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Interactive comment on "Depolymerization and mineralization – investigating N availability by a novel ^{15}N tracing model" *by* Louise C. Andresen et al.

Anonymous Referee #1

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In the manuscript "Deploymerization and mineralization – investigating N availability by a novel 15N tracing model" by Louise C. Andresen et al. the authors compare an analytical approach and a numerical model based on experimental 15N tracing to estimate soil N dynamics. The main N processes discussed are gross rates of protein depolymerization and NH4 mineralization. The authors also calculate microbial nitrogen uses efficiency from the results of the analytical and the numerical approach. The presented manuscript is clearly written, structured well and the results are presented in a meaningful manner. The approach to compare an analytical method and a numerical tracing model is also of great interest. However there are two major concerns at this point: 1. In contrast to the repeatedly mentioned studies by Schimel and Bennett and

Mooshammer et al., the authors of this study do not include microbial biomass as an explicit pool in their model. While neither Schimel and Bennett nor Mooshammer et al. use a numerical model, the concept of a microbial pool can change the interpretation of the results. Without knowing the details of the presented model in this study, I assume that the results might look very different when a microbial pool with a specific turnover time and dynamics is included. This might specifically question the importance and the interpretation of the differences between the two investigated soils regarding the Mson flux in the Ntrace model (see detailed comments). At the very least the authors should discuss how an explicit microbial pool might change their model. 2. The much more severe problem with the experimental setup is the enormous input of amino acids. Although the authors argue that Ntrace is better suited to deal with this surplus of free amino acids, by integrating over a longer time than the analytical methods, the exact opposite could be argued. By introducing this flush of amino acids, peptidases could be inhibited by their potential product and peptidase expression could be down-regulated due to the surplus of amino acids, which would result in lower depolymerization rates later in the incubation. This could be an explanation for the low depolimerization rates derived from Ntrace compared to the analytical approach. It is also not clear to me why the authors chose these high amino acid amendments. The method described by Wanek et al. was developed for leaf litter, which can be expected to have much higher FAA concentrations. Also Wanek et al. mention twice in their paper that FAA concentrations should be determined beforehand and only 25% of the amino acid pool should be amended to avoid the effects the authors of this study discuss. The drastic change in the amino acid pool by these high amendments might thus bias both the analytical and the numerical approach. Neither of the approaches might thus represent realistic N dynamics in the investigated soils. I am afraid the only way to overcome this problem and to sustain the current line of argumentation is to repeat the experiment with lower amendments of amino acids.

Specific comments: Abstract: Page 1, lines 16-17: while stated here and repeatedly throughout the manuscript, that the numerical approach is superior to the analytical

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method, later in the manuscript (page 8, lines 12-13) it is argued that the numerical model is valid because it produces results for Dson that are similar to the analytical approach. This is contradictory. Introduction: The Introduction should be concluded with concrete, testable hypotheses, similar to those presented in the abstract. These hypotheses should be revisited in the discussion. Page 2, lines 23-24: Please state some of these obvious limitations. Page 2 Lines 26-27: This sentence should be in past tense.

Methods: Page 7, lines 4-5: The underlying concept of a microbial N pool in Mooshammer et al. however also allows for the interpretation that any changes in these dynamics might be caused by changes in the microbial N pool. This interpretation is not possible with the Ntrace model.

Results and discussion: Page 7, lines 16-17: As mentioned above, the integration over a longer time does however not consider any physiological adaptations of the microbial community to the amino acid flush. Page 7, lines 17-19 and Page 9, lines 25-31: This problem has been addressed by Wanek et al., who suggested to determine the FAA pool and only amend 25 % of that pool. Page 7, line 24: Since both of the presented approaches have their limitations and are biased by the large amount of amended amino acids, I think it is not possible to tell which method is more realistic. It would be interesting to compare the numeric model with the analytical approach and lower amino acid amendments. This might also help to evaluate if it is necessary to include an explicit microbial N pool in models for soil N dynamics. Page 8, lines 5-6: This might again be caused by the large amounts of amended amino acids. Page 8, Lines 21-26: When microbes are included in the interpretation of these results, it could also mean, that the addition of amino acids led to an increased uptake of amino acids but also an increased release of excess N as NH4 from the microbial biomass. Together with a potential down-regulation of peptidase activity this could be the reason for the observed results. Page9,lines 1-6: In this model the Mson pathway is relevant, when changes in the NH4 pool cannot fully be described by the changes in the FAA pool.

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If a microbial pool was included in the model, changes in this pool, which should be situated between FAA and NH4 could be responsible for the observed dynamics. Page 10, lines 12-14: Especially for the amino acid pool dilution method a longer incubation time of 6h might result in problems with recycled labelled N. Figures: Please stat for all figures that include error bars what these are and what the sample size was. Figure 1: The second formula for NUE should have IFAA+MFAA in the denominator.

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