



中国科学院南京地理与湖泊研究所

Nanjing Institute of Geography & Limnology, Chinese Academy of Sciences



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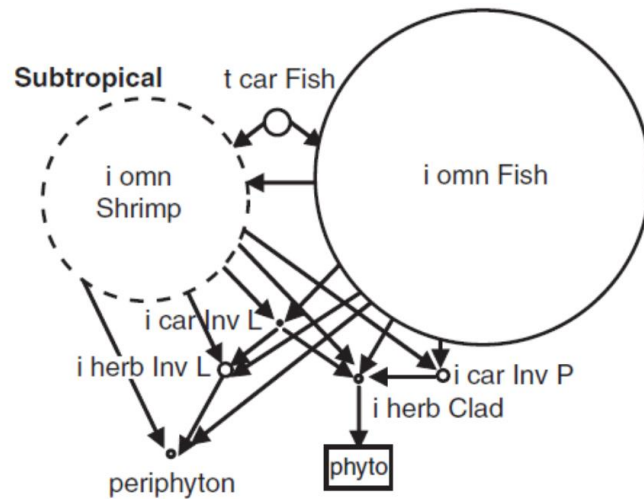
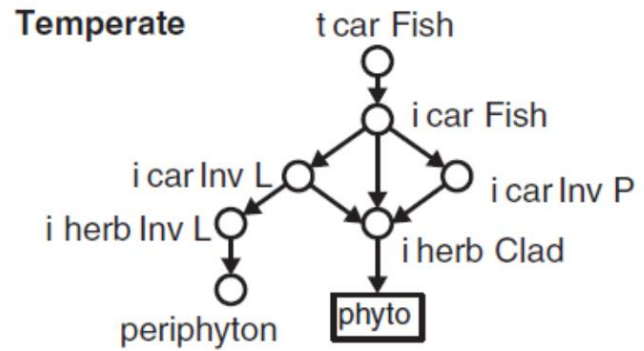
WET模型 模块化构建原理与应用

