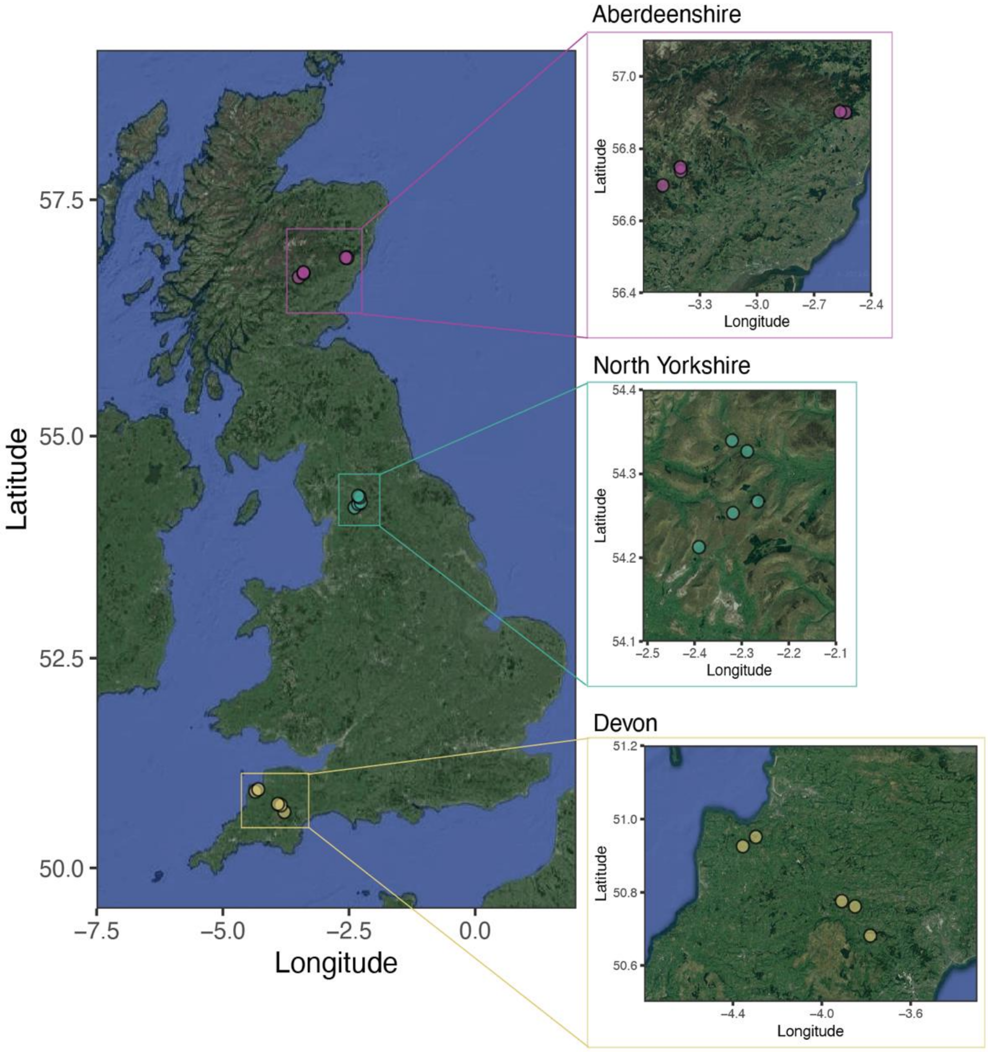
SUPPLEMENTARY INFORMATION



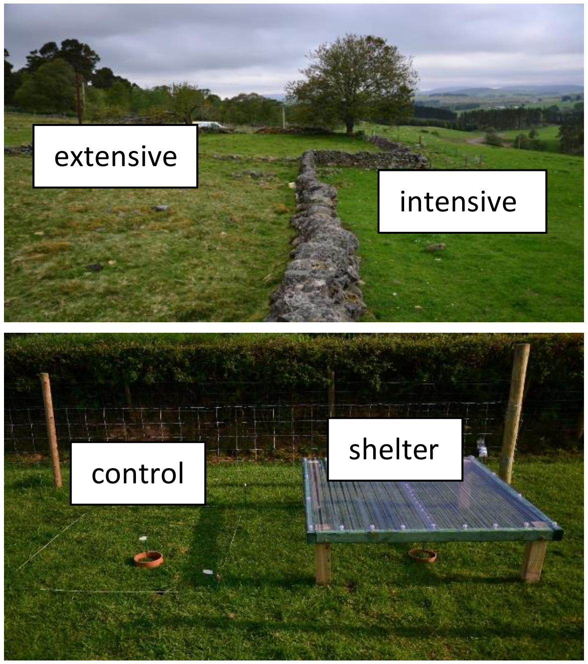


Figure S1. Experimental locations in Devon, North Yorkshire, Aberdeenshire (UK). Each point represents one site, and within each site there were two paired fields with contrasting management (extensive, intensive), resulting in a total of 30 fields. In each fields, there were three drought and three control plots, for a total of 60 experimental units resulting from averaging the data of the three plots per condition (drought vs control) in each field. Modified from Lavallee et al 2023.

