

Supporting Information for “Modeled microbial dynamics explain the apparent temperature-sensitivity of wetland methane emissions”

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1. Figures S1 to S10

References

- Juottonen, H., Tuittila, E.-S., Juutinen, S., Fritze, H., & Yrjälä, K. (2008). Seasonality of rdna-and rrna-derived archaeal communities and methanogenic potential in a boreal mire. *The ISME Journal*, 2(11), 1157–1168.
- van Hulzen, J., Segers, R., van Bodegom, P., & Leffelaar, P. (1999). Temperature effects on soil methane production: an explanation for observed variability. *Soil Biology and Biochemistry*, 31(14), 1919 - 1929. Retrieved from <http://www.sciencedirect>
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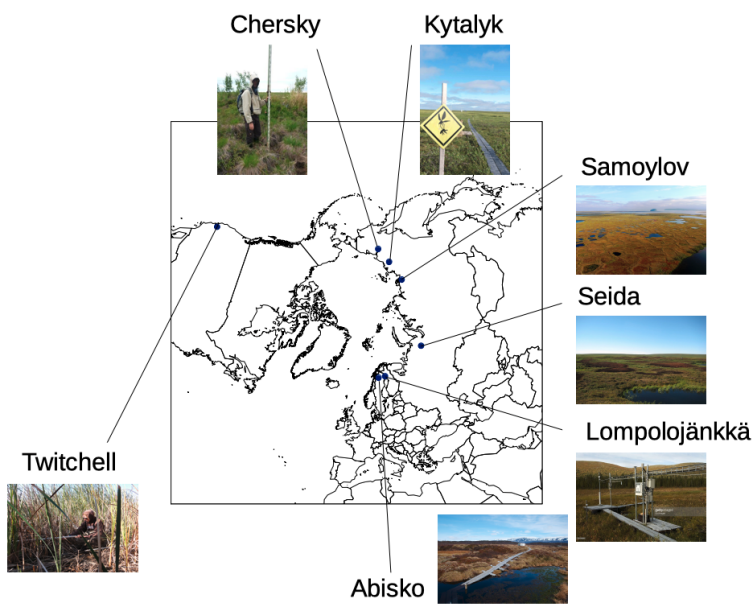
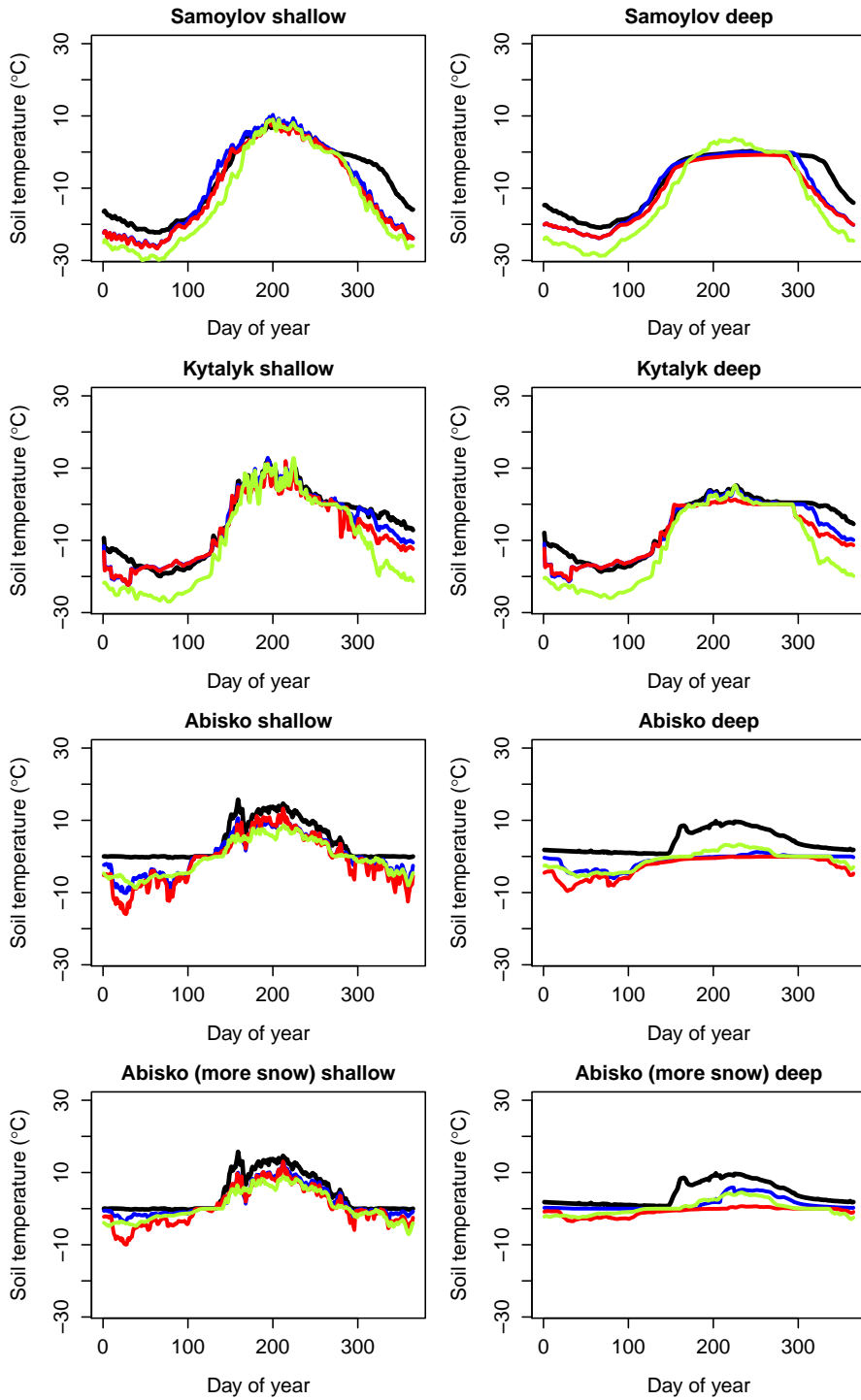


