

The influence of soil communities on the temperature sensitivity of soil respiration

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Accepted Version

Johnston, A. S. A. and Sibly, R. M. (2018) The influence of soil communities on the temperature sensitivity of soil respiration. *Nature Ecology & Evolution*, 2. pp. 1597-1602. ISSN 2397-334X doi: <https://doi.org/10.1038/s41559-018-0648-6> Available at <https://centaur.reading.ac.uk/78849/>

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To link to this article DOI: <http://dx.doi.org/10.1038/s41559-018-0648-6>

Publisher: Nature

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1 **The influence of soil communities on the temperature sensitivity of soil respiration**

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8

9 **Soil respiration represents a major carbon flux between terrestrial ecosystems and the**
10 **atmosphere, and is expected to accelerate under climate warming. Despite its importance in**
11 **climate change forecasts, however, our understanding of the effects of temperature on soil**
12 **respiration (R_S) is incomplete. Using a metabolic ecology approach we link soil biota**
13 **metabolism, community composition and heterotrophic activity, to predict R_S rates across**
14 **five biomes. We find that accounting for the ecological mechanisms underpinning**
15 **decomposition processes predicts climatological R_S variations observed in an independent**
16 **dataset ($n = 312$). The importance of community composition is evident because without it R_S**
17 **is substantially underestimated. With increasing temperature, we predict a latitudinal**
18 **increase in R_S temperature sensitivity, with Q_{10} values ranging between 2.33 ± 0.01 in tropical**
19 **forests to 2.72 ± 0.03 in tundra. This global trend has been widely observed, but has not**
20 **previously been linked to soil communities.**

21

22 Soils store the majority of Earth's terrestrial carbon, and so play a crucial role in the direction and
23 magnitude of future climate changes¹. However, the influence of ongoing climate change on the soil
24 carbon sink is a major area of uncertainty²⁻⁴. Temperature-associated increases in the global soil
25 CO₂ flux (soil respiration, R_S) has led to the supposition that global warming will drive a positive soil-
26 climate feedback^{5,6}. Of particular concern is the potential long-term vulnerability of large soil C
27 stocks at high latitudes⁷. However, our incomplete understanding of the temperature – R_S
28 relationship limits constrained forecasts of terrestrial carbon fluxes in the future⁸.

29

30 The temperature sensitivity of R_S across ecosystems is a key determinant of the soil-climate
31 feedback, but it is difficult to quantify due to the many confounding factors that affect soil metabolic
32 rates^{2,9}. For instance, Q_{10} values (the proportional increase in R_S with a 10 °C increase in
33 temperature) are highly variable across different vegetation types and climates^{2,10}. Nevertheless,
34 Earth system models (ESMs) typically assume a globally constant temperature sensitivity by
35 incorporating fixed Q_{10} values of around 2 (that is, R_S rates double with an increase in temperature
36 of 10 °C)^{11,12}. Thus, while there is a growing consensus that future warming will enhance R_S rates,
37 how the response will vary across climatic regions and soil characteristics is not well

38 established^{13,14}. Here, we propose that a better understanding of R_S temperature sensitivity can be
39 gained by accounting for the various organisms that live in the soil.

40

41 Soil respiration is the biotic conversion of organic C to CO₂ by all of the organisms (heterotrophs:
42 soil microbes and fauna, and autotrophs: plant roots and their mycorrhizal symbionts) that live in the
43 soil. Thus, R_S rates are the product of the body sizes, metabolic rates, abundances and community
44 composition of soil-inhabiting organisms¹⁵⁻¹⁸. Because individual metabolic rates exhibit varying
45 temperature sensitivities¹⁹, we would also expect R_S responses to increasing temperatures to
46 fluctuate according to soil community composition. However, empirical quantification of soil biota
47 contributions to R_S at large spatio-temporal scales is complicated by the vast biodiversity and
48 complexity of soil systems²⁰.

49

50 In this study, we use a model derived from metabolic theory²¹ to integrate soil biota metabolism,
51 community composition and heterotrophic activity in R_S estimates across biomes. The model
52 accounts for the way in which metabolic rates vary with temperature and body size between soil
53 community groups. We then extrapolate to heterotrophic respiration (R_H) rates by accounting for the
54 abundance of soil biota across tundra, boreal forest, temperate forest, temperate grassland and
55 tropical forest soils. By quantifying the contribution of R_H to R_S , using an R_H fraction (H_F) which
56 accounts for autotrophs (plant roots and their symbiotic mycorrhizae) not modelled here, we predict
57 R_S across biomes and mean annual temperature (MAT) ranges. To test the hypothesis that soil
58 community traits strongly influence R_S temperature sensitivities, we compare models that do or do
59 not account for metabolic variation of soil biota. To test how predictive our approach is, we make a
60 further comparison with a classical linear regression fitted to the R_S data. Finally, we increase study-
61 specific MAT's by 10 °C to compare Q₁₀ estimates with available data across the five biomes, and
62 discuss how these compare to those Q₁₀'s used in ESMs and observed in long-term field
63 experiments.

