Ecological clustering of the Red Sea and parallel 1D-ecological simulations

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

Abstract

1. Introduction

3D ecological models are expensive to run. Can we divide the Red Sea into regions and have 1D models running in each of them in parallel?

In this article we cluster the Red Sea in 3 different eco-regions using automatic unsupervised learning algorithms. We then run an assimilative 1D ecological model on each of the region and analyze the results.

2. Data

2.1. Chlorophyll data

We use CCI monthly and 8-days CHL data.

---

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

2.2. DINEOF

CCI data present missing data, in particular, in the southern Red Sea during summer. In order to have a complete dataset on which can apply a clustering algorithm, we use DINEOF, a data filling algorithm. The Chl data is averaged over each region to give a data time-series for each of them.

2.3. Clustering

We use clustering algorithm to divide the Red Sea into regions with similar behavior. We tried K-means and Gaussian Mixture Model, a generalization of the former.GMM was found to give better results.

3. Model and Assimilation

3.1. 1D-ERSEM model

We use a 1D coupled ERSEM model. The physical forcing comes from a 3D circulation simulation of the Red Sea [Yao 2014]. The ecological models are initialized with the results of the 3D Red Sea ecology simulation [Triantfyllou2013].

3.2. Data Assimilation

To improve the results of the simulation we use the hybrid-SEIK assimilation scheme, detailed in this subsection.

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?

Acknowledgment

6. Bibliography