

## ***Interactive comment on “Stable isotopes dissect food webs from top to the bottom” by J. J. Middelburg***

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Natural food webs comprise primary producers and consumers, microbes as well as metazoans. However, most food-web studies are limited in coverage and truncated, in particular at the bottom where microbial producers, consumers and detrital resources are not resolved. Stable isotopes of metazoan consumers together with isotope characterization of microbial biomarkers and detrital compartments might resolve this, but there are still some issues with these tools as mentioned by referee # 2. I agree and will based on the feedback received elaborate on the pros and cons of biomarker approaches (offset between biomarker and total cells signature, among biomarkers).

The referee has a few main points and multiple smaller technical corrections. The latter will all, but one, be implemented in the revision (thanks for identifying those). Table 1

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will be retained since it provides the first systematic comparison on the use of stable isotopes at natural abundance and as tracer.

The reviewer identified “some gaps that have to be filled in before the acceptance of this manuscript. The latter concerns weaknesses of some tools that need to be discussed and the recent development of models that represent avenues for future use of stable isotopes in food-web reconstructions and that need to be cited in this manuscript”

As already alluded to above and in the response to referee #1, I will revise the text to more extensively discuss the pros and cons of the various approaches (natural abundance as well as tracer approaches, biomarker strengths and weaknesses). I agree that a more in-depth treatment of data handling and modeling might strengthen this paper (as also suggested by referee #1) and will therefore add a new section in which I will present and discuss the approaches and modeling tools. The referee emphasized the need for coupling of stable isotopes and inverse modeling and suggested to include the very recent paper by Pacella et al. (2013, *Ecological Modelling*, 267, 127–137). Thank you for suggesting this paper. However, I already cited prior work of van Oevelen et al. (2006, 2010) that included stable isotope data in the inverse analysis. In the revised version, I will explicitly present procedures to link stable isotopes (at natural abundance as well as tracer) with biomass and other ecosystem data.

The referee made some useful suggestions on potential enrichment of carbon isotopes during trophic transfer and difference in isotopic values among the tissues analyzed. The text will be modified to include this, but with the overall constraint that sections 2 and 3 (on natural abundance) will be shortened. Dynamic Energy Budget models with isotopes are indeed powerful to increase our understanding of trophic enrichment and we will add the reference to complement the meta-analysis, observational citations.

Finally, indeed the manuscript deals primarily with aquatic ecosystems and I will add aquatic to the title of the revised manuscript.