We want to thank the reviewers for their valuable, encouraging and constructive comments.

They both were mostly concerned with lack of clarity in details of the model description. With the improved description, these issues have been better explained. Moreover, we extended our analysis by including another strategy in the comparison (EnzMax of Averill 2014), and we looked at the consequences of not accounting for the soil-microbial loop, i.e. the mineralization of microbial turnover, in the model calibration.

In the following we answer point by point to their comments (set in monospace blue font).

Reviewer #1: This was a very interesting and detailed modeling study that integrated several ideas on resource allocation by microorganisms to extracellular enzymes that optimize growth and concomitant impacts on decomposition. The rationale for this study, selection of alternative models, and choice of basic simulation scenarios were logical and easy to follow. I had difficulties understanding some of the modeling details (some comments follow), so that clearer explanations would be helpful in some places.

In the revised manuscript, the explanation of modelling details has been improved and extended. At the same time we aimed at keeping it as concise in order to focus on the general ideas.

The general patterns of alternative model behaviors seemed reasonable, and explanations were largely insightful in both qualitative and semi-quantitative ways. Results demonstrated the utility of a composite microbial community approach rather than explicitly modeling multiple distinct groups (guilds?), i.e., capturing functional shifts in community behavior rather than changing compositional structure (and subsequent function) of the community. However, much of the output is speculative or blackboxed with limited validation, for example, were there any comparative observations of enzyme activities? Of course, the substrate pools were complex, containing both C and N resources, complicating the interpretation of empirical enzyme data.

Comparison of model results to observations of stoichiometry of enzyme activities from literature are discussed in a dedicated section 4.3 (LL 389ffXX). We did not perform own measurements of variability of stoichiometry of enzyme activities.

I'm not sure that the Match strategy was used appropriately; it was apparently based on the EEZY model by Moorhead et al. (2012) and wasn't devised to operate as a decomposition model. It simply estimated the impacts of varying substrate qualities and microbial characteristics on enzyme allocation to balance microbial stoichiometry. The analytical solution to that problem (alpha) was its objective, and as Averill (2014) noted, doesn't maximize microbial growth or biomass. This limits its responsiveness in several dimensions, e.g., in the substrate-feedback experiment (lines 288-290). It will generate the smallest biomass of the strategies under any scenario in which C is limiting. Moreover, it doesn't consider inorganic N sources … did the authors revise the allocation routine in EEZY to compensate? See also Section 4.1: The Match strategy is not devised to address this issue. Averill (2014) addressed this limitation, noting that a microbial strategy emphasizing biomass

growth would generate different enzyme allocations. In essence, Averill's model has a similar rationale to SEAM in that maximized growth return per investment in enzymes albeit also using the EEZY solution to estimate alpha when C was not limiting. In any case, the current manuscript should reference the work by Averill (2014) as very similar in key respects

We adopted the EEZY approach has computing the partitioning coefficient alpha by equation the stoichiometry of decomposition fluxes and microbial demands. However, we extended it 1) to account for N immobilization and a 2) to separate between microbial efficiency into first, an anabolic microbial efficiency accounting for growth respiration and second, a maintenance component. See eq. (3) LL174ff XX. The analytical equation for the partitioning coefficient alpha, therefore, became more complicated but was still possible.  
In the revised manuscript, we incorporated the model of the partitioning coefficient alpha by Averill 2014 as another strategy in the comparison. Averill (2014) came to similar conclusions as our study regarding the importance of growth versus substrate use efficiencies. However, our study greatly extends Averill’s work by accounting for feedbacks to substrate pools, and for exchange with inorganic N pools. There is also a strong model difference: Averill’s decomposition rate of a substrate was completely independent of size of the substrate pool. See a new discussion paragraph at LL 424 XX.

The hypothetical grazing impacts currently appear to be largely a post hoc rationalization for otherwise unknown turnover processes. If model behavior is substantially affected by this turnover, which appears to be true, then it deserves more attention, perhaps worthy of sensitivity analysis.

