Grassroots network of limnologists, information technology experts, and engineers who have a common goal of building a scalable, persistent network of lake ecology observatories

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GLEON Ad hoc Mendota Modeling Researchers (GLAMMR)
Report on workshop outcomes

Participants

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Introduction

The group met for one week, primarily at the Trout Lake Station in northern Wisconsin, to devise a modeling strategy for Lake Mendota phytoplankton dynamics, based on data obtained during the summer of 2008. Participants represented a diverse set of disciplines, including hydrodynamic modeling, water quality modeling, phytoplankton and zooplankton ecology, carbon cycling, and microbial ecology. The group settled on three science themes, each of which contains a set of science questions: (1) understanding bloom dynamics; (2) connecting bloom dynamics to microbial community dynamics; (3) discovering emergent ecosystem characteristics. More detail on science provided below. This progression of themes maps onto the process of conducting the science in a graduated fashion. Firstly, analyses will use ELCOM-CAEDYM (EC) to model the ecosystem. During the workshop, we made tremendous progress in parameterizing the model, formatting driver data, and assembling observations for state variables. The working model forms the basis for the first theme. The output of the model, in terms of state variables, such as organic carbon and nutrient stoichiometry, will be compared with microbial data in support of theme two. Finally, system dynamics will be observed across multiple space and time scales to address questions in the third group, emergent characteristics.

The group has developed collaboration sites to help organize activity and maintain momentum. A GoogleDocs site holds a reference list, the parameter set, and supporting documents. An FTP site has driver and response variable observational data, as well as simulation files. These materials will grow as the project proceeds.

Timeline for work is aggressive, with the following milestones:

August: A workshop on running the latest DC (possibly EC, too) version of the model will take place at the UW CFL. This hands-on activity will enable all who are interested to run the models on their computers.

August: Default parameter set for the model will be finalized.

October (GLEON 9 meeting): Initial science results for the three topical areas will be presented at the "cool things" symposium.

The moderate-term (1 year) outcome of the group will be a series of manuscripts related to the three thematic areas of science.

Science Themes (more science detail available on the Google docs site):

1. What are the primary controls on bloom dynamics? (Lead: Matt, David H., Paul, David M., Luke, Emily, Yvonne, Evelyn, Chin)
    a. How well do our models capture bloom dynamics (and results of bloom including DO)?
    b. What features are consistent, and what features are not?
    c. Also look at process values from the model
    d. Generate hypotheses based on marked discrepancies
    e. Novel approach of constraining model using high resolution time series
    f. Can we explain the rise and fall of DO early/late in the day?
    g. E.g. new values for primary production rates based on signal processing of buoy data, to improve accuracy
    h. How does the nutrient field vary in time and space?
    i. Use to inform future field campaigns (GLIDERS!!!!)
2. Which features of model output can inform our understanding of microbial community dynamics? (Lead: Lucas, Trina, Stefan, Todd, Matt, David M.)
    a. Can we incorporate DOM exudates from phytoplankton into model and see if these drive dynamics
    b. Water column stability creating isolated pockets. What features of the pocket can explain bacteria? E.g. temperature, nutrients, light. This can inform what we focus on with the model
    c. We hypothesize that highest rates of BCC change will be related to space and time variation in (1) temperature, (2) algal DOM, (3) nutrients
    d. Can we create an index from raw phyto data to put in model that will drive exudate production or

   e. Can grazing rates be incorporated into model and used to explain busts in bacterial populations
   f. Long-term fantasies about new model components: viruses, discrete bacterial groups
   g. Include diverse exudate features, allow them to be dynamic and driven by other model parameters like phyto, zoops
   h. Early - very tasty, low MW
   i. Late - due to mortality, composition reflects phyto composition
   j. Can we use calculated BP to guide future field efforts
3. What kinds of emergent properties map back to the ecosystem level? (Lead: Paul, Chin, David M., David, Kevin, Matt)
   a. Responses
      i. Ecosystem respiration
      ii. Scaling laws of physics, chemistry, biology. Are they similar?
      iii. Patchiness in x-y (under which time scales does it collapse?)
   b. Under what conditions is the model unlikely to do a poor job of reflecting what is happening in the lake?
   c. Under what conditions does the lake behave as 1-D vs 2-D vs 3-D
   d. Look at distribution of fluxes across water columns. What are the drivers of variability across these columns? Use this to predict when single-point buoy measurements might be most accurate.
   e. Look for coherence across grid cells or across columns. Does this reflect certain regimes of stability or advective transport.
   f. Edge effects. Is it necessary to include an index that accounts for lack of coherence