Figure S1. Map of sites.



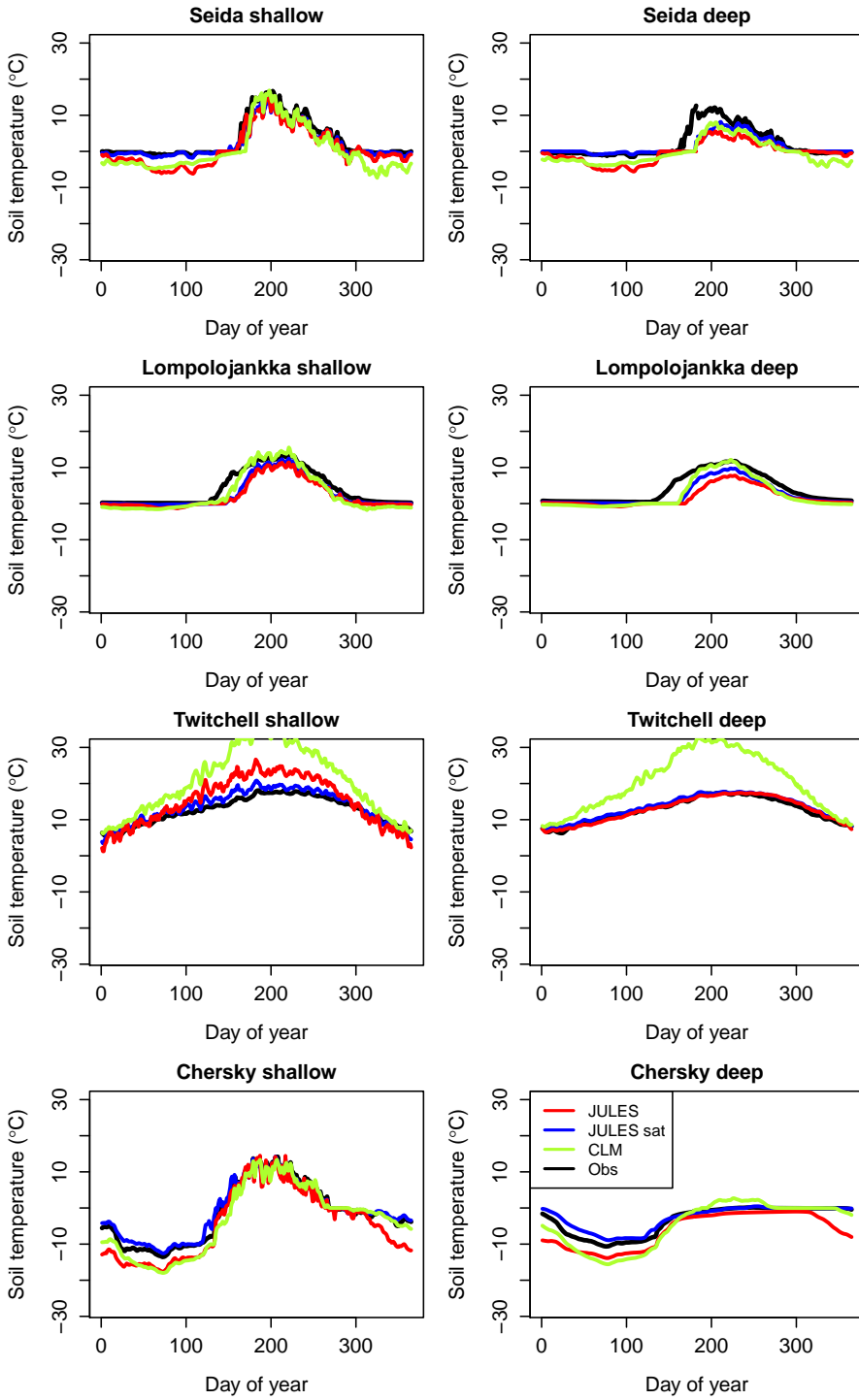


Figure S2. Soil temperature seasonal cycles in upper soil layer (between 1-7cm depth) and deeper soil (between 25-50cm depth), in CLM, JULES (standard version and setting soils to saturated), and observations.