孔祥臻, Tobias K Andersen

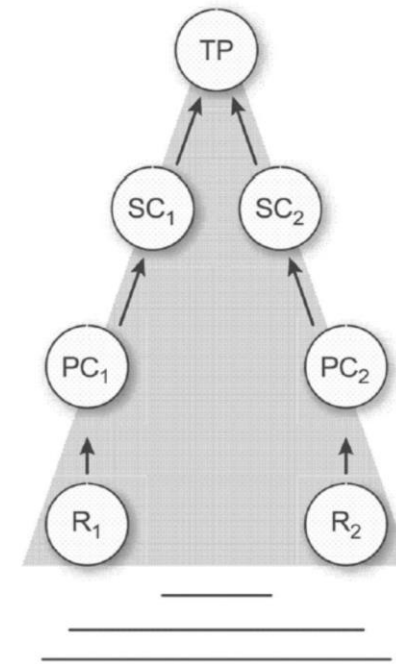
中国科学院南京地理与湖泊研究所 | 丹麦科技大学

2024年10月14日-16日

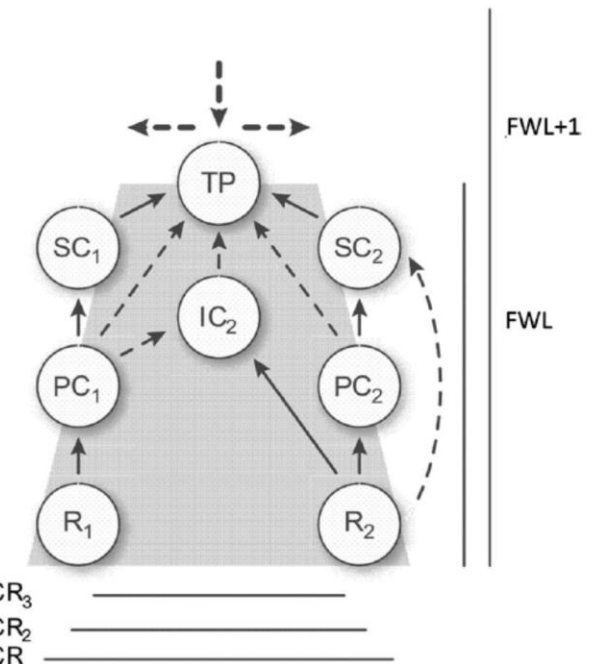
江苏 南京



Temperate



Subtropical

