

Interactive comment on “Partitioning of soil water among canopy trees during a soil desiccation period in a temperate mixed forest” by M. Meißner et al.

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Thank you for your feedback on our manuscript. We appreciate the valuable comments provided. In the following we address your comments and questions. Our replies are written in italics below your comments.

Page 7 lines 21-22: For IsoSource “the fractional increment used in our model calculations was set to 0.1 . . .”. If this means 0.1%, this is too fine an increment and the calculations would take a very long time. If this mean $0.1 \times 100\% = 10\%$, then this is too coarse and numerous possible solutions might be missed as discussed by Phillips Gregg (2003).

We applied a fractional increment of 1% in the IsoSource model calculation as suggested by Phillips Gregg (2003). We will correct the manuscript text accordingly on page 5422, line 9.

Page 8 lines 23-26: Considerably more detail is needed for the data analysis methods. a. How exactly was this ANOVA done for the water uptake fractions from the different horizons? b. Was each feasible solution identified by IsoSource used as a replicate? c. How many were there? d. Large n values lead to statistical significance for even small fractional differences, but n is completely dependent on the choice of the Increment and Tolerance parameters. e. Was a separate ANOVA done for each horizon? These tests are not independent since the water uptake values from the different horizons must sum to 1. Rather than multiple univariate tests of this sort, a multivariate test might have been used that would incorporate this non-independence.

The IsoSource model analysis was separately done for each tree, using the xylem isotopic signature as mixture and the corresponding soil depth as potential sources. For further statistical analysis the mean model outcome of each observation was used as replicate. Hence, with three trees per cluster and four replications per cluster type (Fagus, Tilia, Fraxinus and mixed) there were 12 replicates for single species clusters and 4 for the mixed clusters. Following the discussion with statistical experts we decided to apply a "linear mixed effects model" (model lme from the nlme library implemented in R) to compare fractional water uptake jointly among species and the depth intervals of the entire uptake profile. The model output suggests that the significant effects are soil depth and the depth by species interaction in both single species and the mixed clusters. A post-hoc HSD-test was then conducted for the model output (see page 5423, line 17-23).

Figure 5: a. The same questions about the details of the ANOVA above apply here. b. Distributions of source proportions from mixing models like IsoSource are often quite strongly skewed, making symmetric confidence intervals like

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mean +/- SD not very appropriate. Empirical confidence limits (e.g., 5th %ile to 95th %ile) may be better. c. The means do not seem to always sum to 1. For example, for Fraxinus, the 0.3-0.5 m horizon contributes 0.4, the 0.5-0.7 m horizon contributes >0.7, and the shallower horizons contribute <0.1 each, but more than 0. This appears to sum to at least 1.1.

For statistical analyses the mean of all feasible source contribution estimates (mean model outcome) for a given soil layer was used as provided by the model. We agree, the outcome of the mixing model remains only an approximation. We included a paragraph in the method section addressing this issue (see page 5422, line 10-13).

Technical comments:

1. Page 2 line 23: Insert “rather” between “roughness,” and “than”.

Done accordingly (page 5416, line 25)

2. Page 7 line 22: Change “uncertainty level” to “tolerance” since that is the specific parameter term used in IsoSource.

Done accordingly (page 5422, line 10)

3. Page 12 line 3: Change “futher” to “further”.

Done accordingly (page 5427, line 22)

4. Page 17 line 25: The Phillips Gregg (2003) paper was published in Oecologia, not Ecosystem Ecology.

Done accordingly (page 5432, line 19)

5. Page 27 line 2: I would suggest changing “Shannon index” to “Shannon biodiversity index” to clarify the type of data to which the Shannon index was applied.

Done accordingly (page 5434, line 2)

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