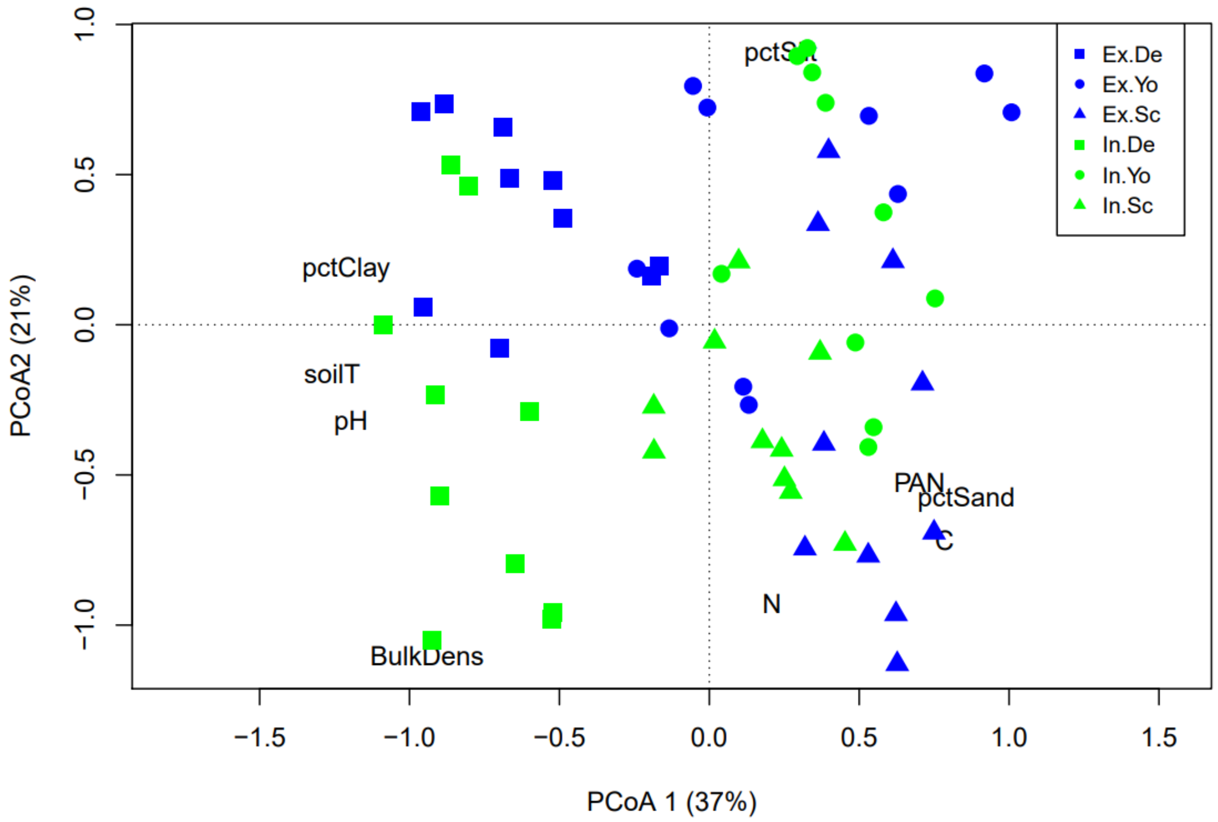


Figure S2. PCoA of the correlation matrix of soil variables across all experimental sites. Observational units are labelled by region (De, Yo and Sc respectively for Devon, Yoirkshire and Aberdeenshire, as per figure S1) and intensive vs extensive management. The actual degree of management intensity varied between sites, as reflected by the variables in the ordination but, overall, it is clear that intensively managed field in the south (e.g. green squares for intensive fields in Devon) were characterized by high pH and Bulk density, finer textures, and lower amount of organic matter. The more extensively managed soil in the north (blue circles and triangle in Yorkshire and Aberdeenshire) had opposite characteristics. Axes 1 and 2 are both necessary to describe the variation in soil from north to south as well as from intensive and extensive management