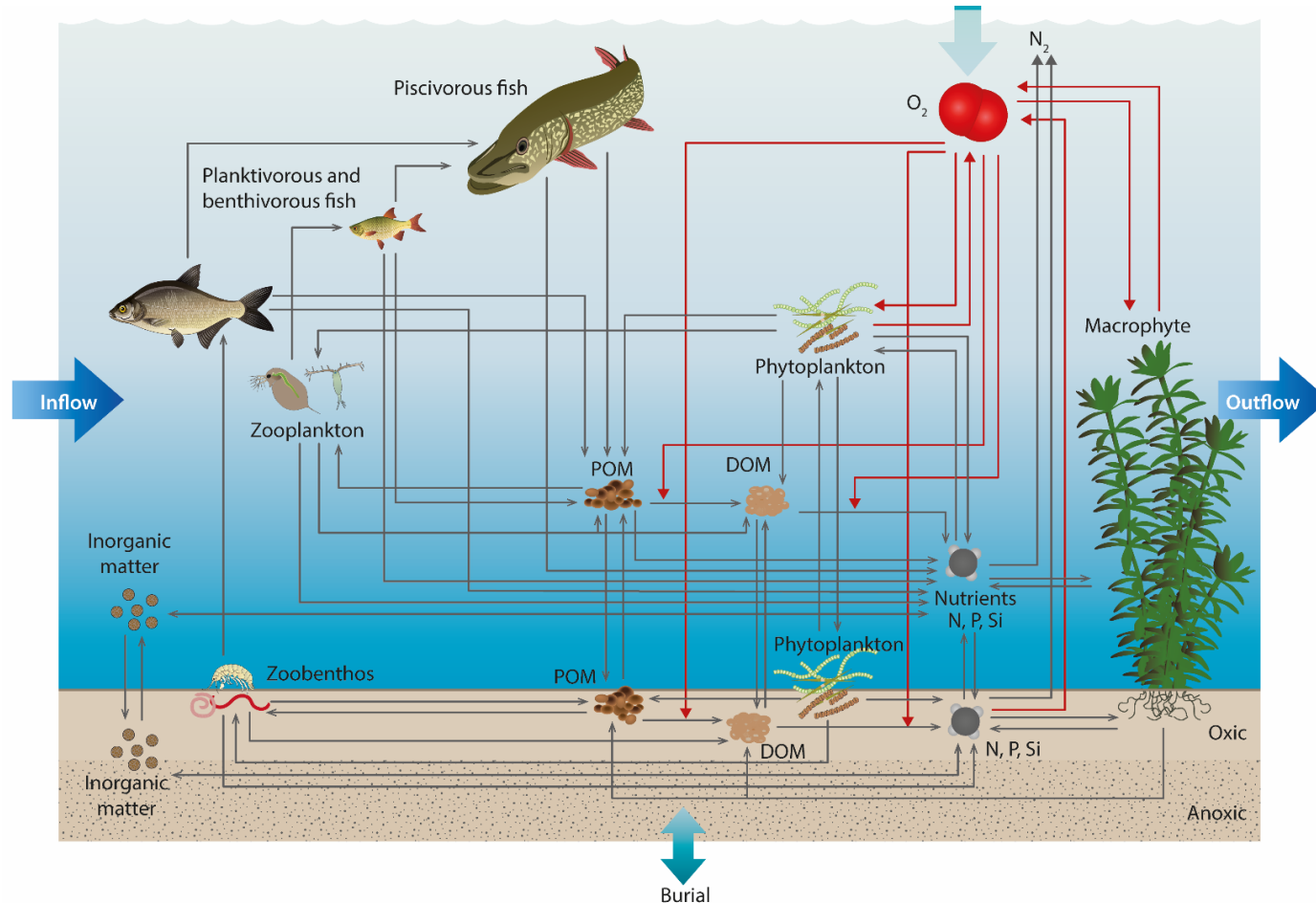


Conceptual model from stable isotope analysis

Iglesias et al (2016) Hydrobiologia

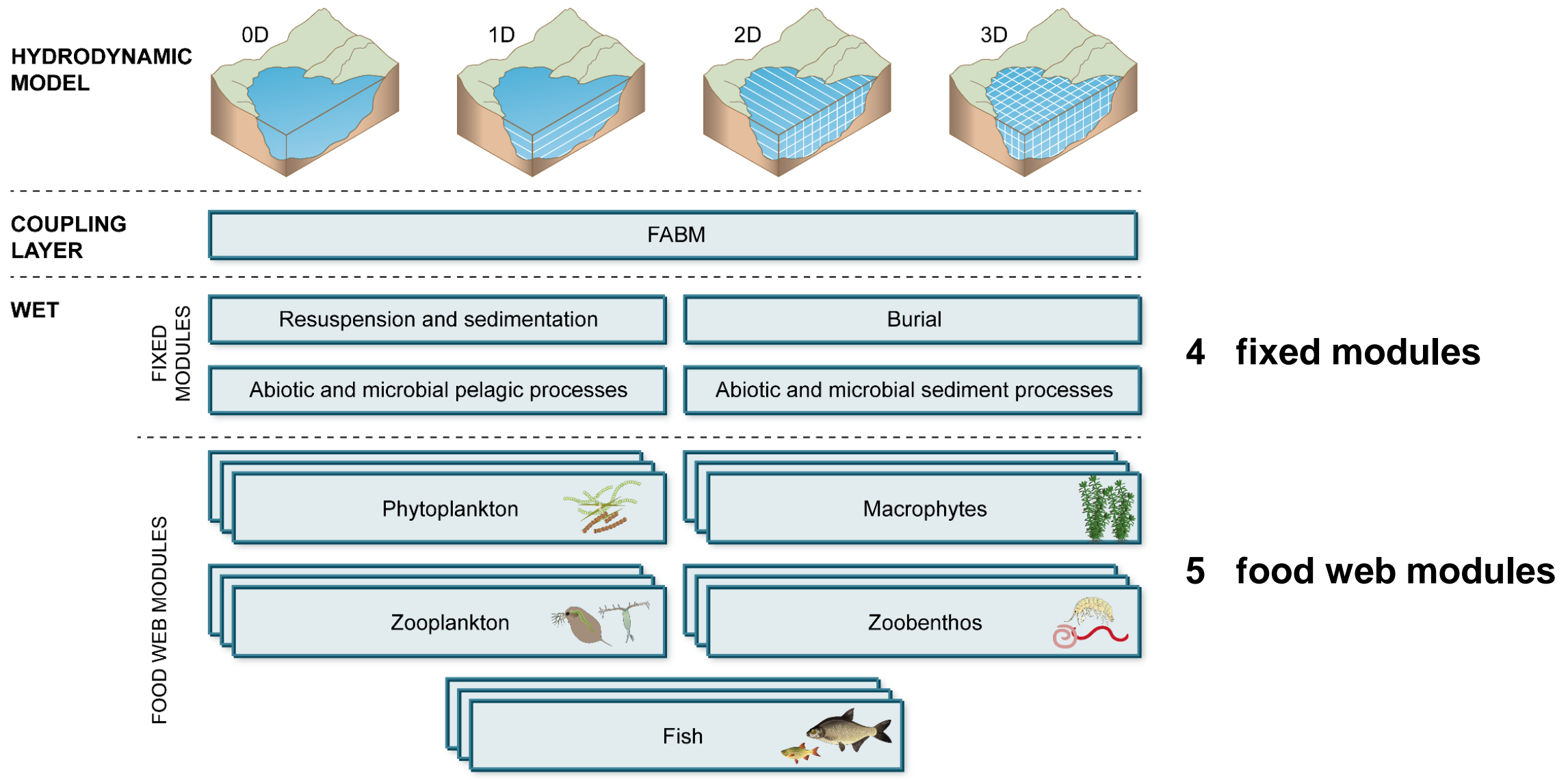
WET (Water Ecosystems Tool)

