

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

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The aim of this review was not to provide an exhaustive account of all stable isotope studies in ecology to date, but to explore the strengths and weaknesses of stable isotope reconstructions of whole food web functioning, i.e. food webs including primary producers and microbial and metazoan consumers. Such end-to-end studies are needed to complement powerful, detailed experimental studies on simplified food webs if we are to advance our understanding of ecosystem functioning in a changing world. The applicability of isotopes in end-to-end food-web reconstructions has rarely been reviewed as such, as confirmed by the referee.

However, in order to keep the manuscript concise (for readability and accessibility), and to keep balance between traditional approaches (natural abundance studies of plants

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and animals) and newer approaches (microbial domain studies using biomarkers, models and deliberate tracer studies), some well-studied aspects had to be covered rather shallow, I fully agree.

Based on the feedback received from referee # 1, I will therefore likely: (1) shorten and merge sections 2 and 3 on the natural abundance approach because this has been extensively covered before (2) elaborate the section 4 on biomarkers to elucidate the microbial domain, including strengths and limitations (isotopic offsets between biomarker and total cell and among various biomarkers) (3) extend section 5 on deliberate tracer approaches, but will not thrive to be complete as this would be a book on its own nowadays. (4) add a new section on data handling and modeling as suggested by both referees. Specifically, I will more explicitly discuss how to use natural abundance isotope data with or without biomass information and tracer isotope data with or without biomass data.

The challenge will be to maintain balance between detail for the isotope specialist and readability for the interested ecosystem scientists, between natural abundance and deliberate tracer approaches and between microbial and metazoan aspects. I acknowledge the referee for his/her advice to provide a more in depth treatment.

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