic module within the eutrophication module JSBACH (De Rooij and Kroot, 1990) with the growth conditions supplied by the chemical model CHARON (De Rooij, 1991); and
- as a semi-dynamic module within the eutrophication model DBS (DELWAQ - BLOOM II - SWITCH, Van der Molen et al., 1994) with growth conditions supplied by the water quality model DELWAQ (Postma, 1984).

In the stand alone version an implementation already existed of a simple, one species zooplankton module, called GRAZIN (Los, 1978). In JSBACH and DBS a more complex multi-species grazing module CONSL has been implemented (Mooij, 1990, and Los, 1992). Implementation of this module in the stand alone version was required by RIZA Lelystad for the analysis of the relation between zooplankton and phytoplankton for the so called Randmeren Lake Wolderwijd and Lake Veluwe. RIZA commissioned the implementation to Delft Hydraulics as assignment number RI-1654 on June 20, 1995.

The aim of this document is the description of the implementation of the CONSL grazing module in the stand alone version of BLOOM II. For a more detailed description of the module itself is referred to Mooij, 1990. Chapter 2 will shortly describe the concepts of BLOOM II and CONSL as far as relevant for the implementation. Chapter 3 gives a technical description of the implementation, while chapter 4 is meant to be a manual for the user.
2 Concepts

The general concept of BLOOM II is the calculation of the species composition of the phytoplankton community by optimization of the primary production rate as a function of the growth conditions and the characteristics of the different species. For the calculation of the effect of zooplankton with the simple zooplankton module GRAZIN, an iterative loop is constructed with the calculation of the effect of zooplankton on algae mortality and the resulting phytoplankton dynamics. In this way a steady state solution is calculated for the phytoplankton species composition as a function of the zooplankton biomass, which is supplied as a forcing function. Stop criteria for the iterative process are:

- the first order grazing rate (unit 1/d) becomes zero;
- the biomass is the same as for the previous iteration step; and
- the maximum iteration number is reached.

The grazing rate is calculated as a function of the zooplankton biomass and the algae biomass according to:

\[
G_j = \alpha_j \cdot \frac{Z_g \cdot Z \cdot (X_e - X_{\text{min}})}{(Z_k + X_e - X_{\text{min}}) \cdot X_e}
\] (1)

with:

- \(G_j\) = mortality rate for algae species j due to grazing by zooplankton (1/d);
- \(\alpha_j\) = preference for algae species j (-);
- \(X_e\) = total biomass of all eatable species multiplied by their preference factor (mg/m³);

\[
X_e = \sum_{j=1}^{j=n} (\alpha_j \cdot x_j)
\]

- \(x_j\) = biomass of algae species j (mg/m³);
- \(n\) = number of algae species (-);
- \(Z_g\) = grazing rate (1/d);
- \(Z\) = biomass of zooplankton (mg/m³);
- \(X_{\text{min}}\) = minimum remaining biomass of edible algae (mg/m³); and
- \(Z_k\) = half saturation constant for the grazing rate (mg/m³).

It should be stressed, that biomass is expressed in BLOOM II for as well phytoplankton as zooplankton in milligram dry weight per cubic meter. The initial grazing rate for each time step, so for the first iteration step, is determined by a specific input parameter, which is multiplied by the grazing preference to obtain the mortality due to grazing for all phytoplankton species.
The CONSL module for multiple grazers has been implemented in JSBACH and DBS for two grazers. In contrast with the GRAZIN module of the stand alone version, the forcing functions of grazer biomass are treated as maximum values and a check is made whether the supplied biomass can be supported by the actual phytoplankton community and whether the changes in biomass do not exceed maximum growth and mortality rates. Because the stand alone version of BLOOM II is a steady state model, these constraints have not been implemented in this version and the supplied biomass of the grazers are treated as forcing functions. The remaining elementary differences with the simple GRAZIN module are:

- the possibility to evaluate the effect of different types of grazers with different characteristics;
- the use of a different food response curve, resulting in a different grazing rate;
- the description of growth and maintenance respiration of the grazers;
- the incorporation of grazing of detritus;
- the evaluation of the effect of temperature on the coefficients; and
- the description of part of the excretion as detritus, while the GRAZIN module assumes changes in zooplankton biomass to affect only the pools of dissolved nutrients.

In the CONSL module the grazing rate is defined as:

\[
G_{ij} = \alpha_{ij} \cdot x_j \cdot Z_i \cdot F_{\max i} \cdot TF_i \cdot \frac{Food_i}{Food_i + \text{HalfSat}_i} \quad \text{for} \quad Food_i \leq \frac{U_{\max i} \cdot TU_i}{F_{\max i} \cdot TF_i} \tag{2}
\]

and

\[
G_{ij} = \alpha_{ij} \cdot x_j \cdot Z_i \cdot U_{\max i} \cdot TU_i \cdot \frac{1}{Food_i} \quad \text{for} \quad Food_i > \frac{U_{\max i} \cdot TU_i}{F_{\max i} \cdot TF_i}
\]

with:

\-
\- \text{\(G_{ij}\)} \quad \text{mortality rate for algae species \(j\) due to grazing by grazer type \(i\)} \quad (1/d);
\-
\- \text{\(\alpha_{ij}\)} \quad \text{preference of grazer type \(i\) for algae species \(j\)} \quad (-);
\-
\- \text{\(Z_i\)} \quad \text{biomass of grazer type \(i\)} \quad (\text{gC/m}^3);
\-
\- \text{\(F_{\max i}\)} \quad \text{maximum filtration rate of grazer type \(j\)} \quad (\ell/\text{mg C grazer/d});
\-
\- \text{\(TF_i\)} \quad \text{temperature correction coefficient for \(F_{\max i}\) for grazer type \(i\)} \quad (1/\degree \text{C});
\-
\- \text{\(Food_i\)} \quad \text{total biomass of all eatable species multiplied by their preference factor for grazer type \(i\)} \quad (\text{gC/m}^3):
\-
\- \text{\(\text{\(Food_i\)} = C_{\text{detr}} \cdot P_{\text{detr} i} + \sum_{j=1}^{j=n} (x_j \cdot P_{\text{alg} ij})\)}
\-
\- \text{\(C_{\text{detr}}\)} \quad \text{concentration of detritus carbon} \quad (\text{gC/m}^3);
\-
\- \text{\(P_{\text{detr} i}\)} \quad \text{preference of grazer type \(i\) for detritus} \quad (-);
\-
\- \text{\(P_{\text{alg} ij}\)} \quad \text{preference of grazer type \(i\) for algae species \(j\)} \quad (-);
\-
\- \text{\(\text{HalfSat}_i\)} \quad \text{Monod half saturation value for the filtration rate of grazer type \(i\) in relation to the food concentration} \quad (\text{gC/m}^3);
\-
\- \text{\(U_{\max i}\)} \quad \text{maximum uptake rate for grazer type \(i\)} \quad (\text{mgC food/mgC grazer}); \quad \text{and}
\-
\- \text{\(TU_i\)} \quad \text{temperature correction coefficient for \(F_{\max i}\) for grazer type \(i\)} \quad (1/\degree \text{C}).

Note that here biomass is expressed as gram carbon per cubic meter.
Figure 2.1 presents a comparison of the mortality rate due to grazing between the GRAZIN module (equation 1) and the CONSBL module (equation 2). The absolute values of the grazing rate are determined by the setting of the coefficients, but the form of the functions is determined by the equations used. The settings used where the advised default values for zooplankton, with a grazing pressure of 1 gC/m³:

\[ Z = 1.0 \text{ gC/m}^3 = 2.5 \text{ g dry weight/m}^3 \]
\[ Z_g = 1.0 \text{ /d} \]
\[ X_{\text{min}} = 0.25 \text{ g/m}^3 \]
\[ Z_k = 2.0 \text{ g/m}^3 \]
\[ F_{\text{max}} = 1.5 \text{ /mgC/d} \]
\[ \text{HalfSat} = 0.1 \text{ gC/m}^3 \]
\[ U_{\text{max}} = 1.5 \text{ mgC/mgC} \]

The temperature was assumed to be 20°C, so no temperature corrections had to be applied.

It appears, that the form of the two functions is quite similar, but that the default settings result in higher grazing rates for the CONSBL than for the GRAZIN module. On average the grazing rates calculated by CONSBL are two times higher. This can be modified by changing the zooplankton characteristics.

Figure 2.1: Comparison of grazing rate calculated by the two modules
In the coupled applications of BLOOM II in JSBACH and DBS, grazing was considered as a separate process having no influence on the phytoplankton dynamics other than an increase of mortality for certain species. BLOOM II, however, did not take into account this increased mortality while calculating the maximum primary production of the phytoplankton community under the given growth conditions. In this way, BLOOM II could calculate dominance of a species of which all biomass is grazed during the same time step, while another species might yield a much higher nett primary production. Therefore, the CONSL module has been implemented in BLOOM II in the same way as the GRAZIN routine: in an iterative loop with the production calculation. The following stop criteria apply:

- the amount of food for the grazers becomes zero;
- the grazing rates of detritus and algae are the same as for the previous iteration step;
- the biomass is the same as for the previous iteration step; and
- the maximum iteration number is reached.

The initialisation of the mortality due to grazing for each time step has been implemented in the same way as has been described for the GRAZIN module, e.g. by multiplication of the preference with a specific input variable.

If a dynamic calculation of the detritus concentration has to be carried out by the BLOOM II model, which is optional, the results of the CONSL grazing module are evaluated after each iteration step for the effect on the following input parameters for the production calculation:

- available dissolved nutrients, calculated as the difference between the total nutrient concentration and the nutrient concentration in algae, detritus and grazers; and
- the contribution of detritus to the extinction of light in the water column.

