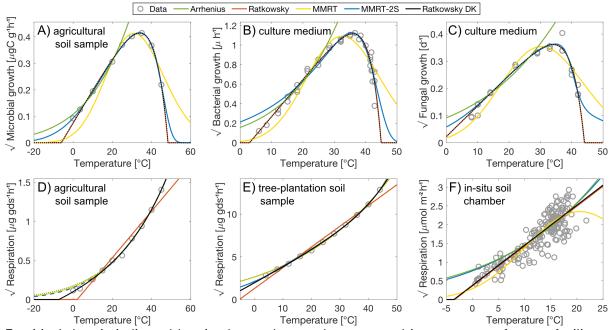
A unified representation of the temperature dependences of soil microbial growth and respiration

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Supplementary Figures/Tables

Supplementary Fig. 1: Examples of temperature relationship patterns from the literature and best-fit obtained using current models.



Empirical data is indicated by circular markers and represented in square-root form to facilitate interpretation of model features. Curves represent the best-fit outcomes for the Arrhenius, Ratkowsky, MMRT, MMRT-2S, and Ratkowsky DK. Refer to Fig. 2 for details.

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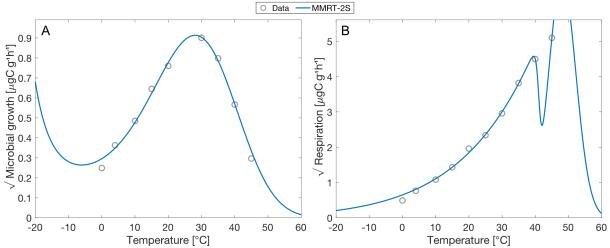
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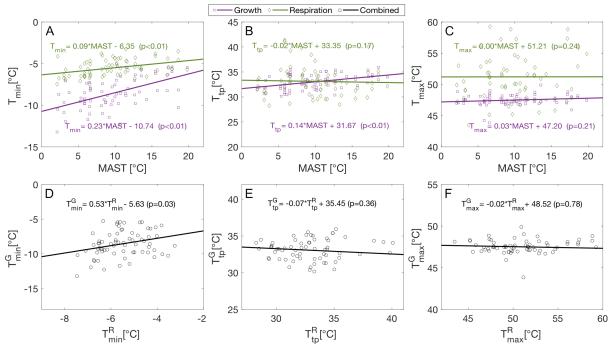
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Supplementary Fig. 2: Example fits of the MMRT-2S model to temperature response curves for microbial growth and respiration.



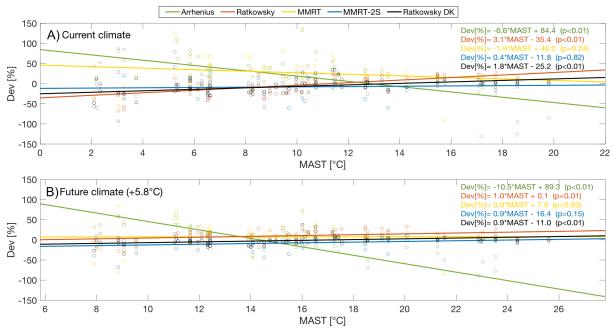
It illustrates that, despite a good fit to the data, the MMRT-2S model can occasionally produce unnaturally shaped curves indicative of overfitting.

Supplementary Fig. 3: Estimates of $T_{\rm min}$ and $T_{\rm tp}$ and $T_{\rm max}$ for microbial growth and respiration across mean annual soil temperatures (MAST), and comparison between growth and respiration estimates.



Parameter estimation was performed using the two-step calibration approach of Ratkowsky DK. The markers represent the calibrated metrics in each site, while the lines and equations illustrate the corresponding linear fits. Superscripts G and R indicate growth and respiration, respectively.

Supplementary Fig. 4: Impact of model choice on cumulative fluxes with potential to alter soil carbon stocks across the mean annual soil temperature (MAST) gradient.



Circular markers represent estimates at each site for the Arrhenius, Ratkowsky, MMRT, MMRT-2S, and Ratkowsky DK under both current (**A**) and future climate change scenarios (**B**). Curves and equations display the results of linear regression, with p-values indicating the statistical significance along the gradient.