The configuration of the conceptual ecosystem model is flexible, but by default it describes interactions between multiple trophic levels, including piscivorous, zooplanktivorous and benthivorous fish, zooplankton, zoobenthos, phytoplankton and rooted macrophytes. The ecosystem model also accounts for oxygen dynamics and a fully closed nutrient cycle for nitrogen and phosphorus.



*WET conceptual model from
Schneider-Meyer et al. in
prep.
Model developed by AU.*

WET allows for flexible model configuration



WET food web configurations

Food web modules

Fish

Zooplankton

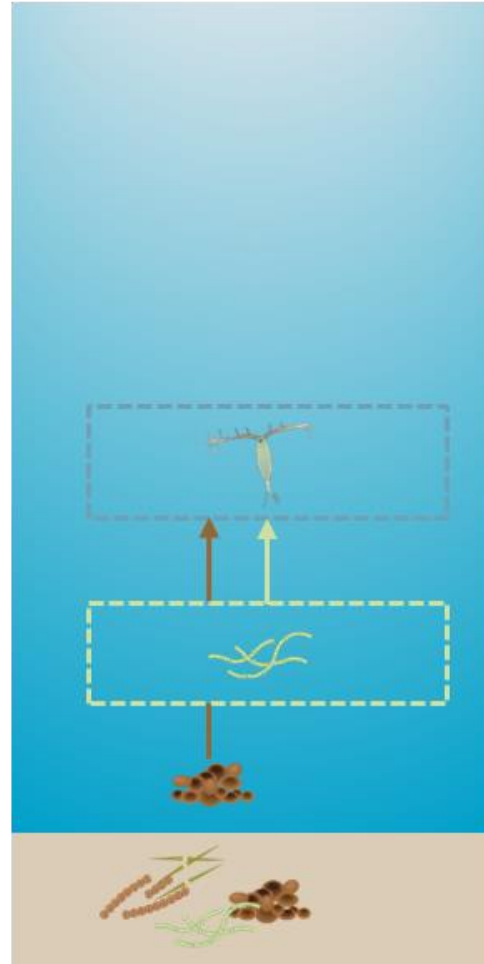
Phytoplankton

Macrophytes

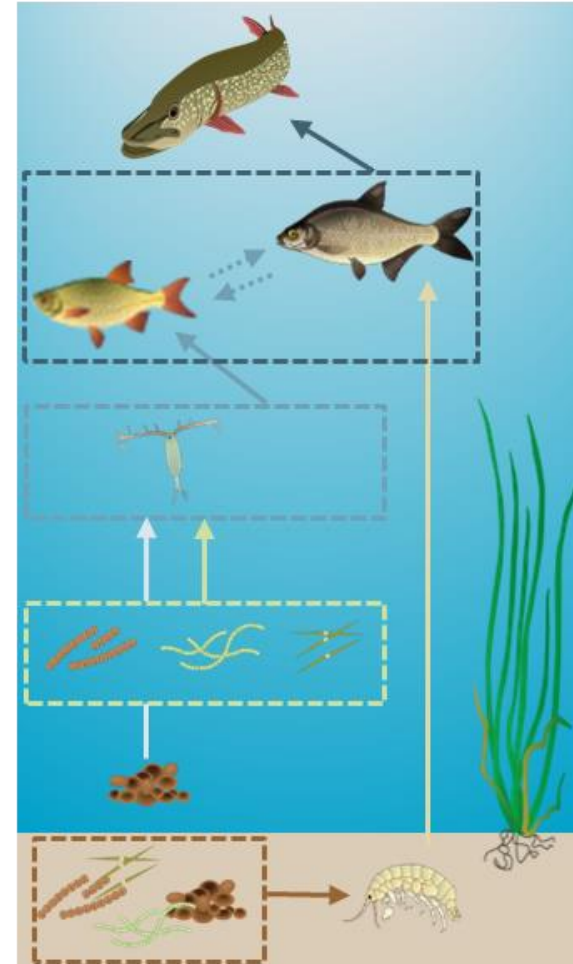
Detritus

Zoobenthos

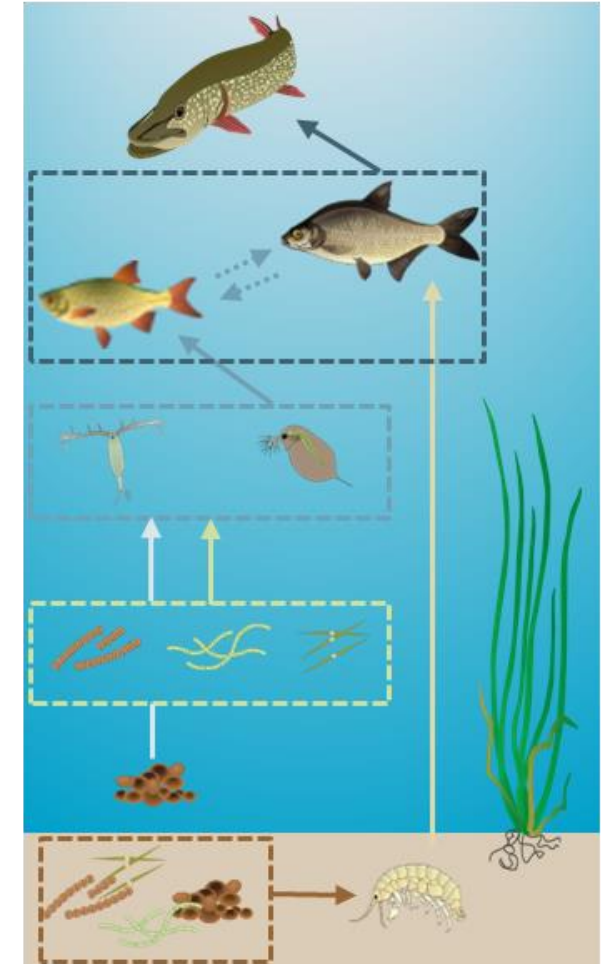
NPZD



WET standard



WET advanced



如何增加一个变量

1. First, copy the lines for an existing species in the configuration file and then change the name of the copy instance.
2. Secondly, one would go through the **couplings and parameters sections** in the new instance, modifying these to fit the desired organism.
3. Finally, one would modify the instances of any predators to include the new instance in their diets.

Thus, adding or subtracting instances to a model setup is relatively easy, and testing for the optimal food web configuration in a specific case is possible, if not usually feasible, by **calibrating several different module setups and comparing their performance.**

Phytoplankton

硅藻

A

绿藻

B

蓝藻

C

diatoms:

long_name: diatom phytoplankton

model: wet/phytoplankton

parameters:

cAffNUpt: 0.2

cAffPUpt: 0.2

cCPerDW: 0.4

cChDMax: 0.01152067786579087

cChDMin: 0.004551645037006276

cDMinS: 1e-05

cDMinW: 0.0001

cExtSp: 0.25

cLOptRef: 14.25958425306334

cMuMax: 2.679774536438407

cNDMax: 0.04543062298800925

cNDMin: 0.008669738123303882

cNFixMax: 0.01

cPDMMax: 0.01003725855292473

cPDMin: 0.002424574658996565

greens:

long_name: green phytoplankton

model: wet/phytoplankton

parameters:

cAffNUpt: 0.2

cAffPUpt: 0.2

cCPerDW: 0.4

cChDMax: 0.007214584180037665

cChDMin: 0.00905217121045621

cDMinS: 1e-05

cDMinW: 0.0001

cExtSp: 0.25

cLOptRef: 40.59286016376461

cMuMax: 0.893404316053331

cNDMax: 0.0912120289848275

cNDMin: 0.01960693948453595

cNFixMax: 0.01

cPDMMax: 0.02111459115262903

cPDMin: 0.001157806782377292

cResusExp: -0.375

cSID: 0.15

cSigTm: 15.34217942225144

cTmOpt: 18.84681634009118

cVNUptMax: 0.07

cVPUptMax: 0.0142463281946629

cVSed: 0.3255787505559667

cVSet: -0.318715127033716

cVSwim: 10

fDCMS: 0.02124417612230302

fDCMW: 0.05823760752712179

fDisaMort: 0.2

fLVMin: 0.025

fMuNFix: 0.9

fNutLimVdown: 0.675

fNutLimVmap: 0.75

hLRef: 4.516178770417071

hO2BOD: 1.0

hSiAss: 0.01

kDResp: 0.075

kMortS: 0.05

kMortW: 0.01

kResusMax: 0.25

lNfix: false

lSi: true

qLightMethod: 2

qTrans: 1

coupling:

DCM_DW_pool_sediment: abiotic_sedimer

DCM_DW_pool_water: abiotic_water/sDDC

DCM_N_pool_sediment: abiotic_sediment

DCM_N_pool_water: abiotic_water/sNDOH

cyanobacteria:

long_name: cyanobacteria

model: wet/phytoplankton

parameters:

cAffNUpt: 0.2

cAffPUpt: 0.8

cCPerDW: 0.4

cChDMax: 0.008412088364390585

cChDMin: 0.004512935215492827

cDMinS: 1e-05

cDMinW: 0.0001

cExtSp: 0.35

cLOptRef: 20.14226790634071

cMuMax: 1.196246880034123

cNDMax: 0.07953522779930783

cNDMin: 0.01086677240813844

cNFixMax: 0.01

cPDMMax: 0.004259340591562401

cPDMin: 0.001764581188430707

cResusExp: -0.375

cSID: 0.15

cSigTm: 8.482930541426433

cTmOpt: 27.62511363911044

cVNUptMax: 0.08

cVPUptMax: 0.03340891092005887

cVSed: 0.1031467018994352

cVSet: -0.02242893726726897

cVSwim: 0.25

fDCMS: 0.09877847265277258

fDCMW: 0.07131369323275408

fDisaMort: 0.3

fLVMin: 0.1295583162307262

fMuNFix: 0.9

fNutLimVdown: 0.67

fNutLimVmap: 0.75

hLRef: 35.59562609331791

hO2BOD: 1.0

hSiAss: 0.09

kDResp: 0.03

kMortS: 0.2

kMortW: 0.01

kResusMax: 0.25

lNfix: false

lSi: false

qLightMethod: 2

qTrans: 3

coupling:

DCM_DW_pool_sediment: abiotic_sedimer

DCM_DW_pool_water: abiotic_water/sDDC

DCM_N_pool_sediment: abiotic_sediment

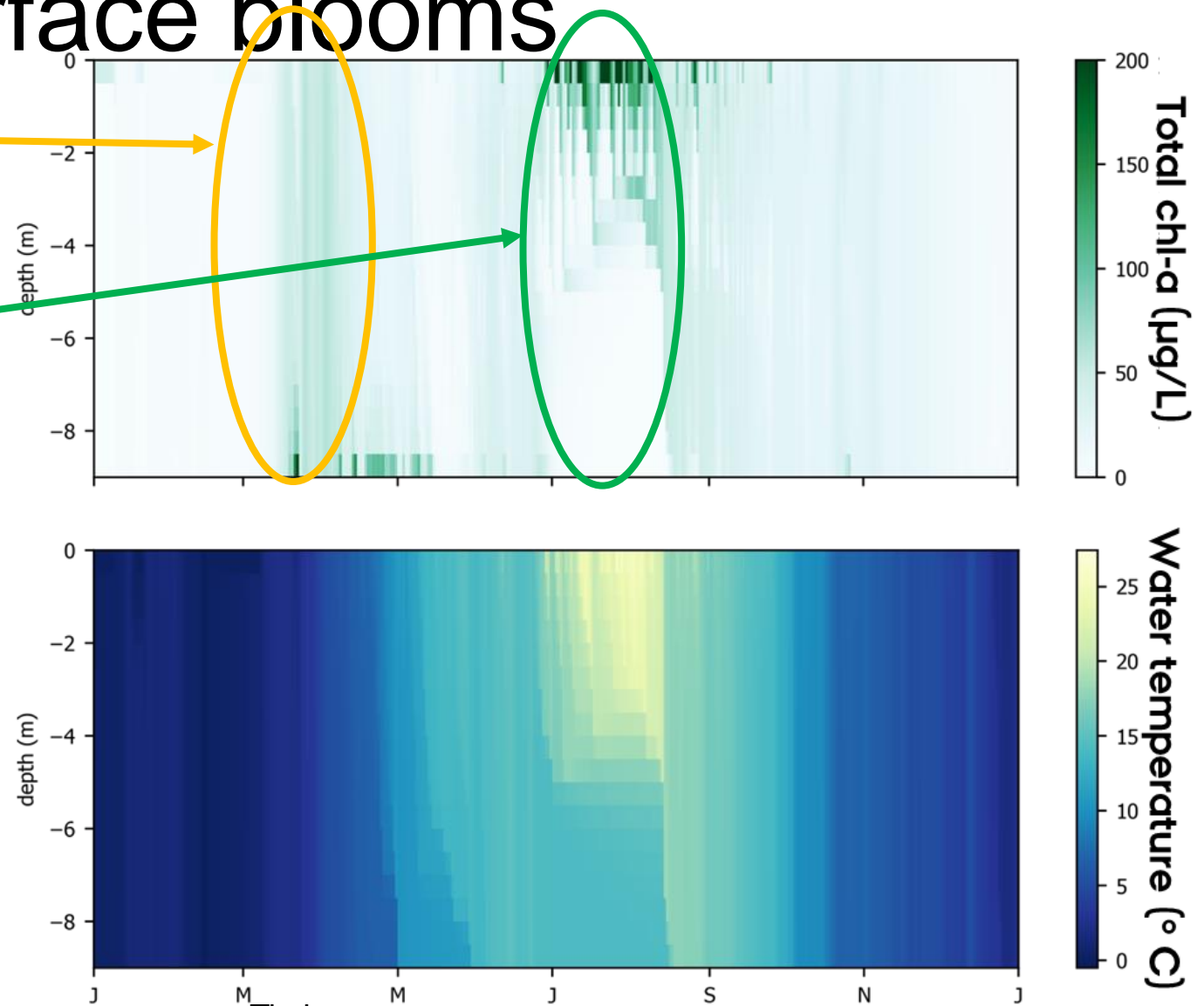
DCM_N_pool_water: abiotic_water/sNDOH

D

WET can simulate cyanobacteria surface blooms

Diatom bloom
Passive settling

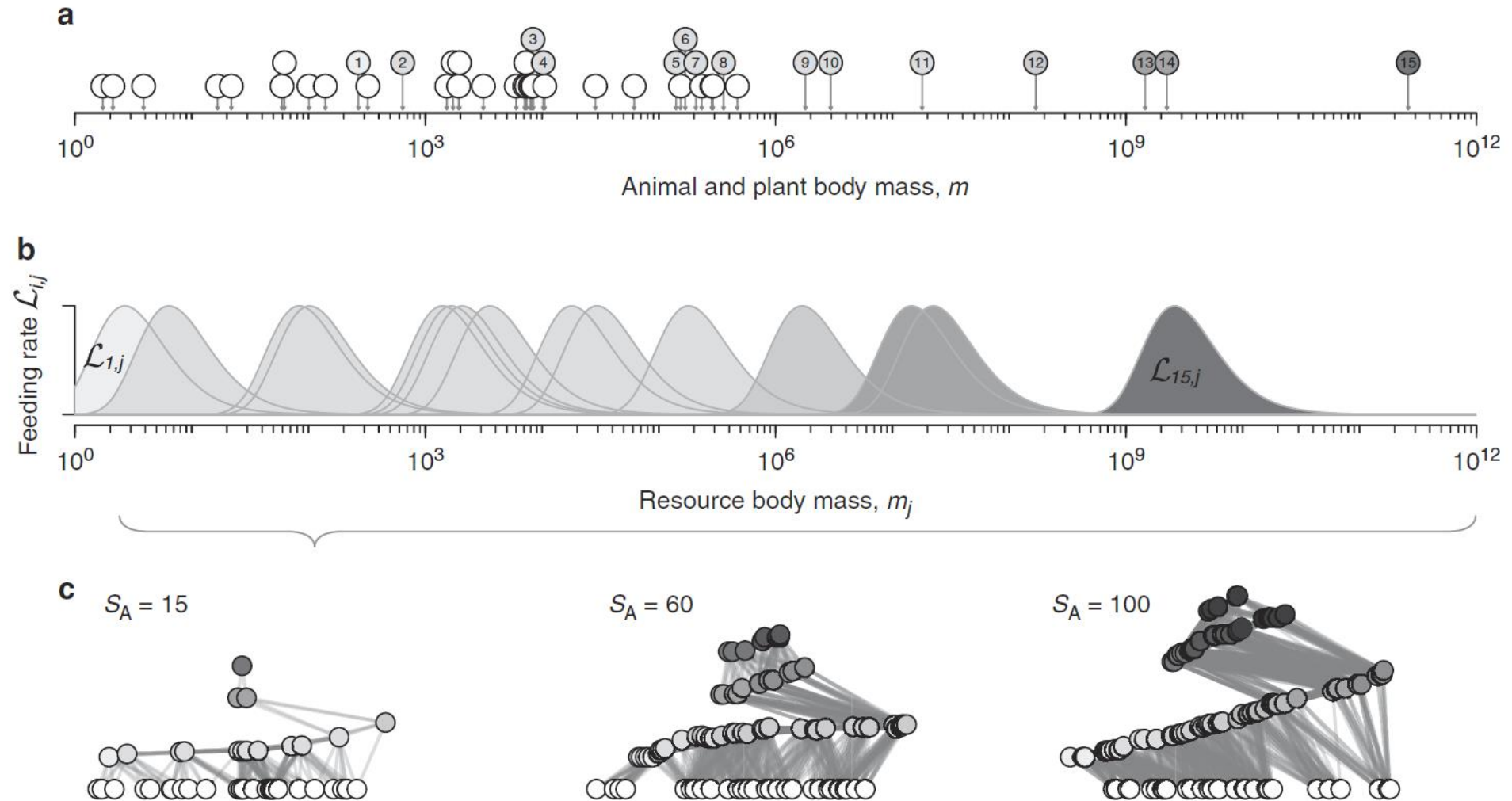