The implementation of CONSL in BLOOM has been carried out in such a way, that the model remains completely backward compatible; input prepared to use the old GRAZIN module can still be used and will provide the same results as before.
3 Implementation

The module INPUT2 reads the general information for BLOOM II as well as the temperature, depth and biomass of grazers from the file on unit 9 with the extension .D09. (Descriptions of this input file as well as the .D11 input file, without the here described modifications for grazers, are presented in Annex A). From the third column of the input table in this file the biomass in mg dry weight per m$^3$ of the zooplankton concentration for the GRAZIN module is read. From the fifth column on, the biomass in mg dry weight per m$^3$ for the grazers for the CONSBL module are read. The current maximum number of grazer types is 25. The first line after the input table provides the information regarding number of algae types and species, nutrients and additional constraints. If no more information is provided on this line, the GRAZIN module is used. Otherwise the number of grazers for CONSBL should be provided between position 69 and 73 on this line. The number of grazers NUGRAZ is used in the rest of the model as a switch to run GRAZIN (NUGRAZ = 0) or CONSBL (NUGRAZ > 0). From the same file is further read the initial grazing rate and the maximum number of iterations. If the maximum number of iterations is less than two, no grazing will be calculated.

The specific input for CONSBL the grazer characteristics are read by the module INPUT4 from the file with extension .D23 on unit 23, if NUGRAZ is greater than zero, and are stored in variables from the common block GRAAS. Table 3.1 presents the input file for two grazers and eight algae types, filled with the default values as used in DBS. The file consists of one column of 10 positions for each grazer. The first grazer type represents zooplankton and the second mussels.

In interactive mode all characteristics can be changed from the menu item ZOOPLANK.

The first major adaptation in the module BLOOM is the initialisation of the algae mortality due to grazing for each time step. The mortality rate is calculated from the initial grazing rate and the preference of the grazers for the algae types. This mortality rate is combined with the faecal fraction of the grazers for the algae types to determine a first order growth rate of the detritus pool. If the option for dynamic calculation of the detritus concentration is chosen, the concentration of available nutrients and the light extinction by detritus are updated.

If the grazing description of the CONSBL module is selected, the option for the calculation of the maximum supported grazing rate is also selected. The calculated maximum grazing rate GRAMX is used as input for the CONSBL subroutine to limit the grazing rate in order to avoid instabilities and resulting negative concentrations.

Furthermore a call is added to CONSBL for the calculation of the first order mortality rates of the algae and detritus due to grazing. Note that the calculated mortality rate for detritus can be negative, reflecting growth of the detritus pool due to excretion of the grazers. The mortality rates are used for the adaptation of the nutrient concentrations and the detritus extinction in a similar way as described for the initial grazing.

Further adaptations in the sources of BLOOM II deal with the output and the dimensions of the arrays for zooplankton biomass, which have become two dimensional.
<table>
<thead>
<tr>
<th>Value</th>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.50</td>
<td>0.50</td>
<td>Faecal fractions grazer per column algae types per row [-]</td>
</tr>
<tr>
<td>0.50</td>
<td>0.50</td>
<td>Preferences grazer per column algae type per row [-]</td>
</tr>
<tr>
<td>1.00</td>
<td>1.00</td>
<td>Faecal fraction detritus [-]</td>
</tr>
<tr>
<td>0.05</td>
<td>1.00</td>
<td>Preference grazer for detritus [-]</td>
</tr>
<tr>
<td>1.50</td>
<td>0.05</td>
<td>Maximum filtration rate grazer [l/mg C.d]</td>
</tr>
<tr>
<td>0.50</td>
<td>0.20</td>
<td>Maximum relative growth grazer [/dag]</td>
</tr>
<tr>
<td>0.50</td>
<td>0.20</td>
<td>Maximum relative mortality grazer [/dag]</td>
</tr>
<tr>
<td>0.10</td>
<td>0.10</td>
<td>Monod term filtr.r. in rel. to food [mg C/l]</td>
</tr>
<tr>
<td>0.25</td>
<td>0.20</td>
<td>Routine respiration coefficient [-]</td>
</tr>
<tr>
<td>1.50</td>
<td>0.10</td>
<td>Maximum daily uptake grazer [mg C/mg C.d]</td>
</tr>
<tr>
<td>0.05</td>
<td>0.005</td>
<td>Standard respiration coefficient [/dag]</td>
</tr>
<tr>
<td>0.181</td>
<td>0.181</td>
<td>Stoch. 1ste &amp; 2de grazer N [fr. C]</td>
</tr>
<tr>
<td>0.026</td>
<td>0.026</td>
<td>Stoch. 1ste &amp; 2de grazer P [fr. C]</td>
</tr>
<tr>
<td>0.0</td>
<td>0.0</td>
<td>Stoch. 1ste &amp; 2de grazer SI [fr. C]</td>
</tr>
<tr>
<td>0.04</td>
<td>0.04</td>
<td>Temp. coefficient filtration rate [1 / °C]</td>
</tr>
<tr>
<td>0.04</td>
<td>0.04</td>
<td>Temp. coefficient max. growth rate [1 / °C]</td>
</tr>
<tr>
<td>0.04</td>
<td>0.04</td>
<td>Temp. coefficient max. mortality rate [1 / °C]</td>
</tr>
<tr>
<td>0.04</td>
<td>0.04</td>
<td>Temp. coefficient routine metabolism [1 / °C]</td>
</tr>
<tr>
<td>0.04</td>
<td>0.04</td>
<td>Temp. coefficient feeding rate [1 / °C]</td>
</tr>
<tr>
<td>0.04</td>
<td>0.04</td>
<td>Temp. coefficient standard metabolism [1 / °C]</td>
</tr>
<tr>
<td>1.0</td>
<td>0.0</td>
<td>Fraction of grazer excretion to the water column [-]</td>
</tr>
<tr>
<td>2.5</td>
<td>2.5</td>
<td>Ratio of dry weight to carbon [mg dry weight/mg C]</td>
</tr>
</tbody>
</table>
4 Running BLOOM II with the new grazing module