64

65 **Results**

66

67 ***Metabolic ecology of soil communities***

68 Metabolism underpins fundamental mechanisms of organism-environment interactions, and sets the
69 basis for linking individual to ecosystem processes²². To investigate the temperature sensitivities of
70 metabolism for diverse soil communities, we compiled a metabolic dataset for fourteen soil biota
71 groups (bacteria, protozoa, nematode, collembola, enchytraeidae, acari, ant, beetle, isopod,
72 centipede, spider, termite, millipede, earthworm). The dataset ($n = 3768$) covers nearly 15 orders of
73 magnitude in body mass (M) and temperatures (T) between -2 and 40 °C. In the first instance, the

74 metabolic dataset was fitted to the linear form of the metabolic scaling equation without accounting
 75 for variations in metabolic parameters between soil biota (termed the 'general' model herein):

76

$$77 \quad \ln(B) = \ln(B_0) + a \ln(M) - E/kT \quad (1)$$

78

79 where B is standard metabolic rate (J hr^{-1}), B_0 is a taxon-specific normalisation constant, a
 80 represents the allometric scaling exponent which usually takes a value close to $\frac{3}{4}$, E is the
 81 activation energy (eV), k is Boltzmann's constant ($8.62 \times 10^{-5} \text{ eV K}^{-1}$) and T is experimental
 82 temperature (K)²¹. General model (Equation (1)) regression analysis yields an allometric exponent,
 83 a , of 0.81 (± 0.002) and activation energy, E , of 0.67 (± 0.01) (Supplementary Table 1). Both
 84 metabolic parameters are within the range predicted by the metabolic theory of ecology (MTE), a :
 85 0.67 – 1 and E : 0.6 – 0.7 eV^{23,24}. Yet, while the general model predicts metabolic rates with
 86 individual body mass well, it does not capture the apparent high variation in soil biota temperature
 87 sensitivities (Supplementary Figure 1), indicating the need to account for metabolic traits between
 88 soil community groups.

89

90 Soil biota were classified into community groups according to their body size distribution as
 91 microbes ($< 0.0001 \text{ mg FM}$), mesofauna ($0.0001 - 8 \text{ mg FM}$) or macrofauna ($> 8 \text{ mg FM}$). Microbes
 92 include bacteria, mesofauna include protozoa, nematode, acari, collembola and enchytraeidae
 93 groups, and macrofauna include ant, spider, isopod, centipede, beetle, termite, millipede and
 94 earthworm groups. Although protozoa and nematodes are technically classified as microfauna
 95 rather than mesofauna, the metabolic data for these groups were collected at a single experimental
 96 temperature. Thus, regression analysis by soil biota groupings was not possible. The community
 97 group (CG) model includes two-way interaction terms between CG – body mass and CG –
 98 temperature to yield community-specific metabolic parameters (B_0 , a & E):

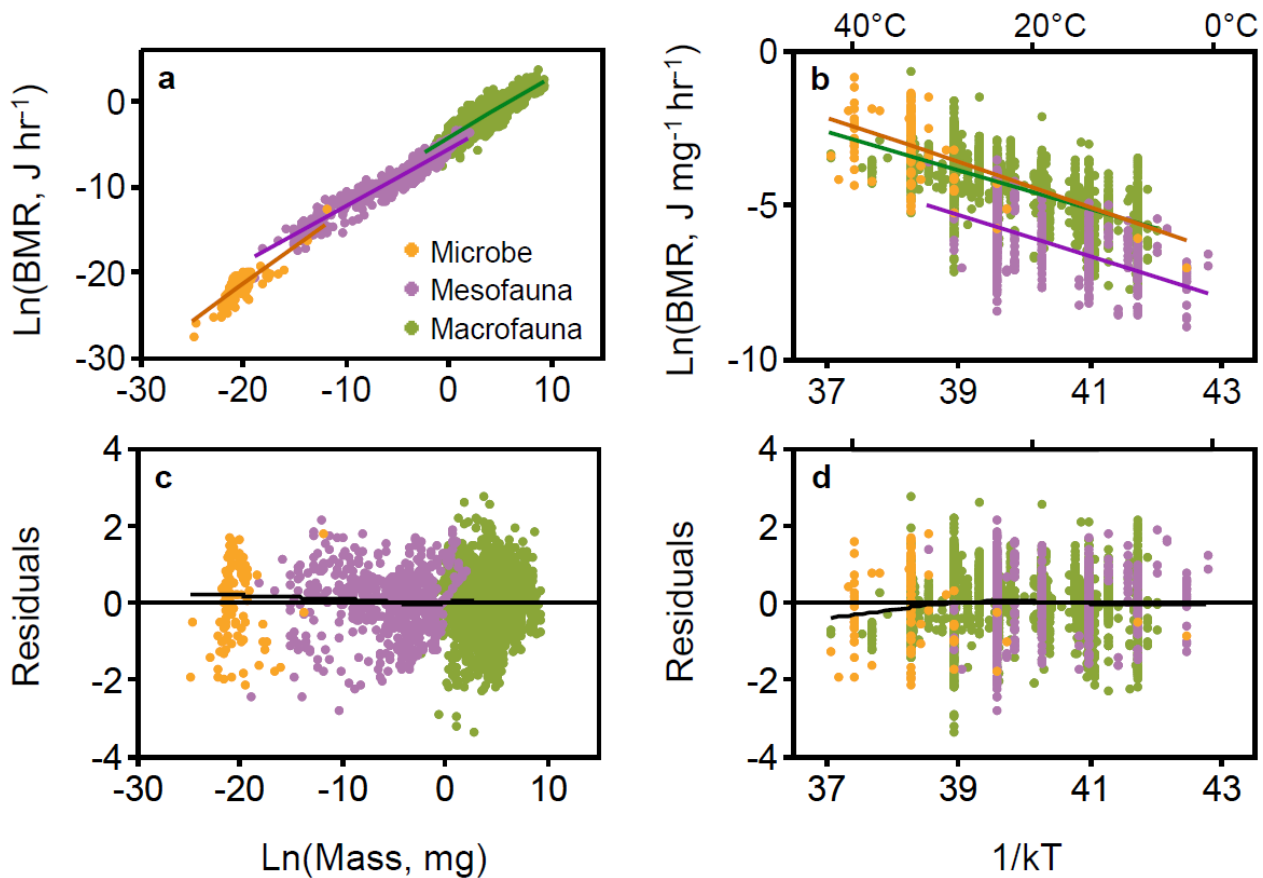
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$$100 \quad \ln(B_{CG}) = \ln(B_{0CG}) + a_{CG} \ln(M) - E_{CG}(1/kT) \quad (2)$$