We agree that little is known about turnover processes. However, the rational was original in model development and not post-hoc but was based on the microbial-loop hypothesis.   
We re-calibrated the model to the intensive pasture site with setting mineralization of microbial turnover to 0 and got a very similar fit and the same conclusions for the simulation scenarios. The change in the turnover mineralization parameter was compensated by changing the fit of the potential turnover of the residues pool (kR) from 1/25years to 1/19 years and by a slightly lower anabolic microbial efficiency (eps). Hence, the fit to this pasture data is not sensitive to the turnover mineralization parameter.   
As long as the other parameters are unconstrained, the model behavior is not substantially affected, and the parameter could be omitted. Nevertheless, to our understanding this process is reasonable and may become important when discussion the sensitivity of the microbial efficiency to temperature or moisture.

Minor issues:

I had trouble following the author's references to appendix materials. For example, the reference to A.7 on line 154 … where is A.7? Readers should not have to wonder.

We hope that the reviewer received a proper version. The equation A.7 (subequations a and b) was correctly given in appendix A , line 621ff on page 39 (in revised line 681XX).

Equation 3, if I interpret it correctly, applies the anabolic microbial efficiency (epsilon) as a constant for both substrates, which assumption should be mentioned because this is often variable across substrate qualities. Also, why is the maintenance respiration included within the parentheses of the numerator, so that epsilon applies to it?

In the revised manuscript, we mention that epsilon, here, is constant across substrates (LL XX). Because we model only two quite abstract substrates, it would be difficult to justify a differing epsilon.  
We defined epsilon as the “anabolic” microbial efficiency accounting of how much carbon needs to be respired for synthesizing one unit of carbon in biomass. Hence it accounts for growth respiration but not for maintenance respiration and needs to be applied only after subtracting the maintenance expenditures. We clarified this in the new manuscript at lines 174 XX.

Equation 4a seems to omit epsilon. If so, then why? Note that I am not R-savvy, so I am relying on others to review the code.  
Equation 4a, of course, indirectly depends on all most model parameters. However, it denotes only the quantities that are changing over the course of the simulation. Epsilon, here the anabolic microbial efficiency, is a fixed model parameter. Contrary, the apparent carbon use efficiency (maybe also denoted by epsilon in some studies) is an emergent property in SEAM, which changes amongst others with stoichiometry of the substrates.

The Revenue strategy applies to the currently limiting nutrient, so either alpha C or N, is determined a priori. This is a clever way of scaling investments, but assumes that potential microbial growth could be reduced in the drive for greater efficiency. Is this reasonable?

Growth can be reduced for greater efficiency with the match strategy. We agree with the reviewer, that it is not a reasonable strategy. The revenue strategy, therefore, assumes that the microbes strive for growth instead of C or N use efficiency. Efficiency, here, means that enzymes yield the greatest return per investment. Growth is reduced by both, lower return or by higher required investments. Note that optimality is thought from a community perspective, which takes into account sharing the returns of enzyme investments with other microbes (new Appendix B).

If the turnover rate coefficient for enzymes is constant across enzymes (equations 6a,b), efficiency is actually a function of enzyme pool sizes rather than turnovers.

I assume that the reviewer used the term “efficiency” as a replacement for “revenue” or “partitioning coefficient”. If the turnover rate is equal in both cases, indeed, it cancels in equations for both terms, and the revenue only depends on current substrate pools and enzyme pools. Conceptually, however, the investment into production of enzymes, i.e. flux instead of a pool, is what is relevant for the microbes. The presented equations can be applied in also in conditions where one has better knowledge on maybe differing turnover of enzymes degrading C-rich versus N rich compounds.

Line 188: Is the reference to table A.5 supposed to be A.1?

We had decided to provide an additional compact manuscript version formatted for the SOIL journal, because it provided a better overview of the text and placed figures near their occurrences in the text. The reference to Table A.5 in the SBB-formatted manuscript correctly referenced the first table in Appendix A.5 on page 44. Unfortunately, in the compact Soil-formatted manuscript it was both referenced and named as A.1. We apologize for this confusion.

Line 211: Was this maximum turnover 10 times per day as opposed to Table A.1 which has 2-5 per year? That's rapid, but maybe plausible if it represents a tiny fraction of SOC stocks. So what's the thinking?