To run BLOOM II with the new grazing module CONSBL the number of grazers in the input file .D09 has to be increased to at least one on the first line after the input table with among others the biomass of the zooplankton. The biomass of the zooplankton (in mg dry weight per m³) has to be supplied from the fifth column on for each period, normally of one week. In the same file the maximum number of iteration steps MAXITER has to be set to a value of at least 2. The advised value is 10. The last variable of importance for CONSBL in this file is the initial grazing rate GRAZINIT. The default value is 0.0. With this value the first iteration step calculates the primary production without grazing, after which the measured grazing pressure is applied.

The characteristics of the grazers are read from the input file with the extension .D23. Table 1 presents an example of this file with an explanation of the different coefficients. For each grazer the data should be applied in a column with a width of ten positions. The model will not run and error message will be displayed, if this input file is not present or not complete, while the number of grazers for CONSBL is one or more.

All characteristics from the input files can be modified in the interactive mode, from the item ZOOPLANK in the PARAM menu (see Table 4.1). The biomass of the grazers can be modified by supplying a multiplication and an addition factor.

BLOOM II produces output in the form of tables and graphs. Regarding the grazers the output files on units 15 and 16, with the extensions .O15 and .O16 are important. The first one contains the results of each individual iteration step, while the second presents for each period the maximum allowed grazing rate GRAMX.

The graphical presentations are performed by the JSPOST program. The program ALTOYS converts the output of the calculations to input for JSPOST. The file ALTOYS.INP describes the parameters to convert the results for. If the name and/or number of types or groups of algae or grazers in BLOOM is changed, this file should be updated as well.

If for the first grazer type for all algae types the preference is greater than zero, the maximum grazing rate GMax (1/day) for this grazer type is calculated. This is the grazing rate for which none of the algae types will be able to grow and therefore the biomass of all types will decrease to zero after a short period. At present, it is not possible to present the corresponding biomass of the first grazer. For a fixed grazing rate, the biomass is a function of among others the available food. Since, for the maximum grazing rate the amount of food will approach zero, the calculation of the biomass is not straightforward. The user can estimate the maximum biomass from a series of iterative calculations with different biomass for the grazer (see Michielsen, 1993).
Table 4.1  Abbreviations used in interactive mode

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>GRAZINIT</td>
<td>Initial grazing rate, applied during the first iteration step for each time step</td>
<td>1 / day</td>
</tr>
<tr>
<td>MAXITER</td>
<td>maximum number of iterations</td>
<td>-</td>
</tr>
<tr>
<td>PHYTFEFR</td>
<td>faecal fraction per grazer for each algae type</td>
<td>-</td>
</tr>
<tr>
<td>PHYTPREF</td>
<td>preferences per grazer for each algae type</td>
<td>-</td>
</tr>
<tr>
<td>DETRFEFR</td>
<td>faecal fraction per grazer for detritus</td>
<td>-</td>
</tr>
<tr>
<td>DETRREF</td>
<td>preference per grazer for detritus</td>
<td>-</td>
</tr>
<tr>
<td>MAXFILT</td>
<td>maximum filtration rate per grazer</td>
<td>l / mg C * d</td>
</tr>
<tr>
<td>MAXGROW</td>
<td>maximum relative growth rate per grazer</td>
<td>1 / day</td>
</tr>
<tr>
<td>MAXMORT</td>
<td>maximum relative mortality per grazer</td>
<td>1 / day</td>
</tr>
<tr>
<td>MONODFIL</td>
<td>half saturation value filtration rate in relation to food per grazer</td>
<td>mg C / l</td>
</tr>
<tr>
<td>ROUTRESP</td>
<td>routine respiration coefficient per grazer</td>
<td>-</td>
</tr>
<tr>
<td>MAXUPT</td>
<td>maximum daily uptake per grazer</td>
<td>1 / day</td>
</tr>
<tr>
<td>STNDRESP</td>
<td>standard respiration coefficient per grazer</td>
<td>1 / day</td>
</tr>
<tr>
<td>NUTCOEFF</td>
<td>nutrient (N,P and Si) content relative to C per grazer</td>
<td>mg N-P-Si/ mg C</td>
</tr>
<tr>
<td>TFILT</td>
<td>temperature coefficient maximum filtration rate per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>TMAXGROW</td>
<td>temperature coefficient maximum relative growth rate per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>TMAXMORT</td>
<td>temperature coefficient maximum relative mortality rate per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>TROUTRESP</td>
<td>temperature coefficient routine respiration per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>TMAXUPT</td>
<td>temperature coefficient maximum uptake per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>TSTNDRES</td>
<td>temperature coefficient standard respiration per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>FREXWAT</td>
<td>fraction of excretion to water column per grazer</td>
<td>1 / °C</td>
</tr>
<tr>
<td>CTODRY</td>
<td>ratio of dry weight to carbon per grazer</td>
<td>mg dry weight/mg C</td>
</tr>
<tr>
<td>CONSCONC</td>
<td>concentration per grazer</td>
<td>mg dry weight/m³</td>
</tr>
<tr>
<td>PRINT</td>
<td>list the current coefficient settings</td>
<td>-</td>
</tr>
</tbody>
</table>
5 References

De Rooij, N.M., and M.P.J.M. Kroot, 1990. CHARON, JSBACH, FUN. DELFT HYDRAULICS.