Cyanobacteria surface bloom
Active upward swim



Cyanobacteria surface blooms occur frequently in Danish Lake Bryrup.

Photo by the Danish EPA.

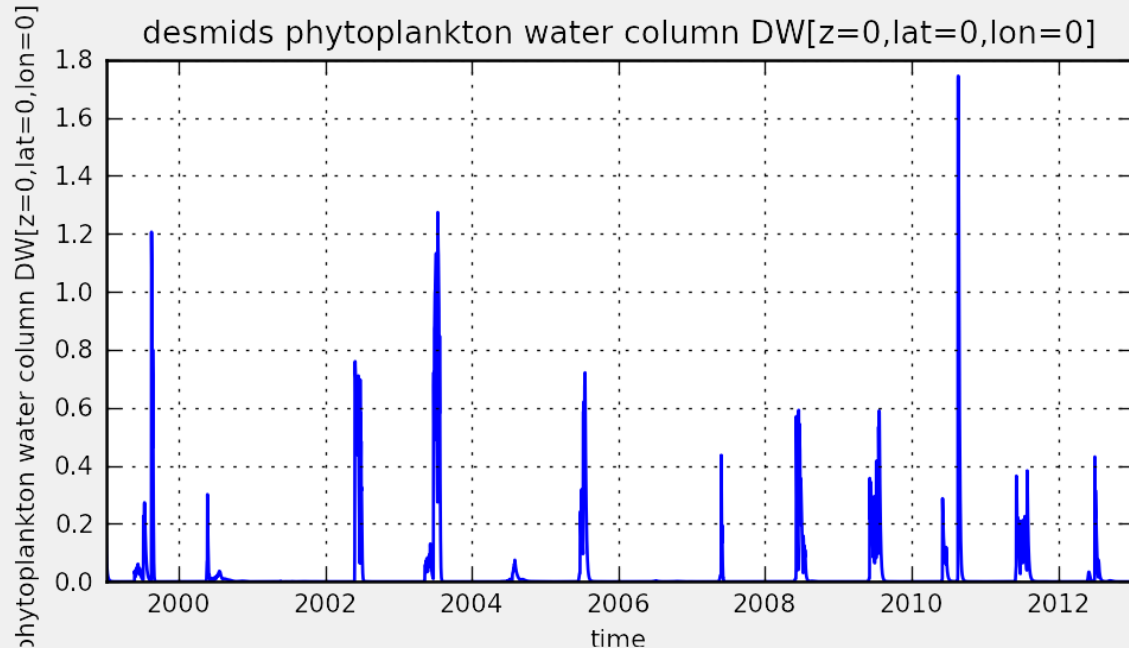
<https://musem.natur-vand/overvaagning-af-vand-og-natur/lokalitetsbeskrivelser/bryrup-langsoe/plankton/>



