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 organic matter-microbial loop, i.e. the mineralization of microbial necromass, 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 (see below) has been improved and extended. At the same time we aimed at keeping it as concise as possible 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 the dedicated section 4.3 (LL 464): “While only low variation in stoichiometry of N-degrading versus C-degrading enzymatic activity is observed across biomes \citep{Sinsabaugh09}, microcosm studies detect short-term changes of enzyme activities with N fertilization \citep{Kumar16}, but their observations differ between different kinds of N-degrading enzymes. Hence, the evidence is mixed. SEAM also predicts accelerated turnover of the residue pool associated with increased enzyme activity of N-degrading enzymes after increased inputs of litter C in relation to litter N. Such patterns are observed at field scale at Duke forest, where \citet{Phillips11} found an increased activity of extracellular enzymes involved in breakdown of organic N associated with accelerated SOM turnover after increased root exudation with elevated \chem{CO\_2}. In an artificial root exudation experiments at the same site, \citet{Drake13} found an increase of N degrading NAG enzyme activity with C-only inputs and a shift from oxidative towards hydrolytic enzymes decomposing low molecular weight (lmw) components with C+N inputs. Assuming that the lmw-components have higher C/N ratios, this observed shift is in line with SEAM predictions.”  
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

Yes, the ideas originate from the EEZY model and we acknowledge this explicitly (“We therefore extended the EEZY model to explore different consequences of alternative enzyme allocation strategies” (L 71 ) or “The adaptation of enzyme allocation was recently formalized using the second strategy by the conceptual EEZY model \citep{Moorhead12} and further developed using the EnzMax allocation strategy by \citep{Averill14}” (L 61).   
In addition, we explain what the conceptual developments from this starting point are. We extended the basic stoichiometric equation of the match strategy 1) to account for N immobilization and 2) to separate between microbial efficiency into the two components: an anabolic microbial efficiency accounting for growth respiration and second, and a maintenance component (See eq. (3) LL172ff ). The analytical solution of the stoichiometry 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 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 445.

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 too little is known about microbial turnover processes. However, the rationale of microbial-loop hypothesis was integral part of model development and not a post-hoc rationalization.   
Generally, the model predictions are sensitive to modifications of the single parameter mineralization of microbial turnover (1-eps\_tvr) , but can be compensated in most cases by adjusting the combination of microbial efficiency (eps), microbial turnover (tau) and the decomposition of the residue pool (kR).  
We re-calibrated the model for 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 mineralization of microbial turnover was compensated by changing the fit of the potential turnover of the residues pool (kR) from 1/25 years-1 to 1/19 years-1 and by a slightly lower anabolic microbial efficiency (eps). Hence, the fit to this pasture with high N inputs data was not sensitive to the mineralization of microbial turnover.   
In addition, we performed a basic sensitivity analysis based on the CO2-Fertilization simulation experiment and discussed this in new appendix C (L 767 ).   
The question whether SEAM is sensitive to the parameterization of microbial turnover can be answered from three perspectives. First, SEAM predictions are sensitive to changes in the eps\_tvr parameter only. Second, SEAM predictions are not as sensitive, if changes in eps\_tvr can be compensated by changes in other parameters. Third, SEAM is sensitive to including microbial turnover in the process descriptions for simulating reasonable dynamics for shifts between C and N limitation.

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.

The equation A.7 (subequations a and b) was correctly given in appendix A, line 621ff on page 39 (in revised line 701). Note that the formatting guidelines demand to not prefix a reference to an equation with “eq.”, which may cause confusion with references to sections.

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 700). Because we model only two quite abstract substrates, it would be difficult to justify a differing efficiency.  
We defined epsilon as the “anabolic” microbial efficiency accounting for 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 179 .

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 almost all model parameters. However, it denotes only the quantities that are changing over the course of the simulation. The anabolic microbial efficiency, here, 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, and overflow respiration.

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 that differs from a single microbe (new Appendix B L 743).

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 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 provide the revised version now only with SBB-formatted style.

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 229).

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 (L268 ). “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 373 “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. We paraphrased “The intensive pasture calibration was tackled only with the Revenue strategy, because the Match and the EnzMax strategies had already shown inadequate for scenarios including feedbacks to substrate pools during in the Substrate-feedback experiment. The control case of the Fixed strategy did not allow for adaptation of microbial enzyme allocation.” (L 271 ).

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 the outlook (L650ff ).

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 L 11 and L650ff).

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 (see below).

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. The revised manuscript tries to make this clearer by starting the paragraphs with “Decomposers can - in principle - adjust in three different ways when faced with imbalances” (L 22 ) and “At least two alternatives exist to represent the effects of microbial diversity at the ecosystem scale.” (L 52).

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 116ff .   
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.

I hope to understand the critique. The C/N ratio of the DOM derives from its different inputs. It may 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 entire available N in the combined decomposition fluxes, i.e DOM. This “additional” N (that cannot be used for biosynthesis) is then mineralized. We added a paragraph for this concept to the introduction (L14ff ,” stoichiometric imbalance”).

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 that these N inputs are unusually high at lines 281ff “The N-balance of the fertilised pasture …”.

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 143). Note that SEAM also assumes gross mineralization and immobilization fluxes when microbes are not organic-N limited (PAR scheme in Manzoni 2008). The concept of organic N limitation applies only, 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 term “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 209ff “The revenue is computed on …”.

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 the appendix in the text explaining the revenue equations (LL 212 “The return is the current …”).

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 the conceptual residue pool is lower than microbial turnover, because enzyme turnover (with lower C/N ratio) contributes to it. When measuring SOM pools one measures a mixture of microbial residues and litter debris, whose C/N ratio is usually wider than the C/N ratio of the decomposers. The used C/N ratio of biomass used in this study is 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 and visualize shifts 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 quasi 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 (which was described in referred former lines 205-211) the litter was added in a single step at the beginning of the experiment (now noted on LL 257 “simulated by a single pulse”). For the CO2 fertilization and the grassland studies, the litter input rate was not changed throughout the year (now noted on LL 266 “assumed constant across the year”). 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 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.

The second alternative is true. We simulated only one litter pool. Hence the assumption of 10 day potential turnover time of the rhizodeposition litter was also applied to the other inputs. This is now explicitly noted on lines 255 “both pulse and continuous”. Note that this fast turnover is only achieved with saturating enzyme levels and the realized turnover rate 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 (Table 4 ,”continued input of increased litter C”).

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 does report 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. For instance, 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 (L 14 “elemental composition between food and the requirement of …”).

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 14 ) and rephrased to “resulted in non-positive imbalance fluxes, i.e. no mineralization of excess N or overflow respiration of excess C. This means, that microbes could utilize all food taken up for productive expenditures.” (L 314 ).   
We extended the figure caption of figure 3 to explain the N imbalance flux “lowest mineralization fluxes (negative or small N mineralization and at the same time no C overflow respiration)”.

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 meant 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 438f “competetive”) 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 Perveen 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 for this accumulation is related to the high N inputs to the system. The SOM buildup was estimated by the 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 true 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 the same properties such as maintenance requirements.” (L 438ff ) Note that Allison 2005 assigns lower expenditures to cheaters who can therefore grow faster on a given (already depolymerized) substrate. Hence, we argue 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 now consistently refer to the bit more complicated but correct “N-rich R-pool degrading enzymes”, e.g. L 481 .

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 am already in contact with investigators of long-term field experiments.

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 “We could assume that community development maximizes biomass production. Such an assumption can be used to compute..” (L 646 ).