regimes. Axis 3, however, also contained variance explainable in terms of intensive vs extensive soil properties, as show below in figure S3. Axis 1 and 2 were thus combined in a composite variable for the SEM of Figure 4 in the main article so to account for major soil properties gradients that were responsive to intensive management.

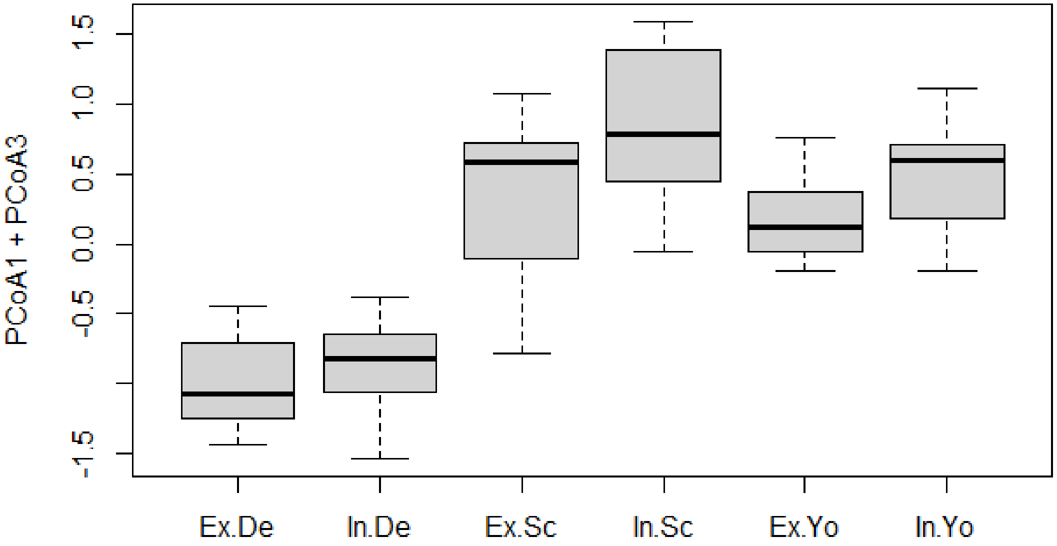


Figure S3. Composite variable of PCoA1 and PCoA3 of the ordination of figure S2. The variable clearly respond to intensive management in a similar manner across the three regions, with higher values in intensive field. An inspection of the eigenvectors revealed that intensively managed fields with high values for the composite had higher bulk density and pH as well as higher N and PAN than less intensively managed soil. That is just a general, average trend, as shown by the width of the box and whiskers in the plot.

