

Reviewer 1

We thank the reviewer for the insightful comments. We have addressed the comments one by one in the following section. *Reviewer comments are written in red and italics.* Our responses are written in blue.

I am intrigued by the approach to estimate the ‘methane exchange velocity’ ... Methane exchange velocity: The authors do not give any information about the assumptions that go in equation

- We have improved the explanation of the derivation of methane exchange velocity. We have also changed our term to “methane transfer velocity”, more commonly reported in the literature. To hold the strict definition of the concept of methane transfer velocity, we have eliminated the assumption of negligible atmospheric methane concentrations, and included the equilibrium concentration of methane in the pore-water according to Henry’s Law (See Eq 3). Since the equilibrium concentrations are virtually constant, the relationships presented previously are maintained and the values for methane transfer velocity adjusted slightly.
- We have included this change in the main text:

By combining pore-water concentration at the surface with the associated fluxes, estimations of methane transfer velocity were obtained as in previous studies in forested ponds and lakes (Holgerson et al., 2017; Schilder et al., 2016; Wanninkhof, 2014). Through this approach, the flux at the water-air interface can be calculated using the bulk formulation:

$$F_{CH_4} = k (C_w - C_{eq}) \quad \text{Eq. (1)}$$

Where F_{CH_4} is the diffusive CH_4 flux ($\text{mol m}^{-2} \text{s}^{-1}$), k is the CH_4 transfer velocity (m s^{-1}), C_w is the concentration of methane in the porewater at the surface (mol m^{-3}), and C_{eq} is the concentration of CH_4 in equilibrium with the atmosphere (mol m^{-3}). C_{eq} can be calculated by multiplying the mixing ratio of CH_4 in the atmosphere (s) by the atmospheric pressure (P , in MPa) and by Henry’s Law coefficient of equilibrium for CH_4 (K_H) of $0.067 \text{ m}^3 \text{ MPa mol}^{-1}$ as in eq. 2:

$$C_{eq} = s P / K_H \quad \text{Eq. (2)}$$

C_{eq} was calculated first with a constant mixing ratio (2 ppm) and second with the value of the average of the initial concentrations of the chamber measurements associated with each flux calculation. These two methods produced nearly identical results in C_{eq} given the much higher values of C_w . The constant mixing ratio was chosen for the rest of the analyses given the uncertainty associated with the initial concentration from the chambers. In the case of our peat bog, C_w can be calculated by multiplying pore-water concentration ($[CH_4]$) by peat porosity, Φ (see ancillary measurements below):

$$C_w = [CH_4] \Phi \quad \text{Eq. (3)}$$

Where $[CH_4]$ was calculated in the top stratigraphic layer of the peat (ca. 10 cm). Finally, methane transfer velocity can be calculated as:

$$k = (F_{CH_4}) / (C_w - C_{eq}) \quad \text{Eq. (4)}$$

It seems that a) ebullition and plant-mediated transport have to be excluded and b) the peat structure and water/air content has to be the same for all sites (i.e. diffusivity is identical as well). Thus, by default, the only remaining factor to explain fluxes is the net methane production (i.e. microbial processes). And that is indeed, what the authors find. Only after reading the whole manuscript, it becomes clear that assumption a) is fulfilled (although the high fluxes in summer 2018 are unexplained).

- We have now included text in the abstract to make this point clearer from the beginning. The high fluxes in summer 2018 remain unexplained since unfortunately microbial data was not available for the hotspots in the Tamarack north transect. This is the text included in the abstract:
 - Ebullition and plant-mediated transport were not important sources of CH_4 , and the peat structure and porosity were similar across the different zones of the bog. We thus conclude that differences in CH_4 transfer velocities, and thus fluxes, are driven by the ratio of the relative abundance of methanogens to methanotrophs close to the bog surface.

Microbial populations and activity: The author correctly state, that their analysis only indicates the presence of microbes, not their activity (i.e. gene expression, as was done in the Lee 2014 paper, which is cited. here). However, this makes the interpretation of Fig. 8 more difficult. I would like to point out FSL-S: Fig. 7 shows that at FSL-S, very close to the top soil, methanotrophs dominate. But for the relation with 'methane exchange velocity', only top soil ratio of methanogens/methanotrophs is used (Fig. 8) – where FSL with both high ratio of methanogens/methanotrophs and high (but variable) methane exchange velocity is clearly needed for the correlation. Given these assumptions, I wonder whether the monthly porewater concentration profiles (Fig. 6 only shows the overall mean profiles) contain more information about production, oxidation and diffusive transport (i.e. the shape of the profile). If so, this can be used as further support of microbial activity as most important driver.