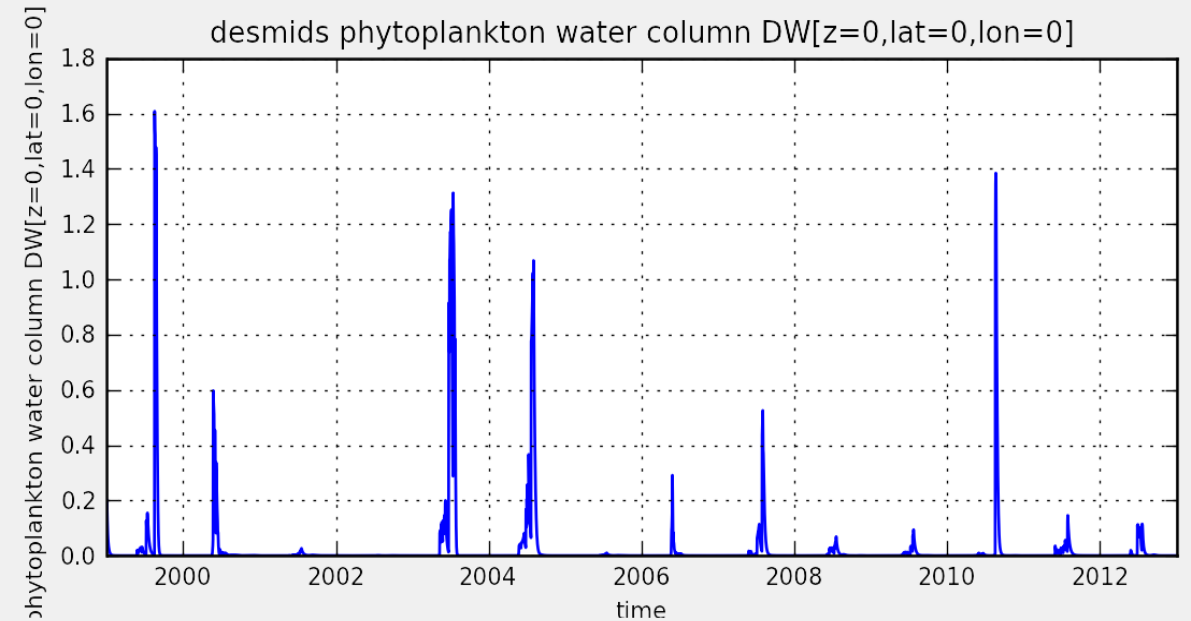
Desmid (帶藻)