Supplemental Description of soil food web data

Table S1. Biomasses of the 13 trophic species in which soil organisms have been functionally grouped to measure energy fluxes in the soil food web. Units are in mg m^{-2} (at a soil sampling depth of 10cm). The biomass of soil animals was estimated by multiplying population densities (estimated directly) by the average mean body mass of a random samples of 20 individual per trophic groups for each site-plot combination. The body mass of each group of soil animal was estimated using allometric equations available in the references cited in the main article (Caruso & Migliorini, 2009; Turnbull et al., 2014). The biomass of fungi and bacteria was estimated using PLFAs as well as fumigation to estimate microbial C. For PLFA, we used the methods detailed in (Chomel et al., 2019). The biomass of roots was measured directly. There are not many reference to which compare our estimates directly but the values of our estimates are consistent with estimates from similar systems and, in general, the ratios usually found between various taxa (e.g. Andrés et al., 2016; Potapov et al., 2019; Van Den Hoogen et al., 2019). The first row of this table is used as example to illustrate the computer codes we use to estimate energy fluxes, fit the network model, and estimate the network entropy as well as the Jacobian matrix to calculate stability metrics analysed in the paper (Moore, J. C., & de Ruiter, P. C., 2012).

Location	Site	Manag.	Shelter	Pred. mites	Pred. nematodes	Collembolans	Oribatids	D Microart.	PF insects	PP nem	OMN Nem	F Nem	B Nem	Fungi	Bacteria	Roots
Devon	S1	Extensive	Yes	344	259	687	633	42	12	1283	811	13	1045	217798	66579	2246877
Devon	S1	Extensive	No	460	167	468	377	342	7	1888	702	19	1089	235959	63732	2473955
Devon	S1	Intensive	Yes	145	139	472	75	12	26	1381	451	34	1189	118640	80431	2414198
Devon	S1	Intensive	No	490	148	404	73	24	46	2057	253	66	2280	126234	80609	2306635
Devon	S2	Extensive	Yes	331	190	968	397	65	13	2620	1293	72	1353	190118	77899	4015696
Devon	S2	Extensive	No	504	197	916	305	806	95	1659	169	51	824	272310	91851	4529609
Devon	S2	Intensive	Yes	266	98	850	194	17	78	2003	578	90	1880	156491	89947	4326434
Devon	S2	Intensive	No	187	91	344	349	12	102	1582	555	34	1319	161136	84456	4350337
Devon	S3	Extensive	Yes	254	110	953	194	38	63	2870	998	101	2292	265610	88452	2605422
Devon	S3	Extensive	No	516	88	829	126	293	70	2965	470	63	2007	200315	80439	2151266
Devon	S3	Intensive	Yes	236	158	1349	78	6	96	4757	1146	73	2540	106139	78121	2031751
Devon	S3	Intensive	No	310	208	608	66	8	57	6266	2814	58	3202	134091	91289	2916160
Devon	S4	Extensive	Yes	158	147	352	420	17	16	2607	498	85	2305	207135	71536	2784694
Devon	S4	Extensive	No	385	150	488	286	363	66	2832	878	71	2427	208897	84765	1936139
Devon	S4	Intensive	Yes	156	138	527	117	5	43	1992	1078	51	1591	132475	78595	4087405
Devon	S4	Intensive	No	224	143	269	163	4	47	2538	1320	93	2022	144432	96250	4649124
Devon	S5	Extensive	Yes	106	109	1612	556	20	57	1641	429	42	978	149205	92032	1709061
Devon	S5	Extensive	No	277	58	862	388	220	46	972	625	15	1131	158248	88198	2832500
Devon	S5	Intensive	Yes	81	73	142	53	9	50	974	1292	96	1120	113089	70717	1756867
Devon	S5	Intensive	No	355	51	223	156	9	166	582	441	112	1555	107145	83346	2533713
Aberdeens.	S1	Extensive	Yes	43	74	332	64	14	19	1799	726	51	1248	128730	43938	1912236

