Simulating the Red Sea Ecology with parallel 1D marine ecosystem models and clustering

Denis Dreano[a], George Triantafyllou[c], Bani Mallick[b], Ibrahim Hoteit[a,*]

[a] *Computer, Electrical and Mathematical Sciences and Engineering Division, King Abdullah University of Science and Technology*
[b] *Department of Statistics, Texas A&M University*
[c] *Hellenic Center for Marine Research*

Abstract

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1. Introduction

3D marine ecological models....

- marine ecology models represent biogeochemical interactions as differential equations.
- Can be as minimal as NPZ or as complete as NPZ

...are useful because....

- HAB affect public health, desalination and coastal economy
- predicting chlorophyll can help fisheries
- For research: better understand the large-scale ecosystem
- Especially usefull because we lack data about the subsurface phenomena

...But expensive and difficult to run.

- (**?**) lot of underdetermination
- circulation model very expensive, because very small grid

*Corresponding author
Email address: `ibrahim.hoteit@kaust.edu.sa` (Ibrahim Hoteit)

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In this article we look at ways to simulate 3D ecosystems more cheaply by running many parallel 1D regional models.

- Divide the Red sea in small regions with similar ecology
- Reduces underdetermination
- Ensure parametrization is better for each region

We are going to test that idea on the Red Sea because....

- Red Sea is an interesting environment: extreme temperatures and salinity
- Very rich and preserved ecosystem
- Unexplored environment
- Lack of data: therefore developing models is important

We will use the hybrid-SEIK data assimilation scheme, because....

- Assimilation constrains the model and reduces underdetermination
- Mitigates the fact that initial conditions are unknown
- SEIK is better than SEEK for strongly nonlinear models
- SEIK is better than EnKF when fewer observations than states
- hybridization reduces the ensemble size and the computational cost

We will assimilate Chl data even if it is imperfect because it is the best available data for the Red Sea.

- Chl data allows to observe large scale ecological patterns with high spatial and temporal coverage.
- Compared with in situ data that are limited in time and space, and expensive.
- However chl data suffers from missing values due clouds, aerosols, etc.

- Also bad values near the coast, case II waters
- Both problem particularly affect the southern Red Sea, that has nearly no observation in the summer during some months.
- However as lack of in situ data, this is the best we have currently in the Red Sea

What we are going to do in this paper step by step.

What is new in this paper and why.

Introduce sections.

2. Data

2.1. CCI chlorophyll data

We use CCI chlorophyll data because it has more coverage..

With a quick look at the data this is what we see....

2.2. DINEOF

There are still missing data in CCI, so we use DINEOF for data filling because....

More or less this is the way DINEOF works....

This is how we applied DINEOF....

Now we show the results of DINEOF.

2.3. Clustering

To do 1D models, we cluster the Red Sea using clustering algorithms. We chose GMM because....

This is more or less the way GMM works....

This is how we used it....

This is what we got....

3. Model and Assimilation

3.1. 1D-ERSEM model

Description of ERSEM.

Initialization/Parameters/Forcing.

3.2. Data Assimilation

We chose hybrid-SEIK DA scheme because....

Equations of hybrid-SEIK.

Parameters.

4. Results

4.1. Model evaluation

Here, we compare the results of the free-run with the assimilated-run. We show that we have a good prediction skill, and that the assimilation improves the model.

4.2. Analysis

Here we look at the results and interpret them biologycally. Do we find comparable results as Acker, Raitsos, Weiker, etc. What can we say about the hypothesis that they made about he process that drive primary productivity in the Red Sea.

5. Conclusion

Are several 1D paralled 1D models a good alternative to 3D simulations?

What did we learn about the Red Sea ecology?

Future works?

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6. Bibliography