Action Items by Paper (which map onto themes)

1. Bloom Controls Paper- Matt, David H., Paul, David M., Luke, Emily, Yvonne, Evelyn, Chin

Action items:

1. Parameter Justifications (most are in tables): Sediment chem.; phytoplankton- see new table "Zoo" doc DH, EK, EG; zoops- see new table DH, EK, EG, KR; Light extinction, photolysis- KR, DM; Bacteria- SB, MH see Nutrient table. Additional metadata and references are here.

2. ELCOM-CAEDYM checks:

1. Water level (outflow), rating curves f cherokee marsh,
2. Tchain
3. Formosat image of mendota query (daily?) - DH
4. nutrient data into validation plots

5. time-series data into validation plots
6. zooplankton data into validation plots- can we get 2008 data from Stanley? PH, TK
7. how do we use phycocyanin to compare with model? conversions/proxies? LW
8. how do we use molecular data TM, MH, TRM
9. pretty conceptual model schematic

3. Parameter adjustments to improve validation

10. group consultation- 1st week in August- Trina will schedule. Running model, sharing
11. re-running (use DYCD?) -
12. run a no buoyancy control scenario
13. Funky plots- PH, LW
14. N:P plankton maps
15. limitation maps - add outputs to NC file
16. N Fixation maps
17. Skeleton outline by October
    Compile references (EK)

2. Bacterial community drivers paper- Lucas, Trina, Stefan, Todd, Matt, David M.,

Rationale: Ultimately we want to put bacteria in the model. We can't put all 200 taxa in the model. We need to lump them. It would be better to lump them based on their ecophysiology. Thus, we will use the model outputs to identify groups of taxa. See Todd's cluster diagram heat map.

Action items:

1. Develop work flow to plug model data into once the model is ready TM, LB, TRM, SB
2. Work with MH to get input needed, integrated samples,
3. Analyze Todd's integrated time series- TRM
4. Bin bacterial populations- TM, SB, LB
5. Identify interesting OTUs- LB

Additional ideas:

Time lag analysis. Correlate individual populations vs. environmental driver variables with variable time-lags (from model output/post-run). Environmental variables could be integrated over previous time steps (e.g. total amount of algal exudate produced during last three time steps). See plot that Matt drew on the easel (on the Google docs site).
Bin bacterial populations into "fast" and "slow" responders (r vs. k strategists). Integrated water samples more valuable since it is less sensitive to vertical entrainment. Can we integrate the water column in silico for Lucas' dataset?

Use model predictions to find conditions during optimal growth (but do we have frequent enough analyses of BCC?)
Use the model to create hypothetical bins of bacteria with different values for growth parameters (e.g. umax,Ks), and ask "does it matter?"
Include diverse exudate features in the model, allow them to be dynamic and driven by other model parameters like phyto, zoops
Early - very tasty, low MW; Late - due to mortality, composition reflects phyto composition
Can we use calculated BP to guide future field efforts

3. Emergent Properties Paper- Paul, Chin, David M., David, Kevin, Matt,

Action items:

1. Refine questions and articulate major ideas (PH, then group).
2. Justify that scaling and hydrodynamics are ok- also happening in Paper 1.
3. Spatial validation on a variable related to metabolism (eg sat chla data)- also in Paper 1
4. Create hypothetical workflow necessary to do analyses (PH, then group).
5. Use Odum model metabolism calculations (Chris Solomon).

Additional ideas:

Possible responses:
- Ecosystem respiration
- Scaling laws of physics, chemistry, biology. Are they similar?
- Patchiness in x-y (under which time scales does it collapse?)

Under what conditions is the model unlikely to do a poor job of reflecting what is happening in the lake?
Under what conditions does the lake behave as 1-D vs 2-D
Look at distribution of fluxes across water columns. What are the drivers of variability across these columns? Use this to predict when single-point buoy measurements might be most accurate.
Look for coherence across grid cells or across columns. Does this reflect certain regimes of stability or advective transport.
Edge effects. Is it necessary to include an index that accounts for lack of coherence