Aberdeens.	S1	Extensive	No	92	28	364	58	14	11	2739	313	53	1057	152138	44957	1960042
Aberdeens.	S1	Intensive	Yes	89	76	319	55	7	0	2022	754	83	1701	90750	70550	340617
Aberdeens.	S1	Intensive	No	67	129	229	138	29	0	3122	793	65	1402	101686	60127	1278808
Aberdeens.	S2	Extensive	Yes	36	64	372	155	29	12	1780	760	56	744	232239	72067	1732964
Aberdeens.	S2	Extensive	No	29	28	166	47	11	4	1859	405	38	580	211362	78993	1876382
Aberdeens.	S2	Intensive	Yes	353	61	272	49	6	1	1625	610	33	1383	116527	71509	1577595
Aberdeens.	S2	Intensive	No	23	55	89	109	19	18	1694	531	67	706	125812	84869	1625401
Aberdeens.	S3	Extensive	Yes	41	233	538	220	38	16	1254	891	20	770	113177	86198	2306635
Aberdeens.	S3	Extensive	No	121	97	311	194	13	26	786	294	9	639	224357	91535	2127363
Aberdeens.	S3	Intensive	Yes	75	81	345	76	25	2	454	545	31	1991	70056	69361	645380
Aberdeens.	S3	Intensive	No	87	19	566	131	1106	27	656	417	26	1410	64260	65525	1039778
Aberdeens.	S4	Extensive	Yes	62	133	375	151	5	32	1398	504	40	993	113432	84942	657331
Aberdeens.	S4	Extensive	No	125	89	362	234	15	44	1690	622	31	1263	122521	58560	812700
Aberdeens.	S4	Intensive	Yes	48	207	195	87	4	3	4328	1446	168	3563	137858	91085	956118
Aberdeens.	S4	Intensive	No	88	80	254	120	21	21	3012	1075	43	2133	139748	81799	1159293
Aberdeens.	S5	Extensive	Yes	29	123	144	37	18	19	4233	698	34	1619	69178	78303	573671
Aberdeens.	S5	Extensive	No	51	66	318	30	33	2	3291	624	59	706	88109	81041	334641
Aberdeens.	S5	Intensive	Yes	111	187	492	31	7	1	2908	1598	103	2047	111210	96532	382447
Aberdeens.	S5	Intensive	No	95	167	394	258	83	3	2182	1112	49	1454	162940	108947	848555
Yorkshire	S1	Extensive	Yes	78	147	794	129	6	15	2070	1012	20	1939	91442	91718	1159293
Yorkshire	S1	Extensive	No	291	75	1513	552	24	15	1466	790	43	1575	95714	94054	1195148
Yorkshire	S1	Intensive	Yes	116	130	303	140	6	50	1051	998	66	1782	62656	89158	1099536
Yorkshire	S1	Intensive	No	334	146	383	19	29	56	1772	1338	40	1474	93221	103615	1254905
Yorkshire	S2	Extensive	Yes	73	50	782	249	9	14	791	739	40	1341	45051	64671	1918212
Yorkshire	S2	Extensive	No	112	43	482	267	15	11	689	588	27	1018	33987	57570	2258829
Yorkshire	S2	Intensive	Yes	92	103	443	103	6	75	849	903	58	1252	33202	54303	1266856
Yorkshire	S2	Intensive	No	113	76	133	17	24	35	745	672	25	861	40219	62911	627691
Yorkshire	S3	Extensive	Yes	101	132	460	236	6	14	1364	1071	48	1525	130939	95172	1936139
Yorkshire	S3	Extensive	No	235	153	607	661	20	11	967	795	70	2256	91426	104591	2653227
Yorkshire	S3	Intensive	Yes	110	70	613	461	11	64	554	321	32	734	63786	65664	1900285
Yorkshire	S3	Intensive	No	161	125	586	69	40	49	758	915	26	1577	40771	55707	1924188
Yorkshire	S4	Extensive	Yes	261	183	711	87	17	59	2336	805	84	1537	71387	60428	3071529
Yorkshire	S4	Extensive	No	340	104	672	83	33	51	2786	645	78	1249	85796	74629	2366392
Yorkshire	S4	Intensive	Yes	296	115	983	202	16	404	3033	1100	89	1675	22813	34110	2067605
Yorkshire	S4	Intensive	No	401	87	745	320	61	201	2359	2721	32	1510	34547	38545	1266856
Yorkshire	S5	Extensive	Yes	349	67	1013	747	16	3	4974	603	107	1040	18182	18885	2533713
Yorkshire	S5	Extensive	No	855	82	215	1752	48	2	5259	731	66	732	21556	25633	2987869
Yorkshire	S5	Intensive	Yes	182	171	735	253	38	20	1796	1102	64	2018	58054	82898	800749

Yorkshire	S5	Intensive	No	611	75	623	33	112	116	1542	1935	68	2423	55733	77067	1027827