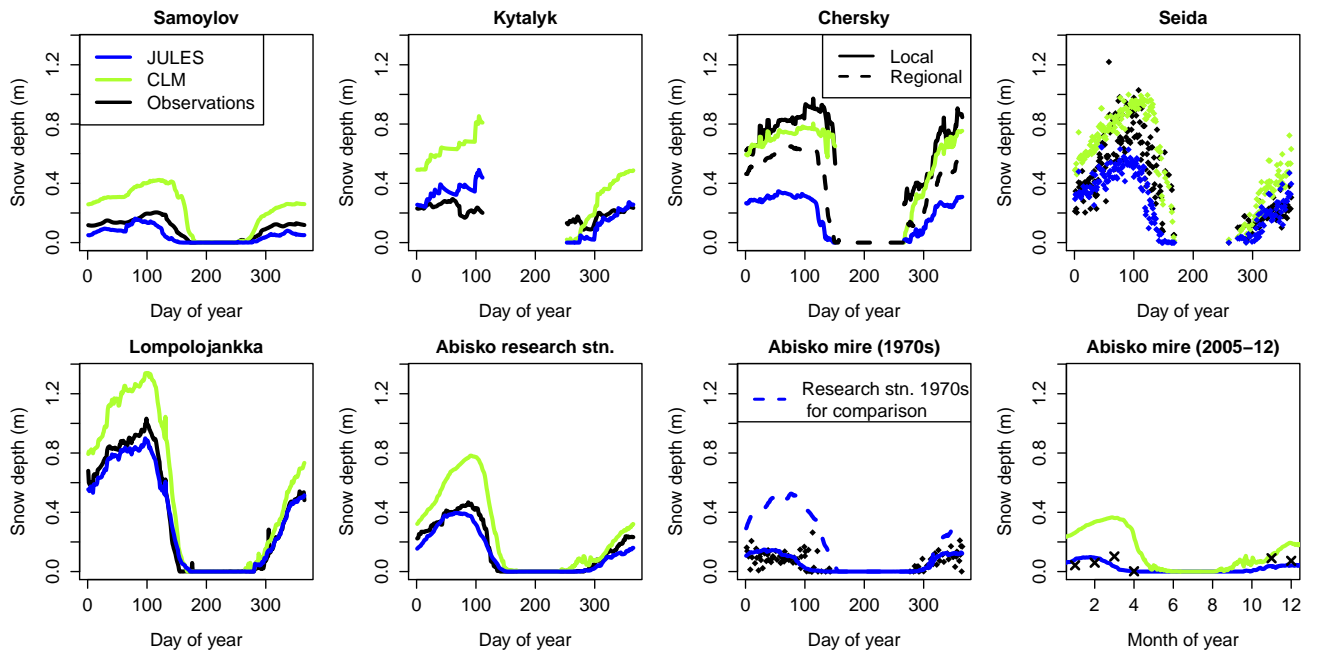


Figure S3. Snow depth seasonal cycle simulated by JULES and CLM, compared with observations.

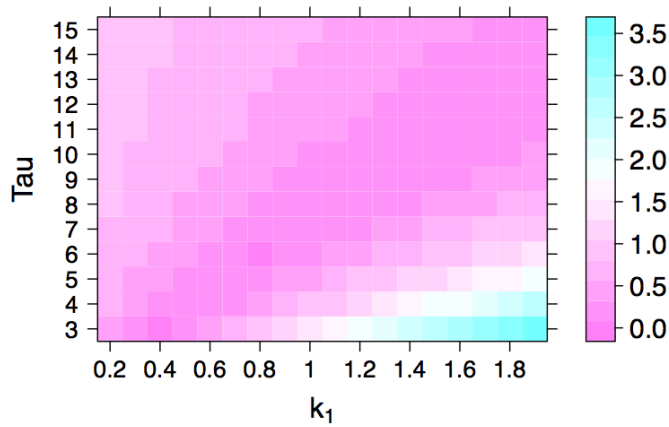


Figure S4. RMSE for optimisation of k_1 and τ described in Section 2.2.4 of main text. Optimal values are $\tau = 6.5$ and $k_1 = 0.925$.