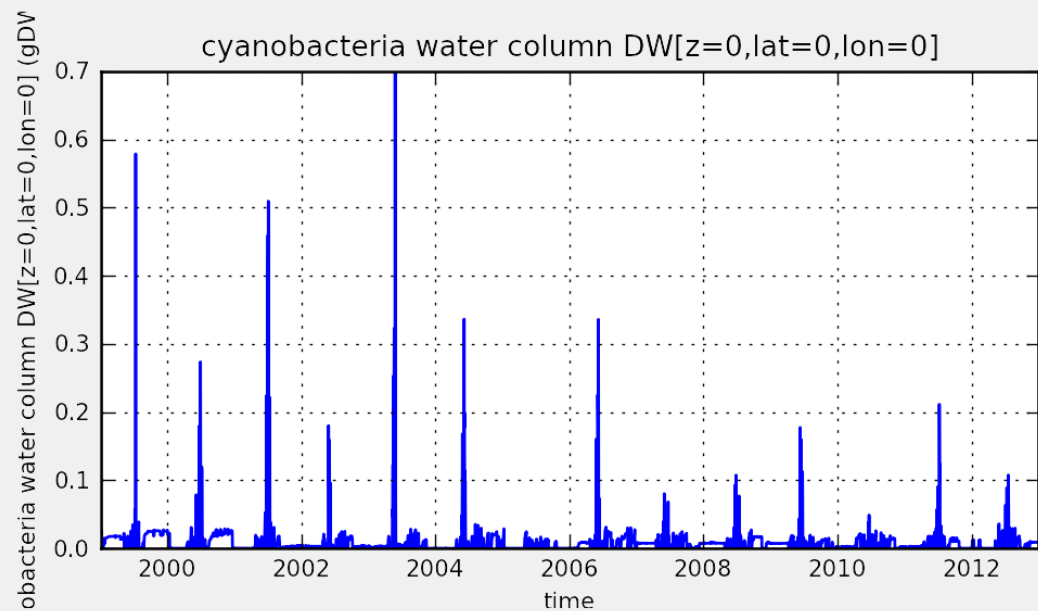
Original



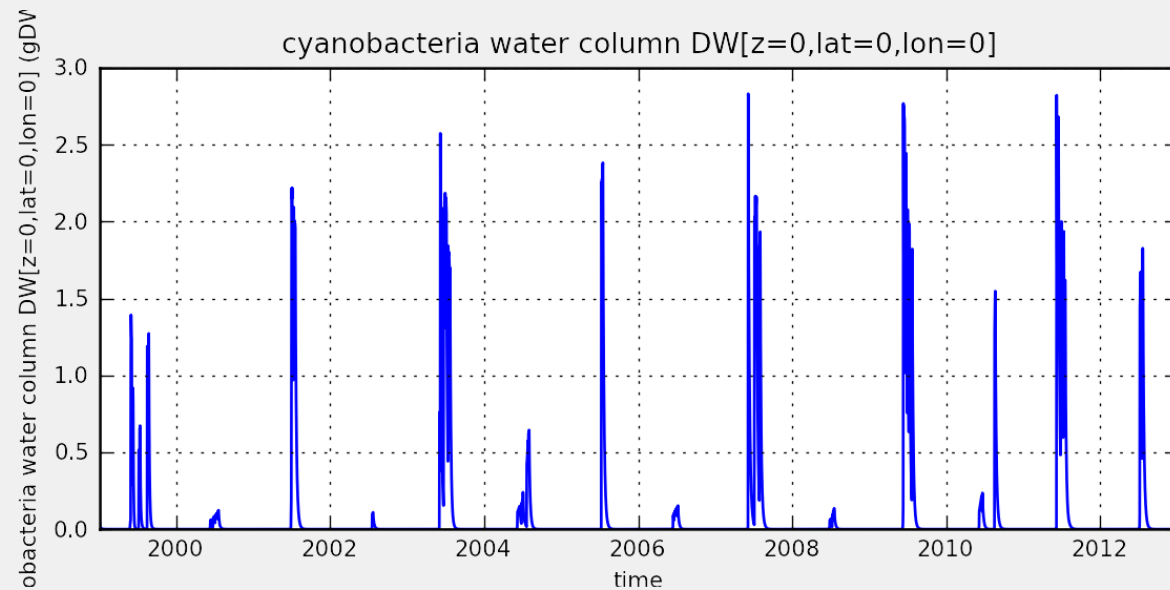
Add dinoflagellatas



Original



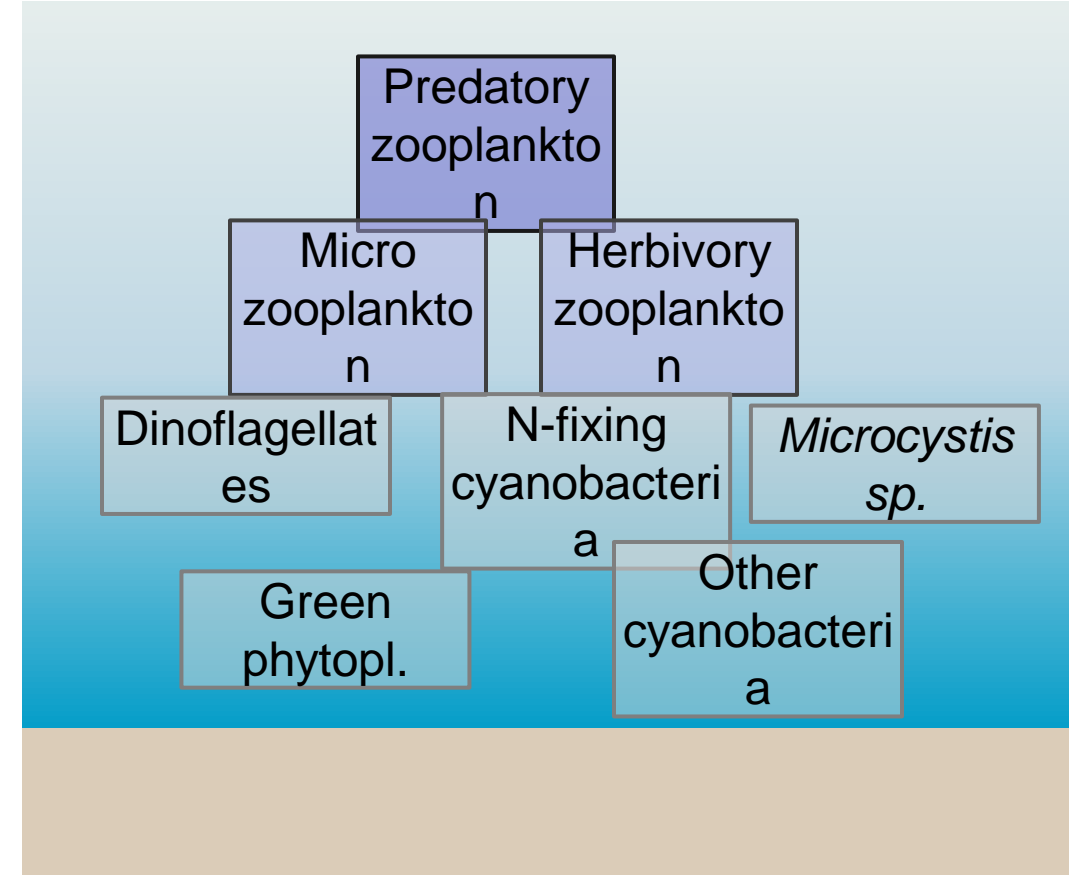
Fish removal



CSPS framework: a WET example

Regev, Carmel, Gal (2023)
Environ. Model. Softw.

Modelling Lake Kinneret (Sea of Galilee), a warm monomictic lake



GMD paper WET

Geosci. Model Dev., 15, 3861–3878, 2022

<https://doi.org/10.5194/gmd-15-3861-2022>

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Water Ecosystems Tool (WET) 1.0 – a new generation of flexible aquatic ecosystem model

Nicolas Azaña Schnedler-Meyer¹, Tobias Kuhlmann Andersen^{2,3}, Fenjuan Rose Schmidt Hu², Karsten Bolding^{2,3,4}, Anders Nielsen^{2,3}, and Dennis Trolle^{2,3}