In typical priming experiment (discusses in section of Line 211), usually, the soil is amended with a very labile substrate that is usually much faster degraded than litter input to a soil. This is also thought true for root exudates. Therefore the priming experiment used a different value for the labile pool than the other experiments. The manuscript notes “used parameter values given in Table A.5 unless stated otherwise” (L XX 186).

Section 2.5. By this point in the manuscript, the reason for such a calibration study is difficult to remember. Perhaps mentioning that the Perveen et al. (2014) study provides a validation of your model would be useful to remind readers.

We revised the introduction of the section 2.5 (L255 XX). “To test the capacity of SEAM to simulate …”

Line 316: Does this statement mean that the microbial N-use strategy simply made more N available for plant uptake?

In effect yes. There was a transfer from SOM R pool to living biomass to microbial turnover that was mineralized. The turnover of the increased microbial biomass returned more N to the mineral N pool than taken by immobilization flux of living microbes. The increased mineral N pool helped plants to grow. We put this explanation to the revised manuscript (LL 359 “helped plants”).

A stronger explanation and/or justification for using only the Revenue strategy for pasture simulations to compare to the Laqueuille data would be reasonable.

Thanks for this suggestion. See line (L 257 XX “tackled only”).

Incorporating SEAM as a direct, interactive component of ESMs seems unlikely, given the differences in scale. However, results could be used to generate simpler, phenomenological links between key drivers and microbial responses that could be included more empirically, such as the recent work by Xu et al. (2014). A recent rationale for this type of approach was published by Todd-Brown et al. (2012) that might be worth mentioning.

We agree with the reviewer. While this study is at higher level of microbial detail than the study of Xu, it is an important step of abstraction compared to models that account for changes in microbial community by explicitly simulating several guilds. We extended the discussion in lines XX .

Suggested references:

Averill 2014 Divergence in plant and microbial allocation strategies explains continental patterns in microbial allocation and biogeochemical fluxes. Ecology Letters 17:1202-1210. doi: 10.1111/ele.12324

Todd-Brown et al. 2012. A framework for representing microbial decomposition in coupled climate models. Biogeochemistry 109:19-33. Doi 10.1007/s10533-011-9635-6

Xu, X, et al. 2014. Substrate and environmental controls on microbial assimilation of soil organic carbon: a framework for Earth system models. Ecology Letters 15:547-555. doi:10.1111ele. 12254

Thanks for making us aware of the Averill study. We added the strategy to the comparison among allocation strategies with the artificial experiments. And thanks for reminding us of the value of the Todd-Brown and the Xu studies that we cite in the revised manuscript in appropriate context (e.g XX and XX).

Reviewer #2: The authors of the manuscript "Adaptation of microbial resource allocation affects modeled long term soil organic matter and nutrient cycling" present a very interesting modelling approach which integrates microbial regulation of C and N turnover. This approach is designed for application in large-scale models, which is of particular importance if we want to reduce the uncertainty in model predictions of land atmosphere feedbacks. The manuscript, therefore, fits well into the scope of SBB, is well written, sound and will be of big interest for modelers, but also for soil ecologists who are interested in microbial regulation of soil processes and how this regulation could be integrated into modelling. Still, I have some issues which need revision before the manuscript could be accepted for publication in SBB. Most of the issues are related to model assumptions and explanation of the modeling approach. Improvements of these issues would foster the impact and

understandability of this paper, particularly in the soil ecologists community.

Thank you for these encouraging comments. In the revised manuscript we improved and extended the explanation of modelling assumptions.

Specific comments

L 39-51 As I understand it, the two alternatives here are similar to the alternatives 2 and 3 in the paragraph L 10-26. I was first confused about which alternative you are talking about in your objectives. I, therefore, suggest avoidung this redundancy.

These are, actually, two separate issues. L 10-26 talked about strategies how microbes deal with stoichiometrically imbalanced food, whereas L 39-51 talked about how to represent microbial diversity in models.

Figure 1 What is the difference between fluxes and mass fluxes? From my point of view DOM and CO2 are also pools (here they are presented as disks and therefore as fluxes). Later on you talk about the DOM pool. Why do the arrows with white arrow heads have dashed line, do they really represent N fluxes? TVR is not explained (turnover?). Please comment on this and change accordingly if necessary.