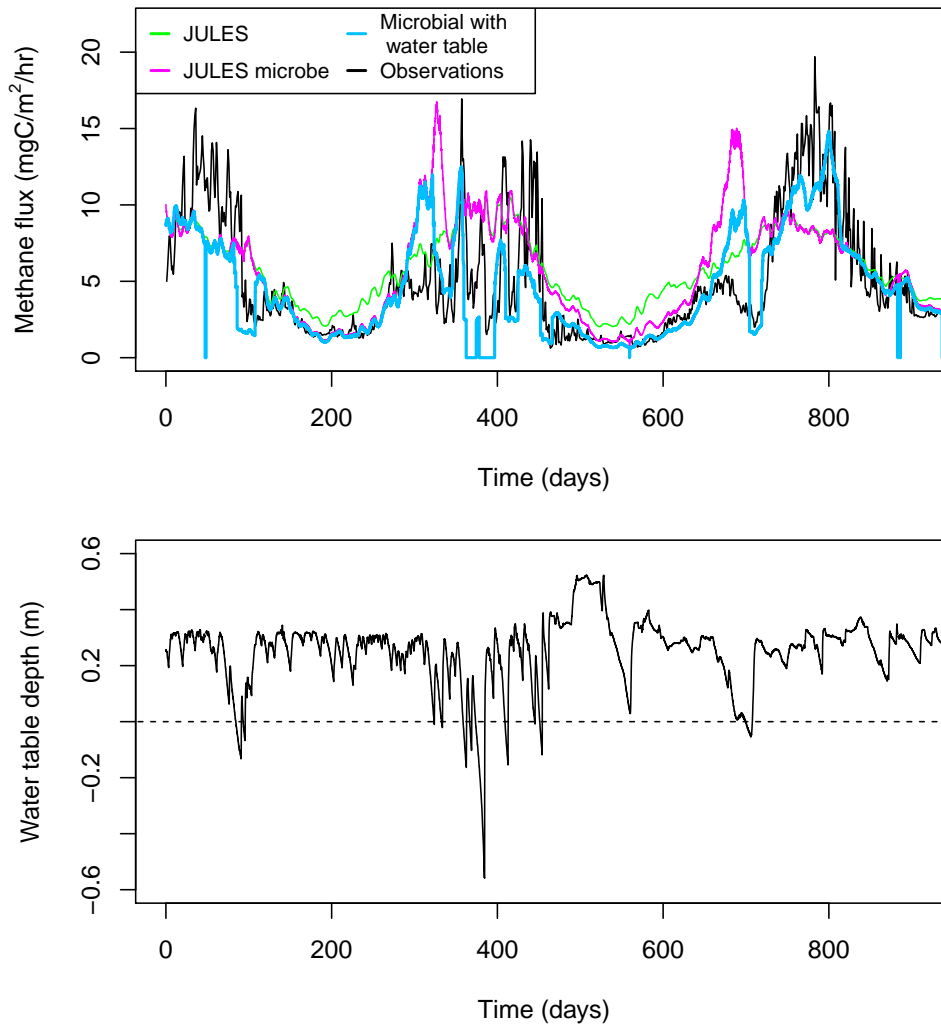


Figure S5. Including water table impact on microbial dynamics at Twitchell: Upper panel shows methane emissions from observations and from the different model versions. Lower panel shows the observed water table depth which drives the ‘microbial with water table’ model in the top panel.

