Interactive comment on “Differences and implications in biogeochemistry from maximizing entropy production locally versus globally” by J. J. Vallino

Anonymous Referee #1

Received and published: 1 March 2011

In this manuscript, the author propose a simply two reaction, coupled model that represents autotrophy and metabolism. Then using Monte Carlo approach to investigate the model domain space and demonstrate some important results. 1) that there are many micropath solutions that produce the same macropath state and 2) global optimum does not correspond to local optimums. Overall, this paper is an elegant and important work that contributes to our understanding of the thermodynamic development of simple ecological systems. It could be published with minor revisions.

Technical comments: In the Introduction, the author expounds on the rationale for a thermodynamic approach, but omits the basic fact that ecosystems are open, energetic systems. What better reason is there to apply thermodynamics?

On Page 3, Page 18 when the MEP principle is introduced, correctly, it could also be mentioned that the goal function in fact depends on the stage of development, which was investigated in Aoki 2008, Ecological Modelling 215, 89–92.

On page 5, line 7, please correct the mistake that Equation (2) applies to heterotrophic organisms, since all organisms metabolize (plants and animals).

On Page 6, line 5, eq (4). When reading it I wanted to see the units presented with the equation. After struggling with it for some time found them described about 2 paragraphs away. Please move this to right when the equation is introduced (particularly kappa).

On page 15, lines 1-3, please clarify what might happen if the N constraint is released. Was this scenario investigated?

I really found the discussion to be inspiring, particularly, the paradigm shift (noted in the quote from Lineweaver and Egan) and the proposition that information exchange could occur over large spatial scales. I also agree with the author that decoding the environmental genomic data is not well developed and will be an important next step.