- Thank you for this interesting observation. You are right that the high abundance of methanotrophs in the top profile of the FSL-S location can be confusing. Some points to clarify about this data: The first section contains the first stratigraphic layer of the core going from ~0-6 cm, while the following section encompasses a core section from ~7-16 cm. We focus on the top section because, first, this is the section where the atmospheric exchange occurs. Secondly, this section should be the most active one for both methanogens and methanotrophs (Angle, 2017) since it includes the more aerobic acrotelm as well as less well-humified peat (greater labile C availability). Both are likely to favor greater microbial abundance. The distinction between the two sections was one based on peat stratigraphy so these two layers should be distinct in many respects. We

hypothesize that the high abundance of methanotrophs may be correlated to higher root density transporting more oxygen to this section but we did not test this hypothesis. We previously calculated relationships between microbial activity and the porewater concentrations for the whole peat profile but did not find the same patterns as just considering the top profile, likely because methane consumption mainly occurs in the upper layers. We have begun to interpret the growth of the concentration profile with time to say something about production and consumption zones within the profile, but such analysis was not within the scope of this study.

- We have included this clarification in the methods section for calculation of CH_4 exchange velocity

Minor comments

Considering the high fluxes in summer 2018, I wonder whether the starting point may already have been high (i.e. an ebullition event early on)? Could be helpful to include the graph in the Appendix

- We have clarified in the manuscript that this is not a part of an ebullition event and have included in the appendix the raw data from the chamber to show the steady increase in concentration:

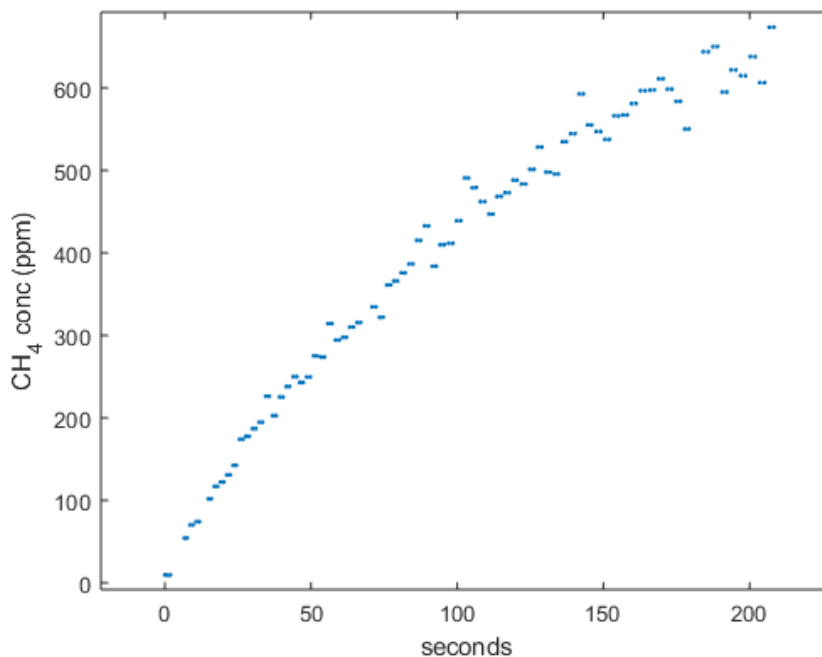


Fig S3. Chamber measurement during the September hotspot in the Tam-N location. Note the steady increase in concentration that indicates that ebullition was not the reason for the high magnitude of the flux at this location.

I understand why and how you do the up-scaling of chamber fluxes. However, there really is no way of evaluating that number and given the temporal variability there is the possibility that the large integrated flux is due to that (but temperature as discussed is possible as well)

- We understand the limitations of this scaling approach. We provide cautious interpretation regarding how this estimate can be used to study other peat bogs. We have, however, decided to keep this estimate to provide an alternative approach to evaluate the heterogeneity in peat bogs through bottom-up measurements.

Page 17: Is there an explanation for the result, that the instantaneous water table does not have a significant effect, but the one a month earlier has?

- The average water level data throughout 30 days prior to the flux measurement had a significant effect in CH₄ fluxes. This was an interesting result and the hypothesis behind it is that the methanogens are responding to average conditions in previous weeks. In particular, we hypothesize that it takes several weeks for methanogens to acclimate to new water levels after the water level has been raised. Therefore, they do not respond instantaneously to changes in water level. From an ecological perspective, it is known that the relative abundance of organisms integrates variation in abiotic drivers over a pre-measurement time window. The length of that window will be a function of the life history and longevity of the organism. Therefore, community composition lags behind that environmental change.
- We have clarified the phrasing in page 17 and included this analysis in the discussion of water level dynamics in section 4.3

Given the importance of the methane exchange velocity, I would move the figure from the appendix up to the main text and also discuss its error (from the figure it looks like that only for FSL and TMW the estimate is significant?).

- We have moved the graph to the main text and now focus exclusively on those measurements of methane exchange velocity that are specific to the analyses of microbiological data rather than including measurements from other locations/months that were not used in the microbiological analysis.
- We have noted that the error in this bar plot is not being transferred to the relationship in Fig 8, since we have decided to plot the individual points rather than the average presented in this figure.