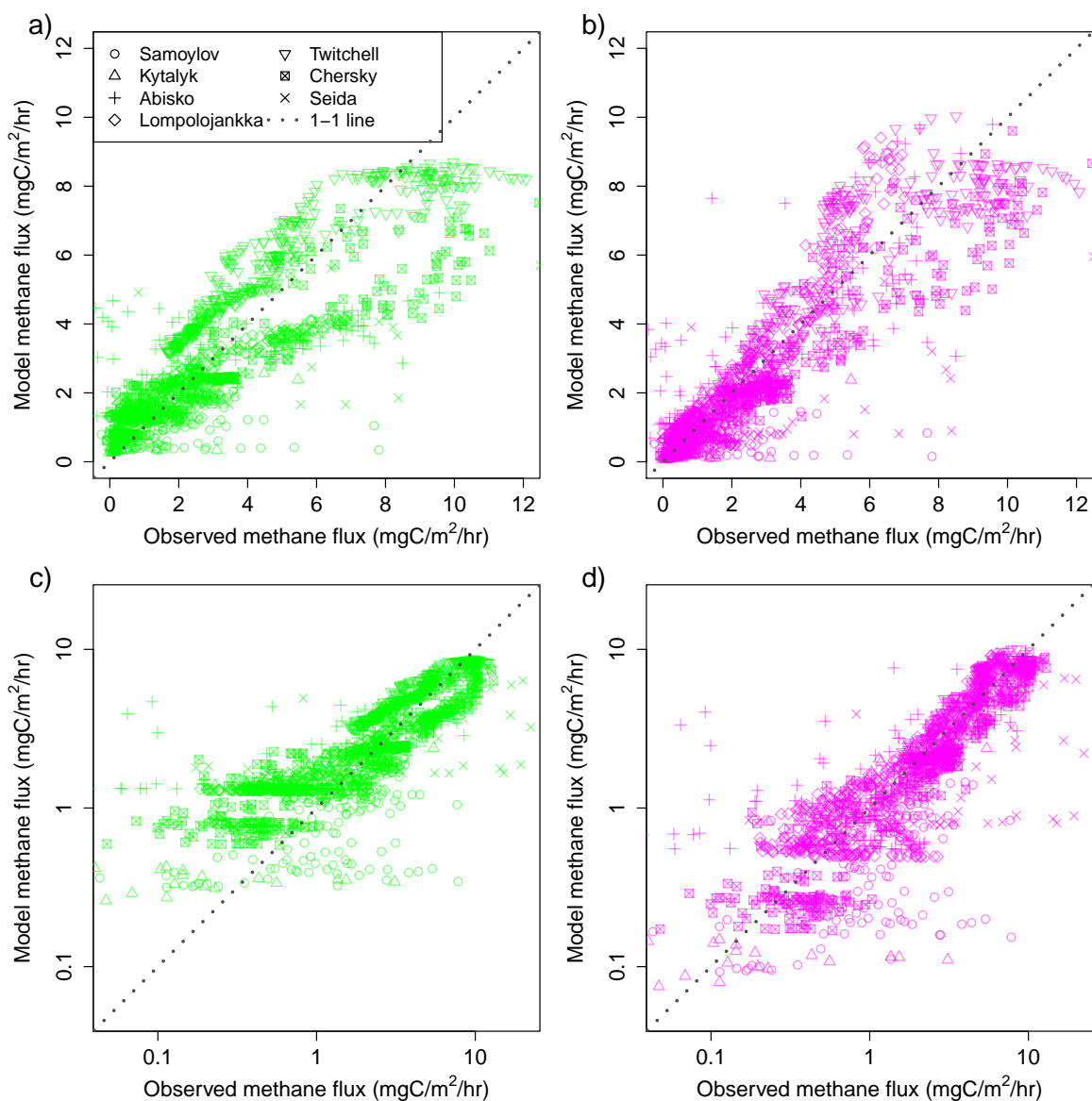


Figure S6. This shows the same data as on Figure 7 in the main manuscript, but with observations plotted on the x-axes and modelled values on the y-axes. a) and c) show the non-microbial methane scheme from JULES and b) and d) show the JULES-microbe scheme. They are plotted both on linear axes (a,b) and log axes (c,d). Note that the methane schemes are forced with observed soil carbon and soil temperature in these plots.