101

102 CG model (Equation (2)) analysis yields ranges in a from 0.66 to 0.87 and E from 0.64 to 0.74 eV
 103 (Figs. 1a & b, Supplementary Table 1). Interestingly, analysis of the CG model reveals that the
 104 temperature sensitivity of metabolism (E) increases with decreasing body size, from 0.64 (± 0.01) for
 105 macrofauna to 0.74 (± 0.19) for microbes (Supplementary Table 1). That is, smaller sized soil
 106 community groups exhibit a greater proportional increase in their metabolic rates with a given
 107 increase in temperature, than individuals belonging to larger size community groups. This suggests
 108 a higher contribution of soil microbes (in particular, as mass-specific metabolic rates in mesofauna
 109 are lower) to R_S rates at increasing temperatures, if resources are available to fulfil higher energy
 110 requirements. The distribution of the CG model residuals against the independent variables (body

111 mass and temperature, Figs. 1c & d) and fitted lowess line, further indicate an absence of
 112 systematic errors, which are much greater for the general model (Supplementary Figure 1).
 113



114
 115 **Figure 1. Metabolic scaling relationships in soil communities.** Left-hand plots (a & c) show individual metabolic rates
 116 (B), corrected to a temperature of 20 °C using equation (2), plotted against individual body mass (M , mg FM). Right-hand
 117 plots (b & d) show B , corrected to a body mass of 1 mg using equation (2), plotted against temperature in an Arrhenius
 118 plot. Top plots (a & b) show community group (CG) model predictions of metabolic rates with individual body mass and
 119 temperature, and bottom plots (c & d) show distributions of the CG model residuals, with deviations of the data from model
 120 predictions characterised by lowess fits (black curves). Microbes (orange) include bacteria, mesofauna (purple) include
 121 protozoa, nematodes, acari, collembola and enchytraeidae, and macrofauna (green) include ant, spider, isopod,
 122 centipede, beetle, termite, millipede and earthworm groups ($n = 3768$). Metabolic parameter values are provided in
 123 Supplementary Table 1.

124

125 **Linking soil metabolism to biome-specific R_S rates**

126 Linking the individual metabolic rates of soil biota to biome-specific R_S ($\text{g C m}^{-2} \text{ year}^{-1}$) requires
 127 quantification of soil biota population abundances (A , no. m^{-2}) and R_H fractions (H_F , which measure
 128 the proportion of R_S contributed by heterotrophs and so also accounts for autotrophs) across
 129 biomes. First, individual-level metabolic rates (B , as in equation (2)) for each soil biota group (i)
 130 were calculated for an individual of average body mass (M) at a given MAT (T). B is then converted
 131 to respiration rate units (g C yr^{-1}) by using the conversion factors $37490 \text{ J gC}^{-1} = 20100 \text{ J LO}_2^{-1} \times (1 /$
 132 $0.5363 \text{ g C LO}_2^{-1})^{25,26}$ and 8760 hr yr^{-1} . The heterotrophic respiration rate (R_H) is the soil