Trophic species abbreviations: Pred mites, predatory mites; Pred. nem, predaceous nematodes; D microart., detritivorous microarthropods such as come diptera insect larvae or mites; PF feeders, root feeders such as aphids, some insect larvae or some mites; PP nem, plant parasitic or feeder nematodes; OMN nem, omnivorous nematodes; F nem, fungivorous nematodes; B nem, bacterivorous nematodes;

Table S2

Linear mixed effect model (with gaussian error distribution) to test the effect of Management (two levels: intensive and extensive), Drought (two levels: control vs drought), and their interaction on soil moisture. We averaged the plot level data across the four sampling times to match the data with the soil food web model, which integrates the response of soil biota over the four sampling in times following the release of the perturbation. The factor “Region” was treated as “random” to account for regional variation in climate and soil. The distance between the experimental sites in each region was such that we could not detect any spatial autocorrelation patterns in the data and we did therefore not need to introduce auto-correlation functions in the model. We detected some heterogeneous variance in the interaction between drought and management and we explicitly modelled that heterogeneity rather than transforming the data to meet the assumption of homogeneity. The fixed part of the model returned the following estimates:

Fixed effects: Moisture ~ Drought + Management + Drought:Management

	Value	Std.Error	DF	t-value	p-value
control-extensive	47.20	6.65	54	7.10	0.0000
drought	-13.65	4.12	54	-3.31	0.0016
intensive	2.38	3.31	54	0.72	0.4752
drought:intensive	3.47	5.14	54	0.68	0.5023

These results indicate an average reduction of approximately 30% over the two months following the removal of the shelters. It also shows no detectable effect of management on soil moisture, neither detectable interaction.

Table S3. As Table S2 but with Ecosystem respiration as response variable

Fixed effects: Moisture ~ Drought + Management + Drought:Management

	Value	Std.Error	DF	t-value	p-value
control-extensive	3.57	0.23	54	15.63	0.0000
drought	-0.79	0.20	54	-3.89	0.0003
intensive	0.55	0.27	54	2.01	0.0490
drought:intensive	-0.02	0.34	54	-0.06	0.9542

These results indicate an average reduction of approximately 22% over the two months following the removal of the shelters. It also shows a detectable effect of management, with intensive management increasing respiration of approximately 15%.

Benchmarking of estimated total food web fluxes and ecosystem respiration.

Food web fluxes

Our estimates of the total flux through the soil food web (i.e. from the basal microbes and roots to the top predaceous mites and nematodes), varied from approximately 250 to 1600 J h^{-1} m^{-2} . These estimates do not include the energy entering the microbes through the detritus and are likely missing some important contribution from neglected groups such as protists, which are only indirectly accounted for within the fluxes of their nematode consumers. On average, however, the total flux observed equals 640 J h^{-1} m^{-2} (at a soil depth between 0 and 10cm) and this is in line with previous estimates of soil food web fluxes. For example, for a similar food web in American grassland (Andrés et al., 2016) total fluxes around 700 J h^{-1} m^{-2} have been estimated. In a different types of soil food web but with very similar methods of flux estimate Potapov et al. (2019) presented total flux estimates in the order of 800 J h^{-1} m^{-2} . Although direct comparisons are not currently easy to conduct because of differences in units of measurements and scale of sampling, and also differences in how the food web are assembled functionally (e.g. definition of trophic groups), our comparisons suggest that our estimates are within the order of magnitude expected for soil food webs. Assuming a conversion coefficient for units of J to units of C as recommended by Peters (1983), that is 1 kg fresh mass = 7 × 106 J, we can then express our average fluxes as approximately 0.25 Kg C yr^{-1} m^{-2}. Potentially, this type of conversion into units of C, while relaying on some simplistic assumptions, still allow a first estimate of ratios between the fluxes of C estimated within the food web and the fluxes of C measured directly as ecosystem respiration.