Indeed, one could consider DOM and CO2 as pools. However, for CO2 we are not primarily interested in integrated respiration flux in the model (We would only use it during model data integration with incubations where cumulative CO2 production has been measured). The DOM pool has a very high turnover rate and is very fast in a quasi-steady state with its inputs and outputs. Therefore, we assumed that the inputs equal outputs (see also: Wutzler T & Reichstein M (2013) Biogeosciences, 10, 2089-2103). By this we can compute the size of the DOM pool but do not need to integrate it separately over time. In the revised manuscript this is explained better at lines 117ff XX.   
The control fluxes are not N mass fluxes. We adapted the Fig 1 by changing to solid lines. Microbial turnover (tvr) is now explained in the figure legend.

L 94-95 How could additional N be mineralized if the C/N ratio of the decomposition flux is equal and fixed to the C/N ratio of the respective pool? What is then the source of additional N? Please comment on this and better explain already here.

The C/N ratio of the DOM derives from its different inputs. It may hay have a lower C/N ratio than what is required by microbial biomass (including necessary growth and maintenance respiration). Then the microbial biomass is substrate C-limited and cannot make use of the additional N. This N is then mineralized. We added a paragraph for this concept to the introduction (LL12ff).

Table 1 inorganic N input is about 230 kg N ha-1, which would be an intensively fertilized arable soil. In unfertilized grassland or a forest soil atmospheric deposition would be about 20-40 kg N ha-1. Maybe it becomes clearer in you examples, but I suggest explaining this high value here to avoid confusion.

We noted the these N inputs are unually high at lines 268ff XX.

L 108 Do you mean "inorganic nitrogen pool"?

Yes, we corrected this typo.

L 124 I have some problems with the term "organic N limitation" and the hierarchy of limitations you are presenting here. It suggests that all microbes first take up organic N and if this is not available in sufficient amounts they take up mineral N. However, there are extracellular enzymes which release ammonia from organic compounds, which only makes sense if the microbes producing these enzymes prefer taking up mineral nitrogen. Therefore, introducing these terms is o.k. for the purpose of modelling in this study, but the introduction as general terms may induce more confusion than clarity. I, therefore, suggest restricting these terms to this study and presenting them as a new, general terminology.

We made clear, that these terms are modelling concepts (LL 145XX). Note that SEAM also assumes gross mineralization and immobilization fluxes also when microbes are not organic-N limited (PAR scheme in Manzoni 2008). The concept organic N limitation applies, when the net imbalance flux to the mineral pool (mineralization – immobilization) is negative.

L 171-172 If the investment is equal to the turnover, how could the microbes then change the size of the enzyme pool? What exactly is meant with "...ensure that...is proportional to its revenue"? Does this mean that enzyme synthesis is not further increased if the ratio return:investment is decreasing with additional enzymes? I suggest that you better explain the revenue strategy, particularly because this seems to be the most promising model alternative.

Beware of confusing the computation of the revenues and the change in allocation. The revenue is computed on the current status quo, i.e. the current enzyme levels. This revenue computation involves the “investment is equal to the turnover”. If the revenue for a specific type of enzymes is higher than that of others, microbes will adapt and re-allocate to more production of this type of enzyme. We extended the explanation at lines 206ff XX.

Equation 6a and b I don't understand why E\*S is included in these equations. I thought that the return comes from the decomposition of the pools L and R and not from the decomposition of the enzyme pool E\*S? Please explain.

Decomposition is a flux that needs to be computed on current state variables, i.e. pools. The decomposition of pools L and R depends on current enzyme levels E\*S and E\*R (eq. A.4). Therefore, they are required in this equation. We referenced the decomposition and turnover equation from appendix in the text explaining the revenue equations (LL 215XX).