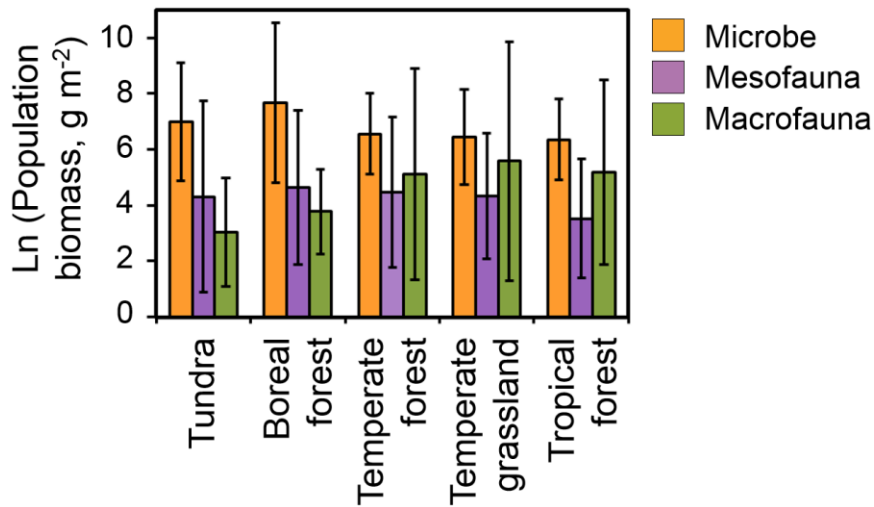
133 community's respiration rate, which is calculated according to individual-level respiration rates (r_i)
134 and population abundance (A_i) as: $R_H = \sum_i r_i A_i$, where the summation is over the soil biota groups
135 in the biome. Our R_H predictions are compared to independent data in Supplementary Figures 2 &
136 3. Finally, accounting for H_F 's reported in the Bond-Lamberty and Thomson²⁷ dataset
137 (Supplementary Figure 4, $n = 66$) gives: $R_S = \frac{1}{H_F} \sum_i r_i A_i$. R_S was calculated at MAT for each of the
138 R_S studies used to evaluate our approaches predictions ($n = 312$), using metabolic parameters,
139 individual body masses and soil biota population abundances in Supplementary Tables 2, 3 & 4
140 respectively.

141

142 ***Soil community composition across biomes***

143 Population biomass (g FM m⁻²) and abundance (number m⁻²) measurements for the fourteen soil
144 biota groups for which metabolic data is available were collected across tundra, boreal forest,
145 temperate forest, temperate grassland and tropical forest soils ($n = 2187$). Community group
146 biomasses across the five biomes investigated here were significantly different ($p = 0.000$,
147 Supplementary Table 5). In general, high latitude (tundra and boreal) soils harbour more soil
148 microbes and mesofauna by biomass than temperate and tropical soils. Soil macrofauna follow an
149 inverse trend, increasing in biomass from tundra to temperate grasslands and tropical forests (Fig.
150 2). Given the higher temperature sensitivity of smaller sized soil biota (Fig. 1), we would expect
151 higher abundances of soil microbes and mesofauna in tundra and boreal soils to be linked to higher
152 R_S temperature sensitivities at high latitudes.

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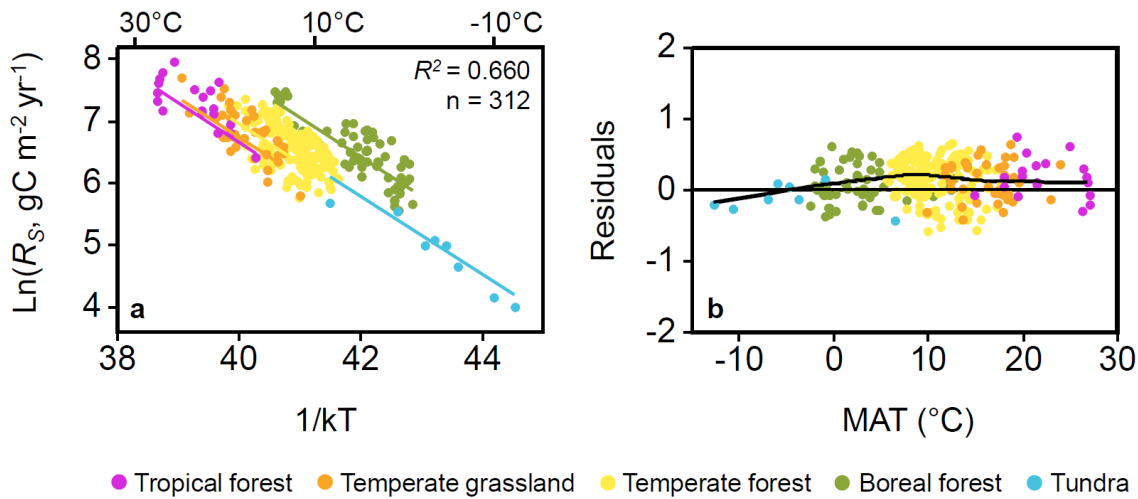
155 **Figure 2. Soil community composition across biomes.** Soil community groups are classified by body size distribution
 156 (microbe, mesofauna and macrofauna). Biomass (g fresh mass m⁻²) measurements incorporate the sum of soil biota
 157 population biomasses for each community group. Average biome-specific soil microbial biomasses were taken from the
 158 study of Xu et al. ²⁸, while soil mesofauna and macrofauna data were compiled in this study (n = 2187, Supplementary
 159 Figure). Presented values are means ± reported standard errors for microbes, while error bars for mesofauna and
 160 macrofauna were calculated as the square root of the summed variances for soil biota group population biomasses.
 161 Differences in community group biomass are significantly different across biomes ($p = 0.000$, Supplementary Table 5).