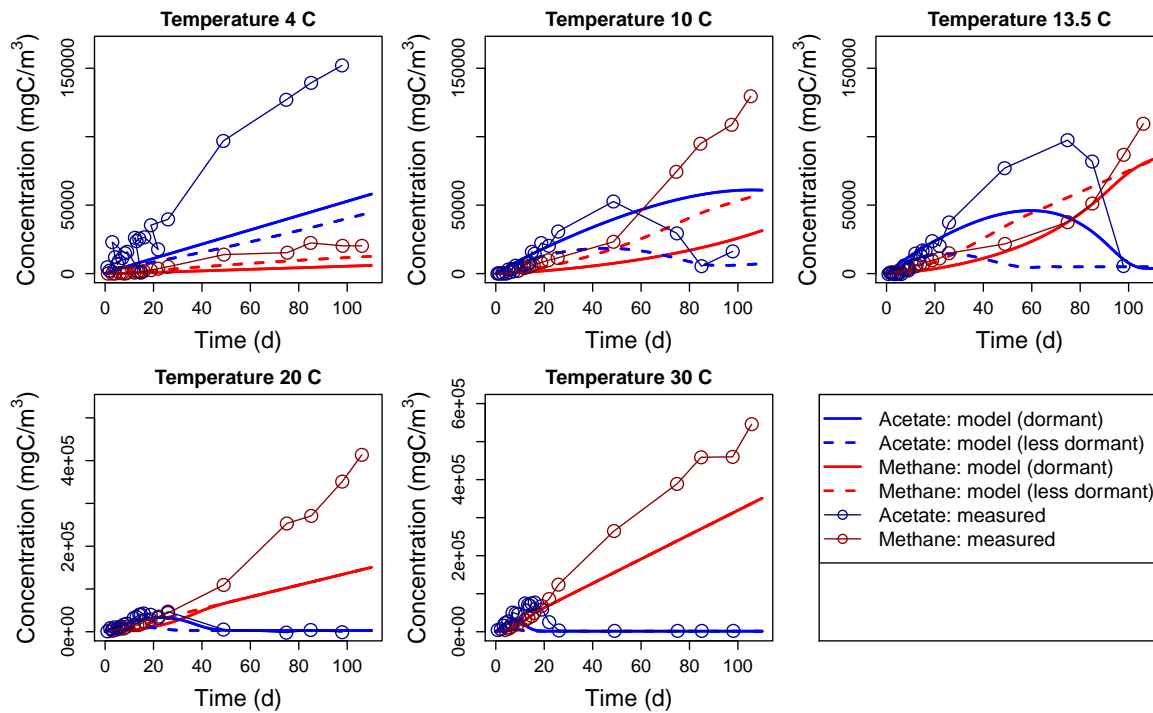


Figure S7. Recreating incubation study from van Hulzen et al. (1999) with JULES-microbe. Comparison of dissolved substrate concentration and methane production simulated by the microbial methane scheme with incubation study by van Hulzen et al. (1999). Modelled results include two different starting values of microbial biomass activity level, and the initial biomass was set to the mean biomass for the equivalent soil carbon density in global JULES-microbe simulation. Soil carbon was not recorded in the study, however soils are peat so carbon was taken as 50% of soil density, which is reasonable for pure peat.

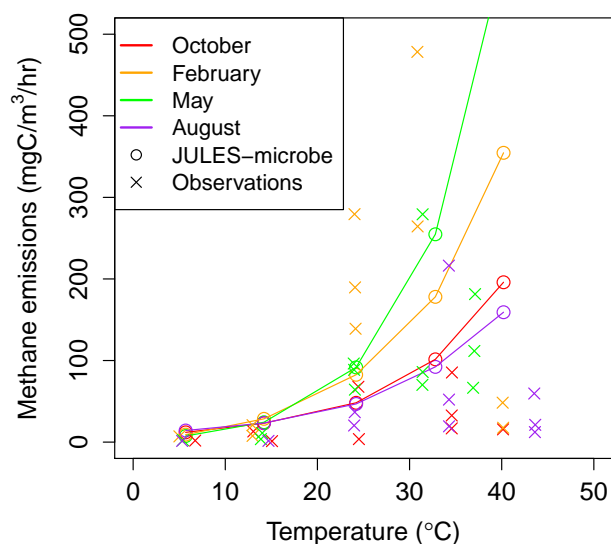


Figure S8. Recreation of incubation study included in Juottonen et al. (2008) (Figure 4) using the JULES-microbe model with prescribed observed soil temperature. Their site was