De Rooij, N.M., 1991. Description of CHARON. DELFT HYDRAULICS.


Annex A  Description of the BLOOM input files

In the following pages the part of the original documentation of BLOOM is presented in which the input files with the extension .D09 and .D11 are described. This description does not include the modifications for grazers as described in this report. In the following, the filename FT05F001 refers to the .D09 input file and FT11F001 to the .D11 file.
5.0 THE STANDARD INPUT OF BLOOM II

As may be seen in Figure 4.1 on page 48 BLOOM's standard input data are divided over three different files:

1. File FT05F001 has a length of 80 columns and contains lake-specific as well as universal (model coefficients) input. Normally it contains some, but in a batch job all instructions for non-standard program options.

2. File FT11F001 is an 80 column file containing the remaining lake-specific data.

3. File FT12F001 is a variable format file containing the integrated photosynthetic efficiency curves of the phytoplankton species.

Except for the last section of file FT05F001, the three files are read sequentially in the order shown above. After the third file is read, the standard input is completed and the program returns to file FT05F001 to read one or several program instructions. This is the start of the optional input (conversational) part of the program. In a batch run each instruction is included in file FT05F001, i.e. the program continues to read from this file. In an interactive run, however, reading of file FT05F001 is stopped at a certain point and from that moment on the program only reads instructions from the terminal.

5.1 INPUT FILE FT05F001

This file contains all sorts of data and therefore has a rather complicated structure. As shown in Figure 5.1 on page 58 we may, however, distinguish six different sections.

Section 1 consists of three lines. The first contains the year number, and the main title. The last characters of the title (following column 72) are not read, but will be set by the program to the current date.
Format is I4,1X,9A8.
The other two lines are subtitles intended to contain details about a particular run. They can be changed between different series of computations within one computer job (See 'The optional input of BLOOM II' on page 63).
Format is 9A8.

Section 2 consists of a variable number of lines. The first line contains the number of periods (NDEC) for which data are to be read (usually 52).
Format is I5.
The remaining NDEC lines contain the values of four different variables in each period:

1. The day length in hours.
2. The natural mortality rate constant per day.
3. The zooplankton concentration in mg dry weight per m³.
4. The water depth, in m.
In most applications the column for the natural mortality rate constant (M) contains no data (or 0.0) in each period, because M is computed by the model and not read. Furthermore data for zooplankton are frequently missing.
Format is 4F10.0.

**Section 3** contains information on coefficient values and variable names. However, some strings (words) are only included as comment rather than as a name or program instruction.

Several input lines are searched for the occurrence of the word 'NOMINAL'. If it appears, the program skips reading that line. The input values of a parameter will be used in each time-step. If 'NOMINAL' does not appear, however, the program reads a multiplication and an incremental coefficient value to compute the value of a parameter according to the general equation:

\[
\text{Parm value} = \text{Mult factor} \times \text{Input} + \text{Increm factor} \quad (5.1)
\]

The line marked 'TYPES' reads the number of phytoplankton types, the number of phytoplankton species, the number of nutrient constraints and the number of additional constraints. The latter should always be 1 in the current version of the program. All strings are comments.
Format is 4(8X,I5,2X).

The line marked 'FIRST' reads the initial time-period for the computations, the final time-period, the increment (time-step size) and the number of successive runs (NRUN). Usually the latter is 0 or 1 and the computations stop after those for the final period. If

\[\text{NRUN} = 2, 3, \ldots, 10,\]

the following input lines contain initial, final and incremental values for the 2nd, 3rd, ..., 10th run. In this case the program starts a new series of computations for each specified period. No parameter values or options can be reset between the runs. Using NRUN values of 2 or more is useful to make separate computations in different parts of the year, or to vary the time-step size of the model in different periods.

If the increment is larger than 1, all inputs to the program are averaged for each period.
All strings are comments.
Format is 4(8X,I5,2X).

The next lines in the example starting with 'NITROGEN' contain information for the nutrient constraints. Usually there are 3 of these constraints (see also the first line of input section 3). The order of the nutrients here should be consistent with the order of nutrients in Figure 5.2 on page 61 (input file FT11F001).
Each line contains eight (or less) tokens:

**Token 1:** the eight character name of a nutrient.
**Token 2:** A program instruction. If it equals 'TEMPDEP', the program computes the remineralization of the nutrient as a linear function of temperature. Otherwise remineralization is constant.
**Token 3:** The temperature multiplier of the remineralization rate constant ('TEMPDEP' was specified), or the remineralization rate constant.