L 199-200/Table A5 How could it be that the C/N ratio of the microbial biomass is higher than that of the microbial residues, if the C/N ratio of a decomposition flux is the same as the C/N ratio of the decomposed pool? Is it because microbial residues are mixed in the pool R with inactive enzymes which have a low C/N ratio? Still, the assumed C/N ratio of 11 for the microbial biomass is very high and is usually between 6 and 8. Please explain this high value for microbial C/N ratios. Why is the C/N ratio of the litter calibrated if this could easily be measured? Please explain.

L 201 Name of this experiment differs from Table 4.

Yes, C/N ratio of residue pool is lower as microbial turnover, because enzyme turnover (with lower C/N ratio) contributes to it. Indeed, the used C/N ratio of biomass is quite high but well inside the range of observed values. It was taken as reported from the study of Perveen et al. 2014 for the Laqueuille site, where it was set to the measured C/N ratio of SOM. For consistency, we used the same value also in the prototypical examples. In all presented experiments, except the VarN incubation the C/N ratio of the residue pool emerged from the simulations, and was always lower than the C/N ratio of the microbial biomass, although not as low as in the VarN incubation, where we wanted to demonstrate shift between two contrasting substrates.  
C/N ratio of the litter was prescribed to measured values. Only the potential turnover rate of Litter, k\_L, was calibrated.  
We updated the experiment name in Table 4.

L 205-211 What is the temporal resolution of the models and how are the yearly litter inputs distributed across the year? It surely makes a difference if the 30gC are evenly distributed across lets say 365 days and the addition of 50gC is on one of these 365 days or if the temporal resolution is a year and the yearly input simply increases from 30gC to 80gC in one of the 10 years. Providing this information would help the reader to better understand the simulation experiments and their outcomes.

The model has no intrinsic time step but is formulated as a differential equation. It will not resolve dynamics below daily scale, because we assumed steady state of the DOM pool. Furthermore, the discretization of the quality spectrum to just one litter pool with a single turnover time impacts high time resolution where very labile litter dominates. In the priming experiment (described on lines 205-211) the litter was added in a single step at the beginning of the experiment (now noted on LL 258 XX). For the CO2 fertilization and the grassland studies, the litter input rate was not changed throughout the year (now noted on LL 266 XX). For the grassland calibration, changing to a variable litter input probably would influence the exact results of the calibration a bit. However, the introduced uncertainty or bias by wrong assumptions of this time distribution and exact times of measurements of the other properties is potentially larger than the simplifying assumption of constant litter input rate. For the long-term dynamics of the CO2 fertilization experiment we think that distributing the litter across the year would only add some fluctuation to the pools but not change (but rather obscure) the overall behavior.

L 210 Was this assumption valid for the additional litter input or also for the yearly litter input of 30? Please add this information.

Yes. We did simulated only one litter pool. Hence the assumption of 10day potential turnover time of the rhizodeposition litter was also applied to the other inputs. This is now explicitly noted on lines 256 XX). Note that this fast turnover is only achieved with saturating enzyme levels and is usually lower.

L 212-213 continuous litter C input is also expected under ambient CO2 concentrations if you include rhizodeposition as litter input. But the size of the input will be increased. Please clarify.

The word “increased” continuous C input got lost in the old manuscript and is now added back.

L 232 In table 1 a literature value for N input is given. Why is this value taken from the literature if you used a well investigated ecosystem where the N inputs are surely known? For initial litter and SOM pools you used observed values (L 238). Please explain.

The used literature reports the values at the investigated ecosystem.

L 262 What is meant with balanced growth if the microbial biomass was decreasing? Please explain.

Balanced growth is defined as the stoichiometry of the food matching the stoichiometric demands of the feeder (Sterner and Elser, 2002). This is not related to growing biomass. If the stoichiometry of the food is matching, but there is only little food, turnover of feeders will be larger than its growth and biomass is decreasing despite balanced growth. We added a paragraph to the introduction (LL 12ff XX).

L 265 What is meant with "did not need stoichiometric imbalance fluxes"?

I guess this is related to the upper left panel of figure 3, which is poorly explained (What is Min lmb?). If positive values mean that there is a net flow from organic sources into the mineral N pool, than there is an imbalance flow, isn't it? It is not "needed", but it is there. At C/N ratios higher than ~27 this flux turns into negative values. They stay above -0.1, but is this relevant or not? The wording seems to be not accurate enough in this case and I suggest that you better describe what exactly you are meaning. Otherwise it is sometime hard to follow your ideas.