162

163 ***The influence of soil communities on R_S across biomes***

164 Comparison of our R_S predictions (lines) with independent R_S data (symbols) in Fig. 3a
 165 demonstrates good prediction of R_S rates across biomes and MAT's ($R^2 = 0.66$, n = 312, no p -value
 166 can be reported as predictions are independent of the data). Temperature sensitivity differences
 167 across biomes emerge from the approach by integrating variation in the metabolic ecology and
 168 community composition of soils. However, high variability in the R_S data likely points to site-specific
 169 interactions between individual, population and community-level dynamics with other environmental
 170 factors (e.g. resource quantity and quality), as well as temperature (Fig. 3b).

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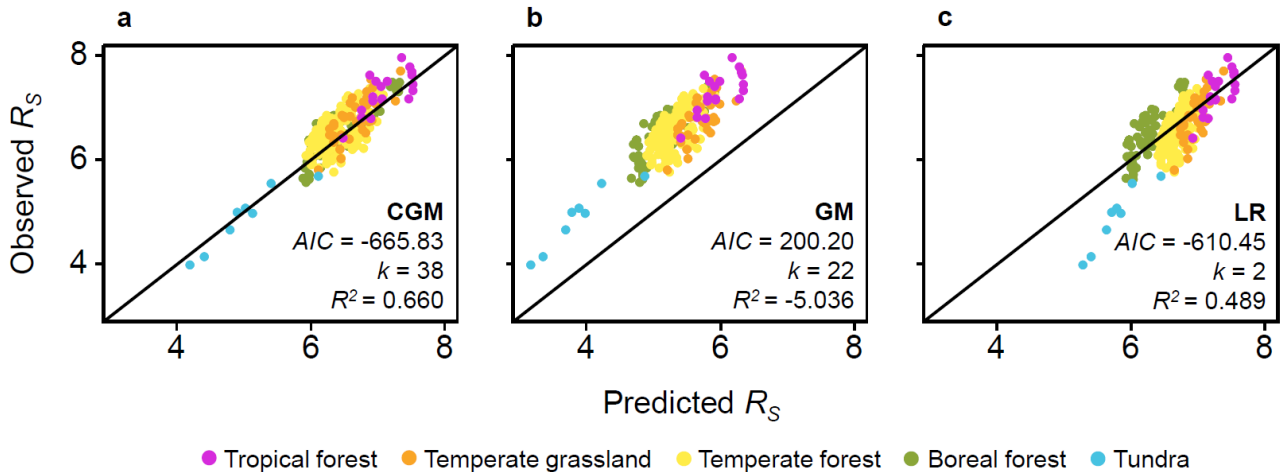
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Figure 3. Temperature sensitivity of soil respiration (R_S) across biomes and MAT's. Plots show a) independent R_S data (symbols: $n = 312$) and predicted R_S from the community group (CG) model presented here (lines) and b) CG model residual distributions against MAT ($^{\circ}\text{C}$) with fitted lowess line (solid black line).

To test whether incorporating the varying temperature sensitivities of soil biota was important in achieving good R_S predictions (Fig. 3 and 4a), we compare the CG model presented here to R_S predictions using the general model (Fig. 4b) and a linear regression between R_S and MAT fitted to the data (Fig. 4c). Not accounting for metabolic variation between soil community groups in the general model significantly reduces the accuracy of the metabolic approach (Fig. 4b). This result indicates that soil community body size distribution and metabolic ecology strongly influence the temperature sensitivity of R_S across the five biomes investigated here. Comparison of the CG model with the linear regression ($\ln(R_S) = 22.54 - 0.388 (1/kT)$, Fig. 4c) and AIC values, further indicates that accounting for soil ecology enables better R_S predictions. Improved prediction of R_S rates are particularly evident in boreal and tundra soils of the CG model, where the data indicate higher R_S temperature sensitivity (Fig. 3a). Weak temperature control in the linear regression presented here and ESMs which implement fixed Q_{10} values are unable to capture these climatological differences in R_S temperature sensitivities⁷, with serious consequences for future climate change projections.