The standard input of BLOOM II 52
Token 4: A program instruction. If it equals 'NOMINAL', the value of this nutrient constraint (B_i) equals the input for each period (read from file FT11F001). The rest of the input line is ignored. In all other cases it is computed according to equation (5.1).

Token 5: A comment signaling the nature of the next coefficient.
Token 6: The value of the multiplier for the nutrient constraint.
Token 7: A comment signaling the nature of the next coefficient.
Token 8: The value of the increment for the nutrient constraint.

Format is: A8,7X,A8,F7.0,A8,7X,2(A8,F7.0)

The line marked 'BACKGROUND EXT' contains information how to compute the background extinction from the input (from file FT11F001). It contains seven tokens:

Token 1: A comment.
Token 2: A comment.
Token 3: A program instruction. If it equals 'NOMINAL', the value of the background extinction equals the input for each period (read from file FT11F001). The rest of the input line is ignored. In all other cases it is computed according to equation (5.1).
Token 4: A comment signaling the nature of the next coefficient.
Token 5: The value of the multiplier for the background extinction.
Token 6: A comment signaling the nature of the next coefficient.
Token 7: The value of the increment for the background extinction.

Format is: 30X,A8,7X,2(A8,F7.0)

The line marked 'TEMPERATURE' contains information how to compute the temperature from the input (from file FT11F001). It contains six tokens:

Token 1: A comment.
Token 2: A program instruction. If it equals 'NOMINAL', the value of the temperature equals the input for each period (read from file FT11F001). The rest of the input line is ignored. In all other cases it is computed according to equation (5.1).
Token 3: A comment signaling the nature of the next coefficient.
Token 4: The value of the multiplier for the temperature.
Token 5: A comment signaling the nature of the next coefficient.
Token 6: The value of the increment for the temperature.

Format is: 30X,A8,7X,2(A8,F7.0)

The line marked 'SOLAR INTENS' contains information how to compute the solar radiation from the input (from file FT11F001). It contains eight tokens:

Token 1: A comment.
Token 2: A comment.
Token 3: A program instruction. If it equals 'TOTALRAD', the solar radiation level for each period is multiplied by a correction factor to convert it from total to photosyntheti-
cally active radiation (PAR). The correction factor used by the model is 0.45.

Token 4: A program instruction. If it equals 'NOMINAL', the value of the solar radiation equals the input for each period (read from file FT11F001) or the input times 0.45. The rest of the input line is ignored. In all other cases the solar intensity is computed according to equation (5.1).

Token 5: A comment signaling the nature of the next coefficient.
Token 6: The value of the multiplier for the solar intensity.
Token 7: A comment signaling the nature of the next coefficient.
Token 8: The value of the increment for the solar intensity.

Format is: 15X,2(A8,7X),2(A8,F7.0)

The line marked 'MIXING DEPTH' contains information how to compute the mixing depth from the input. It contains seven tokens:

Token 1: A comment.
Token 2: A comment.
Token 3: A program instruction. If it equals 'NOMINAL', the value of the mixing depth equals the input for each period. The rest of the input line is ignored. In all other cases it is computed according to equation (5.1).
Token 4: A comment signaling the nature of the next coefficient.
Token 5: The value of the multiplier for the mixing depth.
Token 6: A comment signaling the nature of the next coefficient.
Token 7: The value of the increment for the mixing depth.

Format is: 30X,A8,7X,2(A8,F7.0)

The line marked 'ORGANIC MINERALIZATION' contains information how to compute the remineralization rate of carbon. This value is not used in the actual computations of the model, but only to create a specific (optional) output table (See 'Live and dead phytoplankton pools (FT20F001)' on page 101). It contains three tokens:

Token 1: A comment.
Token 2: A comment.
Token 3: The temperature multiplier for the overall remineralization of detritus produced by phytoplankton. The remineralization rate constant is computed as multiplier times temperature.

Format is: 23X,F7.0

The line marked 'KMIN' contains the names for the energy constraints and the remineralization rate of chlorophyll. It contains six tokens:

Token 1: The name of the lower limit of an extinction interval.
Token 2: The name of the upper limit of an extinction interval.
Token 3: A comment.
Token 4: The (exponential) temperature multiplier for the remineralization of chlorophyll (A).
Token 5: A comment.
Token 6: The temperature constant for the remineralization of chlorophyll (B). The remineralization rate constant
REMCHL is computed as an exponential function of temperature:

\[ \text{REMCHL} = \exp (A \times T - B) \]

Format is: 2(A8,7X),2(8X,F7.0)

The line marked 'MORTALITY' contains information which mortality rate constants will be used by the model. It contains four (or less) tokens:

Token 1: A comment.
Token 2: A program instruction. If Token 2 equals 'NOMINAL', the mortality rates read in Section 2 will be used. If Token 2 equals 'EXPO'NENT', the mortality rates will be computed by an exponential, type dependent function. The coefficients are read according to the description in section 5.
Token 3: A comment.
Token 4: The flushing rate constant per day.

Format is: 15X,A8,15X,F7.0

The line marked 'ZOOPLANKTON' contains zooplankton coefficient values. It contains seven tokens (or more if the number of nutrient constraints exceeds three). The nutrient contents here should be entered in the same order as the names were read earlier from this file.