We introduced the terms balanced growth and imbalance fluxes now with more explanation in the introduction (LL 12 XX) and reworded L 265 to “resulted in non-positive imbalance fluxes. This means, that microbes could utilize all food taken up for productive expenditures.” (LL 316 XX).   
We extended the figure caption of figure 3 to explain the N imbalance flux.

L 286-270 This sentence is poorly connected to the paragraph. What is the reasoning of this sentence since you did not simulate the performance of different microbes? I suggest deleting this sentence.

Assuming the reviewer meat L 268: For some readers it would not be clear, that less biomass means an inferior strategy. Because, this is one important conclusion, we added a paragraph in the discussion (L 436ff XX)and reference it at this part of the text.

L 279 What is meant with "composition flux"? Please explain.

We corrected the typo to “decomposition flux”.

L 301-302 In figure 5 it does not become clear, which N mineralization flux is meant. Here you write about the mineralization flux derived from microbial turnover, but there is also the N mineralization flux from the turnover of the DOM pool. This has to be clearly indicated in figure 5.

We updated the facet labels in Fig 5.

L 322 I wonder why the model was only compared with the measurements of one year. In Perveen et al 2014 it seems that there data available for at least five years. A good fit to a time series of measurements would increase the confidence into your model. Please comment on this.

Table 4 of Perveen et al 2014 that was used for calibration does not report several years. Rather it reports rates, i.e. changes over time. The impression of four years probably is implied by Fig. 2 in Pervee et al 2014 that shows several years of simulation. Fig 8 of this paper also show 5 years, but presents an observation as a point with confidence interval instead of a vertical line.

Figure 8 dR is positive meaning that SOM is build up. Doesn't this mean that the grassland is not in equilibrium? How the change rate of the SOM was exactly measured in the field? Please explain.

Yes it is not in equilibrium. The dataset is a challenge to SOM models, because it reports a continued SOM accumulation. The explanation in this study and in Perveen et al 2014 is related to the high N inputs. The SOM buildup was estimated by ecosystem C-balance. For details see Perveen et al 2014 and references therein: “Mean annual compartment sizes and ecosystem fluxes were quantified in the intensive pasture over the period 2003–2008 and by considering a soil depth of 0–60 cm […] Soil C stock (Cs) was estimated from total C and bulk density. Net carbon flux to soil (dCs/dt) was estimated by the eddy covariance technique combined with specific greenhouse gas measurements such as methane emissions (Klumpp et al., 2011).”

L 375 I suggest being carefully with the statement that such microbes would be outcompeted. You did no simulation including both strategies at the same time. Allsion 2005 showed in theoretical simulations that even microbes without any enzyme production could coexist with enzyme producing microbes.

It is correct that we did not check competition and must be careful. We rephrased to “We argue that producing less biomass means an inferior strategy, because slower growing microbes have a competitive disadvantage to faster growing microbes that have otherwise same properties such as maintenance requirements.” (L 436ff XX) Note that Allison 2005 assigns lower expenditures to cheaters who can therefore grow faster on a given (already depolymerized) substrate. Hence, we think that Allison 2005 supports our argument.

L 382 "..the the..."

We corrected the typo.

L 400 "N-degrading enzymes" is misleading here, because you simulated the enzyme pool degrading the N-rich pool R, but you did not explicitly simulated N-degrading enzymes.

Always referring to the correct “N-rich R pool degrading enzymes” would quite complicate the reading of the manuscript. We introduced our sloppy abbreviated usage of the terms at lines 98 XX.

L 500-501 Although the best argument would be the comparison with measured data from long-term field experiments.

We completely agree. This might be a follow up study and I discussing with Clair Chenu.

L 566 Is this really the case? It is probably a fair assumption for modelling the whole community. However, considering several subpopulations, we have to assume that each subpopulation tries to optimize biomass production, which could be on the expense of the growth of other subpopulations resulting in a lower overall microbial biomass.

We phrased “Community development can be assumed to” (L 645 XX).