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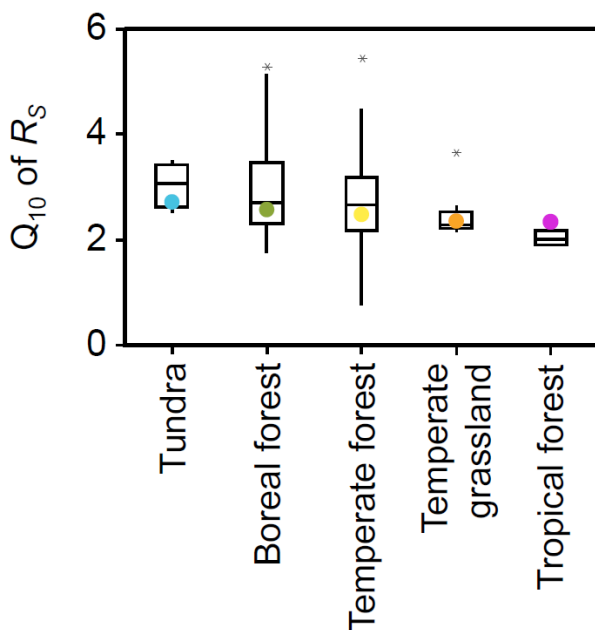
Figure 4. Model comparisons and goodness of fits with independent soil respiration (R_S , $\text{gC m}^{-2} \text{ year}^{-1}$) data. The community group model (CGM) (a) is compared to the general metabolic model (GM) (b) which does not account for metabolic variation in soil communities, and an empirical fitted linear regression (LR) to the R_S data ($\ln(R_S) = 22.54 - 0.388 (1/kT)$, $r^2 = 0.489$, $p < 0.0001$) (c). p -values cannot be calculated for a & b as predictions are independent of the data. Solid black lines are 1:1 lines which would demonstrate perfect prediction and lower AIC values indicate a better goodness of fit to the data while accounting for model complexity (k : number of parameters). Note that the r^2 value for the general model (b) is negative because the residual sum of squares from the model is higher than the total sum of squares from the data.

Biome-specific Q_{10} 's were calculated, using the CG model, by taking R_S rates for study-specific MAT's (MAT₀, $n = 119$) and for an increase in temperature of 10 °C (MAT₊₁₀), to give $Q_{10} = R_S(\text{MAT}_{+10}) / R_S(\text{MAT}_0)$. We compare our median Q_{10} values (symbols) to those reported in the Bond-Lamberty and Thomson²⁷ dataset (boxes) in Fig. 5. With increasing temperature, the metabolic approach indicates that R_S in tundra and boreal soils is more temperature sensitive than temperate and tropical soils, with mean Q_{10} values increasing from 2.33 ± 0.001 in tropical forests to 2.72 ± 0.03 in tundra. Many studies have reported similar climatological responses, in which R_S in colder high latitude climates increase more rapidly with increasing temperature^{7,8,10,27,29-33}, but none have yet linked variations in R_S temperature sensitivity to the mechanisms driving decomposition processes by soil communities. However, our estimates also assume static biome-specific soil communities, and that greater metabolic rates at higher temperatures are met with sufficient food resources.

Temperature, soil water and resource availability interact to affect the provision of food resources to soil communities³⁴, and the inclusion of these environment-community feedbacks would likely result in lower R_S sensitivity predictions in warm climates as the soil biota become food limited¹⁵.

Conversely, freeze-thaw cycles in tundra soils lead to deviation of R_S temperature dependence from thermodynamic laws⁷, increasing below 0 °C as the decomposition of structurally complex molecules by arctic microbes exhibit a higher temperature sensitivity of metabolism³⁵. Our Q_{10}

219 estimates thus overestimate tropical soil and underestimate tundra and boreal soil responses to
 220 increasing temperatures (Fig. 5), in line with long-term field Q_{10} 's of 5.2 ± 2.4 for tundra and boreal,
 221 2.7 ± 1.7 for temperate and 2.2 ± 0.9 for tropical climates³⁶. Exploring alternative thermodynamic
 222 hypotheses, such as non-linear temperature curves and acclimatisation mechanisms, could explain
 223 more of the variability in the Q_{10} data and Q_{10} 's under long-term warming. On the other hand, our
 224 approach estimates much higher Q_{10} values than the static value of 2 used in many ESMs, which
 225 are often parameterised with short-term observations based on eddy covariance fluxes and soil
 226 incubations^{2,37}. This divergence between short- and long-term Q_{10} values has been suggested as
 227 evidence for the inclusion of emergent behaviour over long timescales⁷, which in this study includes
 228 the metabolic response of soil communities and shifts in soil community composition across biomes.
 229



230
 231 **Figure 5. Observed and predicted Q_{10} values for R_S across biomes.** Q_{10} data from the Bond-Lamberty and Thomson
 232 ²⁷ dataset ($n = 119$) presented as boxes with the median and first and third quartiles shown. CG predictions of Q_{10} values
 233 across biomes are given by coloured symbols, showing median predicted values, with imperceptible first and third quartile
 234 whiskers.

235

236 Discussion

237 We use a metabolic ecology approach to better understand the relationships between soil biota
 238 metabolism, community composition and R_S rates. We find that accounting for the metabolic
 239 ecology of soils (Fig. 1) together with soil community composition (Fig. 2) reveals variations in R_S
 240 with MAT across five biomes (Fig. 3). Important in achieving good R_S predictions was incorporating
 241 the varying temperature sensitivities of soil community groups. In comparison, assuming all soil
 242 biota exhibit identical temperature sensitivities resulted in substantial under-estimation of R_S rates
 243 (Fig. 4b). The metabolic ecology and body size distribution of soil communities thus strongly

244 influence the temperature sensitivity of R_S across biomes. With increasing temperature, our
245 approach suggests that R_S would be most strongly enhanced in colder climatic regions (Fig. 5),
246 because of the higher temperature sensitivity of soil biota inhabiting these soils.