Token 1: A comment.
Token 2: A comment.
Token 3: The stochiometric constant for nutrient 1 (nitrogen in the example) in zooplankton.
Token 4: A comment.
Token 5: The stochiometric constant for nutrient 2 (phosphorus in the example) in zooplankton.
Token 6: A comment.
Token 7: The stochiometric constant for nutrient 3 (silicon in the example) in zooplankton.

Format is: 23X,F7.0,2(8X,F7.0)

The line marked 'ZOOK' contains zooplankton coefficient values. There are ten tokens:

Token 1: A comment.
Token 2: The value of the half saturation constant of equation (1.14) to compute the grazing rate constant in mg dry weight of phytoplankton per m^3 per day.
Token 3: A comment.
Token 4: The filtration rate constant per day.
Token 5: A comment.
Token 6: The amount of phytoplankton which escapes grazing by zooplankton in mg dry weight of phytoplankton per m^3 per day.
Token 7: A comment.
Token 8: The initial value of the grazing rate constant for the first iteration.
Token 9: A comment.

The standard input of BLOOM II
Token 10: The maximum number of zooplankton grazing iterations. If this is less or equal to 1, the program will automatically suppress certain output lines because no grazing iterations will be performed (See 'Zooplankton iterations (FT15F001)' on page 86). Format is: 4(8X,F7.0),8X,I4

The line marked 'AUTOLYSE' specifies two additional coefficient values. There are 4 tokens:

Token 1: A comment.
Token 2: The fraction of nutrients of a phytoplankton cell which is instantly released to the dissolved nutrient pool upon dying.
Token 3: A comment.
Token 4: The value of the sedimentation rate constant of detritus per day.
Format is: 2(8X,F7.0)

Section 4 shows the specific coefficients of the phytoplankton types. The first line marked 'STOCHIOM' is a comment line.

The lines beginning with 'DIATOMS' and ending with 'OSCILLAT' contain the specific coefficients of the phytoplankton types. There should be as many input lines here as there are types in the model. This number was read at the beginning of Section 3. For each type there are seven tokens:

Token 1: The name of the species to which a type belongs. (See Section 5).
Token 2: The specific extinction of a phytoplankton type in m² per mg dry weight.
Token 3: The requirement for nutrient 1 (nitrogen in the example; see Section 3) of each type.
Token 4: The requirement for nutrient 2 (phosphor in the example; see Section 3) of each type.
Token 5: The requirement for nutrient 3 (silicon in the example; see Section 3) of each type.
Token 6: The carbon to chlorophyll ratio of each species.
Token 7: The dry weight to carbon ratio of each species.
Format is: A8,2X,D10.0,8F10.0

Section 5 contains the specific coefficients related to production for each phytoplankton type. The first line marked 'PRODUCTION' is a comment line.

The next (in the example fifteen) lines contain the specific coefficients of the phytoplankton types. There should be as many input lines here as there are types in the model. This number was read at the beginning of Section 3. For each type there are ten tokens:

Token 1: The name of each phytoplankton type. Each of the names here should correspond to the type names read in Section 4. If there is no complete correspondence, the program will be terminated abnormally.
The temperature coefficient \( A \) to compute the maximum growth rate constant of each type.

The constant coefficient \( B \) to compute the maximum growth rate constant of each type. Maximum growth rates are computed as:

\[
T \\
U_{\text{max}}(T) = A \times B
\]

or

\[
U_{\text{max}}(T) = A \times (T - B)
\]

(See token 4).

A program instruction. The first (exponential) equation is used when Token 2 equals 'EXPONENT'. The second (linear) equation is used when Token 2 equals 'LINEAR'.

The temperature coefficient \( A \) to compute the natural mortality rate constant of each species.

The constant coefficient \( B \) to compute the natural mortality rate constant of each species. Mortality is computed as:

\[
T \\
M(T) = A \times B
\]

The temperature coefficient \( A \) to compute the respiration rate constant of each species.

The constant coefficient \( B \) to compute the respiration rate constant of each species. Respiration is computed as:

\[
T \\
R(T) = A \times B
\]

The relative mixing depth of each phytoplankton species: the fraction of the total depth over which types with active buoyancy control are mixed (See 'Solution algorithm' on page 27).

The zooplankton preference rate for each phytoplankton species.

Format is: \( 8X,2F8.0,A8,6F8.0 \)

Section 6 is no standard input to the program. It contains one or several optional program instructions, which are only read from file FT05F001 for reasons of convenience (See 'The optional input of BLOOM II' on page 63 for more details).
Figure 5.1 Example of standard input file FT05F001. This dataset contains both lake-specific and universal inputs. The drawn lines and the column lines are not in the input file, but printed for convenience.

Section 1
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Diepte 1.35M; achtergrond extinktie 2.5 per m; Refraktair N = 0.75.
Tentative berekening.