Siikaneva in Finland, and for the model we used Lompolojankka which is the closest site to Siikaneva of the sites that were simulated. The same sample dates were used for initial substrate, biomass and activity level (mean values across the years simulated) and the closest soil layer to the sample depth (20cm).

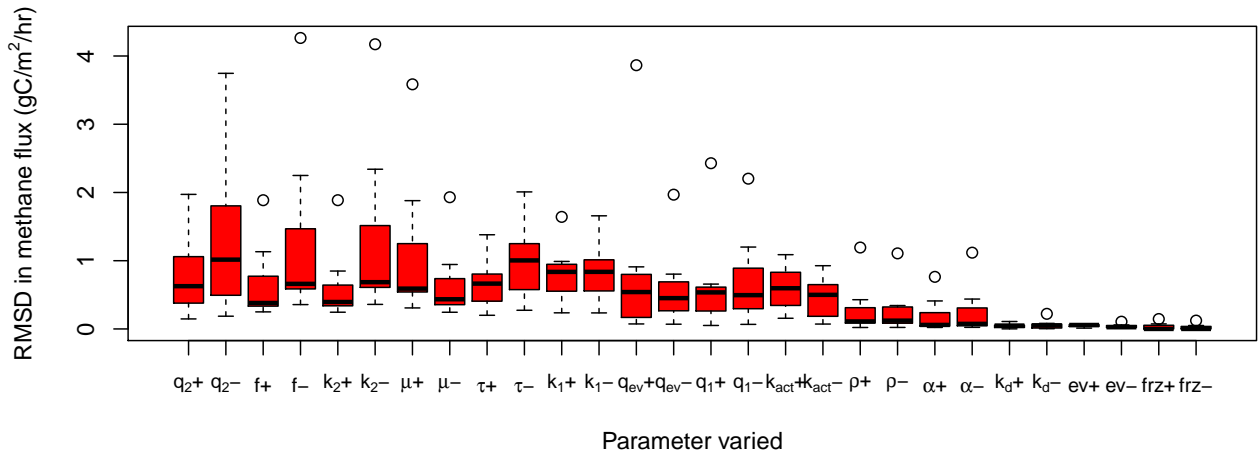


Figure S9. Sensitivity analysis in which all parameters in the JULES-microbe model were varied by $\pm 25\%$ and the root mean squared difference (RMSD) compared with the default simulation was calculated. k_{act} represented the k_2 parameter in the reactivation/dormancy equation (Equation A5), which we varied separately in order to separate the reactivation/dormancy rate from the overall respiration rate for the purpose of the sensitivity test. All of the other parameters are defined in Table A1 in the main manuscript.