247

248 Soil community composition will also be influenced by multiple global drivers (e.g. warming, CO₂
249 fertilisation, N deposition) in the future, which will alter the direction and magnitude of R_S responses.
250 Thus, to better anticipate the effects of global environmental changes on R_S requires a better
251 understanding of the ecological mechanisms underpinning macroecological patterns in soil
252 communities. Yet, fundamental knowledge gaps in soil ecology need to be addressed to understand
253 the primary drivers of soil community composition across a broad spectrum of environmental
254 variables. Unravelling these complex interactions would allow us to represent the mechanistic links
255 between the belowground and aboveground components of terrestrial ecosystems, develop more
256 predictive models of soil systems and improve forecasts of future climate changes on numerous
257 ecosystem functions, including R_S . Our study stresses the importance of considering the soil
258 organisms which facilitate ecosystem functions, and demonstrates the utility of fundamental
259 ecological principles in describing complex soil systems.

260

261 **Methods**

262 **Metabolic ecology of soil biota.** Metabolic data for a wide range of soil biota was compiled from
263 the dataset of Ehnes, et al. ¹⁹, which includes data from the meta-analyses of Meehan ³⁸ and
264 Chown, et al. ³⁹ together with their own measurements for acari, collembola, enchytraeidae,
265 centipedes, millipedes, isopods, spiders, ants, beetles, termites and earthworms (n = 3399). In
266 addition, we compiled data for bacteria from Makarieva, et al. ⁴⁰ (n = 56), protozoa from Laybourn
267 and Finlay ⁴¹ and Fenchel and Finlay ⁴² (n = 143), nematodes from Klekowski, et al. ⁴³ and Ferris, et
268 al. ⁴⁴ (n = 105) and enchytraeidae from Nielsen ⁴⁵ (n = 58). Detailed differences at the species-level
269 are avoided in order to explore the collective metabolism of soil community groups across biomes.
270 All measurements were converted to wet weight (mg) and standard metabolic rate per hour (J hr⁻¹),
271 using a dry to fresh mass ratio of 0.2:1¹⁹, 1 mL O₂ = 20.1 J²⁶ and 1 mL O₂ = 0.5363 mg C²⁵.

272

273 **Soil biota populations and community composition.** Linking individual to population-level
274 metabolism requires estimation of the population abundances of different soil biota across biomes.
275 Here, we extend the dataset of Fierer, et al. ⁴⁶, who collected population biomass data for acari,
276 collembola, enchytraeidae, nematodes and earthworms in tundra, boreal forest, temperate forest,
277 temperate grassland and tropical forest soils (n = 799). We compiled additional data for all of the
278 soil biota groups and biomes of Fierer, et al. ⁴⁶, and for ants, beetles, centipedes, isopods,
279 millipedes, protozoa, spiders and termites in biomes for which data was available (n = 1382).
280 Average biome-specific microbial biomass values were taken from the extensive review of Xu, et al.

281 ²⁸, which compiles 1182 measurements across the biomes investigated here (Supplementary Table
282 4).

283

284 Population biomass measurements required conversion to population abundance by estimates of
285 mean individual body masses (M) for the fourteen different soil biota groups. We assume that M for
286 different soil biota groups are constant across biomes. Although this assumption likely introduces
287 error due to variations in individual life histories across climates, not enough information exists to
288 apply more detailed individual-level relationships. To minimise error we collated data from a number
289 of sources reporting M for the different soil biota groups (Supplementary Table 3). Average M (mg
290 dry mass) used in this study were: protozoa (6.55×10^6), nematodes (0.0020), acari (0.0096),
291 collembola (0.055), enchytraeidae (0.055), ants (2.23), beetles (4.35), isopods (4.47), centipedes
292 (6.59), spiders (7.42), termites (9.90), millipedes (17.06) and earthworms (52.37). All population
293 biomass measurements are expressed here as fresh mass (g FM/m^2) using the conversion to fresh
294 mass of five times dry mass¹⁹. Using a single dry to fresh mass conversion factor for all soil biota
295 groups will also introduce some error, as variations likely exist across soil biota groups and
296 biomes⁴⁷. Measurements given in the dataset of Fierer et al. ⁴⁶ (g C m^{-2}) were further corrected by
297 accounting for a 50 % carbon content. We do not make additional extrapolations to specific soil
298 depths, as this is highly variable between soil biota groups and soil types, and often not reported in
299 field studies. If population measurements were expressed on per mass of dry soil basis, appropriate
300 bulk density values were used to convert these measurements to density (per m^2) for the soil type
301 reported.