Section 2
52 WEEKS TO BE READ
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8.05  0.    1.35
8.30  0.    1.35
8.58  0.    1.35
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9.36  0.    1.35
9.79  0.    1.35
10.24 0.    1.35
...
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7.77  0.    1.35

Section 3
TYPES  12  SPECIES  5  NUTRIENT  3  ADDITION  1
FIRST  1  LAST  52  INCREM  1  NRUN  1
NITROGEN TEMPDEP 0.006 NOTNOM MULTIPLI 1.0 INCREM -0.75
PHOSPHOR TEMPDEP 0.006 NOMINAL MULTIPLI 1.0 INCREM 0.0
SILICON TEMPIND 0.025 NOMINAL MULTIPLI 1.0 INCREM 0.0
BACKGROUND EXT NOMINAL MULTIPLI 1.0 INCREM 0.0
TEMPERATURE NOMINAL MULTIPLI 1.0 INCREM 0.0
SOLAR INTENS TOTALRAD NOMINAL MULTIPLI 1.0 INCREM 0.0
MIXING DEPTH NOMINAL MULTIPLI 1.0 INCREM 0.0
ORGANIC MINERALIZATION 0.006
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MORTALITY EXPONENT FLUSH 0.0
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ZOOK 2000. GRAZRATE 1.0 ESCAPE 250. GRAZINIT 0.0 MAXITER 3
AUTOLYSE 0.5 SEDIMENT 0.0

The standard input of BLOOM II
### Section 4

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### Section 5

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### Section 6

**5.2 INPUT FILE FT11F001**

The second standard input file is an 80 column file such as shown in Figure 5.2 on page 61 containing most of the lake-specific data. Each line corresponds to one time-step, hence there are usually 52 lines of input. This number NDECO was read by the program from input file FT05F001. The following variables are read:

1. The identifier (name) for the time-step (columns 1 through 4).
2. The number for the time-step (columns 6 through 10).
3. The water temperature in °C (columns 11 through 20).
4. The amount of solar radiation in Joules/cm²/week (columns 21 through 30).
5. The measured chlorophyll concentration in mg/m³ (columns 31 through 40).
6. The available concentrations of the nutrients in mg/m³. Usually there are three of them in the order nitrogen, phosphorus and silicon (columns 41 through 70). The number and order of the nutrients is read from the first input file. The consistency of the order is not checked by the program.
7. The Background extinction per m. In the example the background extinction is constant for a whole year (columns 71 through 80).

The input format is A4,IX,I5,7F10.0.

Note: the chlorophyll measurements are only used by the program to create print-plots of computed and measured chlorophyll against time (See 'Print-plot of results (FT45F001)' on page 103). Missing data for chlorophyll should be entered as -1.0, not as 0.0 or as a blank. Under normal conditions these values are not plotted. If, however, the selected time-step size of the model is larger than one week, the chlorophyll measurements are linearly interpolated to prevent that the model consistently plots computed chlorophyll numbers for periods without observations.
Figure 5.2 Example of standard input file FT11F001. This dataset contains lake-specific inputs such as temperature and nutrients. The column lines are not in the input file, but printed for convenience.

<table>
<thead>
<tr>
<th>WK</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>5.0</td>
<td>1599.</td>
<td>128.</td>
<td>3.5470</td>
<td>0.1520</td>
<td>5.0000</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 2</td>
<td>2</td>
<td>1.8</td>
<td>1464.</td>
<td>115.</td>
<td>3.7330</td>
<td>0.1480</td>
<td>4.7500</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 3</td>
<td>3</td>
<td>2.0</td>
<td>1727.</td>
<td>99.</td>
<td>4.1800</td>
<td>0.1570</td>
<td>4.8000</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 4</td>
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<td>2.5</td>
<td>1143.</td>
<td>-1.</td>
<td>4.0400</td>
<td>0.1485</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 5</td>
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<td>2016.</td>
<td>128.</td>
<td>3.9000</td>
<td>0.1400</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
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<td>1783.</td>
<td>-1.</td>
<td>4.1270</td>
<td>0.1530</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 7</td>
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<td>3770.</td>
<td>95.</td>
<td>3.8250</td>
<td>0.1250</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 8</td>
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<td>4251.</td>
<td>-1.</td>
<td>3.6460</td>
<td>0.1150</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
<td>WK 9</td>
<td>9</td>
<td>1.0</td>
<td>3719.</td>
<td>73.</td>
<td>3.4670</td>
<td>0.1050</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
<td>WK10</td>
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<td>2.2</td>
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<td>77.</td>
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<td>0.1130</td>
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<td>2.50</td>
</tr>
<tr>
<td>WK11</td>
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<td>0.1810</td>
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<td>2.50</td>
</tr>
<tr>
<td>WK12</td>
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<td>4331.</td>
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<td>4.3550</td>
<td>0.1785</td>
<td>4.8</td>
<td>2.50</td>
</tr>
<tr>
<td>WK13</td>
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<td>219.</td>
<td>4.4960</td>
<td>0.1760</td>
<td>4.8</td>
<td>2.50</td>
</tr>
</tbody>
</table>

| WK51 | 51 | 1.8| 1501. | -1.  | 3.7825 | 0.1400 | 5.1875 | 2.50 |
| WK52 | 52 | 1.5| 1254. | -1.  | 3.8750 | 0.1400 | 5.2750 | 2.50 |

The standard input of BLOOM II 61