Supplementary Table 1: Median parameter values obtained from the models fitted to microbial growth and respiration data across 70 sites, with interquartile ranges shown in parentheses.

Model	Parameter	Growth	Respiration
Arrhenius	A [μgC g ⁻¹ h ⁻¹]	4.8·10 ¹¹ (6.9·10 ¹²)	1.3·10 ¹² (9.8·10 ¹²)
	μ [J mol ⁻¹]	6.9·10 ⁴ (1.4·10 ⁴)	6.8·10 ⁴ (1.1·10 ⁴)
Ratkowsky	b [(µgC g ⁻¹ h ⁻¹) ^{1/2} °C ⁻¹]	0.02 (0.01)	0.08 (0.04)
	c [°C ⁻¹]	0.09 (0.05)	-
	T _{min} [°C]	-4.1 (4.0) *	-5.5 (4.5) *
	T _{max} [°C]	47.6 (1.4) *	-
Ratkowsky (two-step cal.)	b [(µgC g ⁻¹ h ⁻¹) ^{1/2} °C ⁻¹]	0.02 (0.01)	0.04 (0.02) *
	c [°C ⁻¹]	0.13 (0.03) *	-
	T _{min} [°C]	-8.6 (2.5) **	-5.6 (1.7) ^{**}
	T _{max} [°C]	47.5 (0.9)	-
MMRT	ΔH_0^{\ddagger} [J mol ⁻¹]	8.0·10 ⁴ (3.8·10 ³)	6.9·10 ⁴ (5.8·10 ⁷) *
	ΔS_0^{\ddagger} [J mol ⁻¹ K ⁻¹]	14.1 (8.2)	-7.1 (700) [*]
	$\Delta C_{\mathrm{p}}^{\ddagger}$ [J mol ⁻¹ K ⁻¹]	-7.3·10³ (1.4·10³) *	-75.6 (492.6) *
	T_0 [K]	290.7 (2.49)	3.5·10³ (3.5·10⁵)
MMRT-2S	ΔH_0^{\ddagger} [J mol ⁻¹]	4.5·10 ⁴ (8.9·10 ⁴)	7.1·10³ (8.4·10⁴)
	ΔS_0^{\ddagger} [J mol ⁻¹ K ⁻¹]	-100.1 (354.4)	-174.7 (203.1)

	$\Delta C_{p,l}^{\ddagger}$ [J mol ⁻¹ K ⁻¹]	-2.8·10³ (2.6·10³)	-570.2 (468.4)
	$\Delta C_{\mathrm{p,h}}^{\ddagger}$ [J/mol/K]	-3.5·10 ⁴ (7.0·10 ⁴)	-928 (2.3·10 ⁴)
	$\Delta\Delta H^{\ddagger}$ [J mol ⁻¹]	1.2·10 ⁵ (2.8·10 ⁵)	1.2·10 ⁶ (2.5·10 ⁶)
	<i>T</i> _c [K]	337.8 (143.8)	321.3 (29.5)
	<i>T</i> ₀ [K]	292.6 (33.3)	407.7 (137.0)
Ratkowsky DK	b [(µgC g ⁻¹ h ⁻¹) ^{1/2} °C ⁻¹]	0.02 (0.01)	0.02 (0.01)
	c [°C ⁻¹]	0.09 (0.05)	0.02 (0.01)
	T _{min} [°C]	-4.1 (4.0) *	-0.0 (3.8)
	T _{max} [°C]	47.6 (1.4) *	0.0 (0.4)
Ratkowsky DK (two-	b [(µgC g ⁻¹ h ⁻¹) ^{1/2} °C ⁻¹]	0.02 (0.01)	0.04 (0.02) *
step cal.)	c [°C ⁻¹]	0.12 (0.03) *	0.08 (0.02)
	T _{min} [°C]	-8.6 (2.5) **	-5.6 (1.7) [*]
	T _{max} [°C]	47.5 (0.9)	51.0 (5.5)

Pattern scores were derived from correlation analysis between parameter values and mean annual soil temperature. Values marked with * indicate weak trends (pattern score > 0.1) and bold values marked with ** indicate strong and consistent trends (pattern score > 0.5). The parameters of the MMRT-based models are reported in their standard thermodynamic units, implying the existence of a scaling factor to microbial rate units.