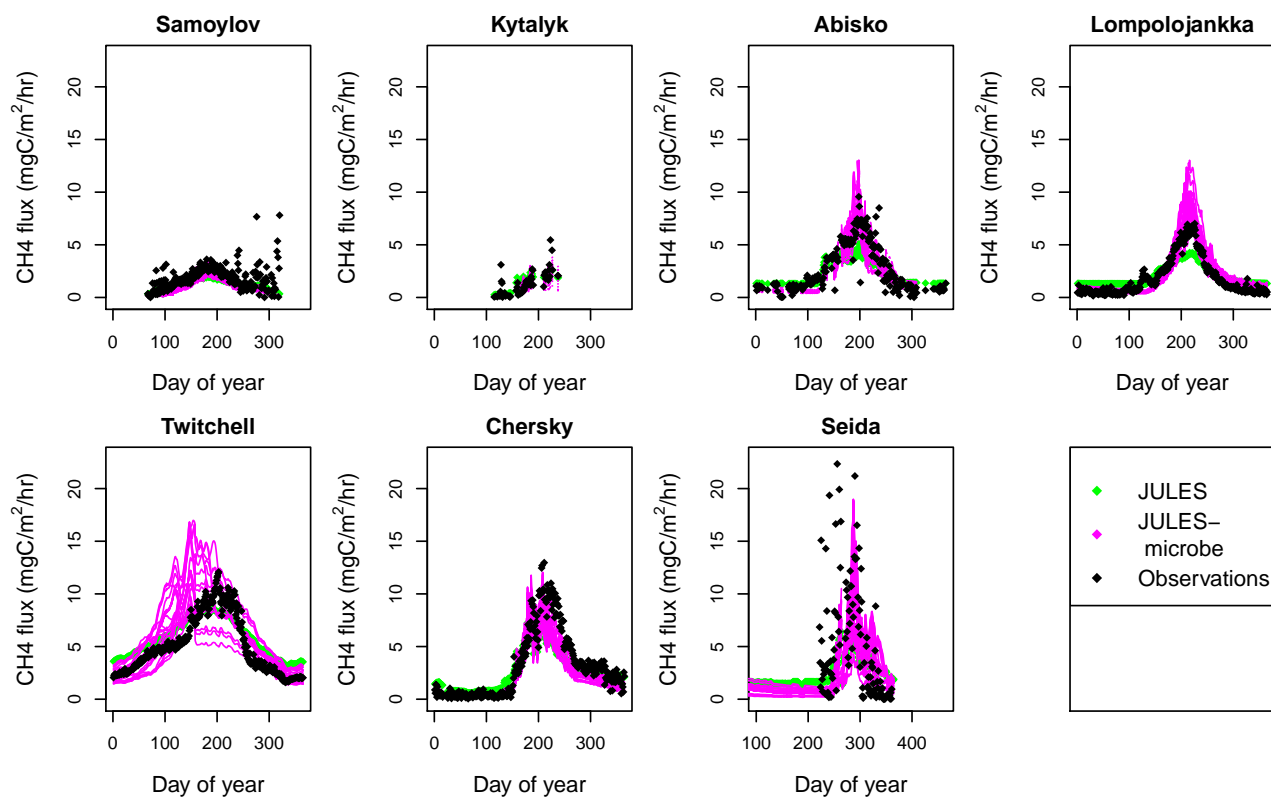


Figure S10. This plot explicitly shows all of the simulations performed in the sensitivity study shown in Figure S9. The sites are all plotted on the same axes for comparability. Observations and JULES results are also included for comparison.