302

303 **Heterotrophic respiration (R_H)**. Using our metabolic approach, R_H rates were estimated by
304 summing the metabolic rates of soil communities at MAT in a given biome. Community-level
305 metabolic rates were calculated by taking metabolic parameters (B_0 , a and E ; Supplementary Table
306 1) for each soil community group, individual body masses (M , mg fresh mass) for each soil biota
307 group (Supplementary Table 3) and their population abundance (A , number m^{-2}) in different biomes
308 (Supplementary Table 4). Metabolic rates were then transformed to respiration rates (g C) by using
309 the conversion factors $37490 \text{ J gC}^{-1} = 20100 \text{ J LO}_2^{-1} \times (1 / 0.5363 \text{ g C LO}_2^{-1})$ ^{25,26} and 8760 hr yr^{-1} .
310 To investigate whether our model predicts R_H rates across biomes and MAT's, prior to extrapolating
311 to R_S as detailed below, we compared our predictions with available R_H data in the Bond-Lamberty
312 and Thomson ²⁷ dataset ($n = 66$). R_H data were compiled for un-manipulated field studies reporting
313 annual R_H and R_S rates, and were averaged for single study years and/or locations where
314 applicable. Measurements were also excluded if reported R_H rates were equal to or higher than
315 reported R_S rates. If MAT's were not reported, or the same MAT was given for multiple years in the
316 same study, NOAA weather stations were used to collect MAT measurements based on the study
317 sites latitude and longitude (<https://www.ncdc.noaa.gov/cdo-web/datatools/findstation>). The CG

318 model's predictions of R_H rates were then evaluated ($r^2 = 0.757$, Supplementary Figure 2), in
319 comparison to the general metabolic model ($r^2 = -2.261$) and a linear regression approach ($r^2 =$
320 0.529) (Supplementary Figure 3). Accounting for model complexity in AIC calculations indicates that
321 the CG model does not perform better than the linear regression given its large number of
322 parameters, but this may be a result of the limited size of the data set. To test whether the CG
323 approach performs better given more data we used the R_H data to calculate an R_H fraction (H_F) for
324 each biome to account for the contribution of heterotrophs to R_S . This allowed us to use the larger
325 R_S data set ($n = 312$) to evaluate the CG model with greater precision as reported in Fig. 4.

326

327 ***R_H fraction (H_F)***

328 R_H fractions (H_F) were calculated as R_H / R_S for studies reporting both annual R_H and R_S rates (g C
329 $m^{-2} yr^{-1}$, $n = 66$) and assuming $R_S = R_H + R_A$ ⁴⁸. By using R_H values, rather than R_A , we avoid some
330 of the issues in separating heterotrophic and autotrophic contributions to R_S , as R_H is typically
331 measured directly whereas R_A is typically derived by calculating the difference between R_S and
332 other ecosystem fluxes⁴⁸. Mean $H_F \pm SE$ across the five biomes investigated here were 0.39 ± 0.10 ,
333 0.63 ± 0.02 , 0.58 ± 0.03 , 0.63 ± 0.04 and 0.77 ± 0.07 for tundra, boreal forest, temperate forest,
334 temperate grassland and tropical forest soils, respectively. Variability in H_F within biomes is likely
335 linked to the experimental difficulties associated with separating the autotrophic and heterotrophic
336 components of soils and the methodology used to do so in the field⁴⁸⁻⁵⁰. To explain some of this
337 variability, and to account for the temperature sensitivity of R_A , we performed a regression analysis
338 between H_F and MAT, which revealed a weak but significant positive correlation ($H_F = 0.54 + 0.0069$
339 MAT ; $r^2 = 0.104$, $p = 0.008$, Supplementary Figure 4). This linear relationship is incorporated in our
340 calculations to extrapolate from R_H to R_S rates across biomes and MAT's.

341

342 ***Soil respiration (R_S)***

343 To compare our R_S estimates with independent data, annual R_S rates (g C $m^{-2} yr^{-1}$) were compiled
344 from the global soil respiration datasets of Bond-Lamberty and Thomson²⁷ and Carey, et al.⁵¹ for
345 tundra, boreal forest, temperate forest, temperate grassland and tropical forest soils ($n = 312$). Data
346 were included from un-manipulated field studies reporting average annual R_S and MAT, and
347 measurements from both datasets were averaged for single study years and/or locations where
348 applicable. R_S measurements compiled from the Bond-Lamberty and Thomson²⁷ dataset included
349 119 Q_{10} values, which were used to evaluate predicted Q_{10} 's across biomes using our CG model.

350

351 **Data availability.** The datasets generated and analysed during the current study are available on
352 Dryad (<https://doi.org/10.5061/dryad.416kv03>).

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472

473 **Acknowledgements**

474 This research has been financially supported by a NERC Soil Security Programme fellowship
475 (NE/N019504/1). We thank Chris Venditti, James Brown, Gabriel Yvon-Durocher, Charles Hall and
476 four anonymous reviewers for their feedback and suggestions on the manuscript.
477

478 **Author contributions**

479 AJ conceived the idea and compiled and analysed the data; AJ and RS developed the methodology
480 and wrote the manuscript.
481

482 **Competing interests**

483 The authors declare no competing financial interests.
484