Table S4. The full output of the SEM graphically presented in Figure 4 is provided below:

Regressions:

	Estimate	Std.Err	z-value	P(>|z|)	Std.lv	Std.all
Soil properties ~						
Location	1.000	0.085	11.804	0.000	1.000	0.820
Intensive Management	0.385	0.138	2.797	0.005	0.385	0.194
Soil Moisture ~						
Drought	-0.764	0.181	-4.232	0.000	-0.764	-0.392
Soil properties	0.568	0.091	6.235	0.000	0.568	0.577
Food Web Total flux ~						
Soil Moisture	-0.283	0.164	-1.730	0.084	-0.283	-0.277
Soil properties	-0.230	0.150	-1.534	0.125	-0.230	-0.229
Drought	-0.340	0.261	-1.303	0.192	-0.340	-0.171
Intensive Management	0.424	0.233	1.817	0.069	0.424	0.213
Entropy ~						
Food Web Total flux	0.406	0.093	4.378	0.000	0.406	0.408
Soil Moisture	-0.493	0.094	-5.240	0.000	-0.493	-0.488
Return Time ~						
Food Web Entropy	-0.442	0.116	-3.809	0.000	-0.442	-0.441
Total Respiration ~						
Drought	-0.854	0.227	-3.762	0.000	-0.854	-0.431
Soil Properties	0.211	0.131	1.613	0.107	0.211	0.212
Soil Moisture	0.116	0.161	0.720	0.471	0.116	0.114
Food Web Total flux	0.191	0.125	1.525	0.127	0.191	0.192
Entropy	0.096	0.145	0.661	0.509	0.096	0.096
Intensive Management	0.511	0.206	2.483	0.013	0.511	0.250

```
Variances:
                                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
  Soil properties                     0.537    0.098    5.477    0.000    0.537    0.546
  Soil Moisture                       0.489    0.089    5.477    0.000    0.489    0.514
  Food Web Total flux                 0.785    0.143    5.477    0.000    0.785    0.792
  Entropy                             0.459    0.084    5.477    0.000    0.459    0.470
  Return Time                         0.791    0.144    5.477    0.000    0.791    0.805
  Total Respiration                   0.579    0.106    5.477    0.000    0.579    0.591
  Location                            0.661    0.121    5.477    0.000    0.661    1.000
  Drought                             0.250    0.046    5.477    0.000    0.250    1.000
  Intensive management                0.250    0.046    5.477    0.000    0.250    1.000

R-Square:
                                   Estimate
    Soil properties                    0.71
    Soil Moisture                      0.49
    Food Web Total flux                0.21
    Entropy                            0.53
    Return  Time                       0.20
    Total Respiration                  0.41
```

This model was fitted to the correlation matrix of the data. We are not reporting estimates of covariances set to zero for obvious reasons (for example, there is obviously no path between location and drought, that both are clearly independent exogenous variables in the model). The final path structure underlying the equations of the regression part of the model was based on the general hypothesis set in Figure 1 of the paper. We needed to consider that the number of observational units limited the number of paths we could fit into a single model (overfitting and degrees of freedom issue), and we thus explored the support for alternative paths that are not included in the final model but that could have been possible. For example, we found very little support for including direct paths from the Location variable (a composite of Latitude and Longitude) to the soil food web metrics and total respiration, as that spatial effect was, not surprisingly, most parsimoniously described by the effects that location has on soil variables. Indeed, the three regions in the south and north of England and in Scotland were selected to maximize environmental gradients across experimental units. Soil moisture is positioned between the food web metrics variables and the exogenous variables (Location, Drought, Soil). This corresponds to our hypothesis that soil environmental gradients, location and rain-out shelters ("drought") all affected Soil Moisture, and soil moisture then affected the food web and total respiration. Drought, however, could have non soil moisture related effects but models with direct paths from drought to food web metrics and soil respiration received very little support and were discarded.

Food web parameters, and computer code to estimate fluxes and network entropy

We provide an exemplar data set of one particular food web and the original Python code to estimate food web fluxes according to the equation we present in the method of the main article. The code can be run suing the file "Example.py", which calls the python module (that is the computing functions) in the file "Mass_Balance.py". There are two files in input: one with the topology of the web (topology.txt) and another (info_for_example.csv) that lists the biomass of all trophic species (the example is based on S1, in Devon, drought, that is row one of Table S1), the "metabolism" (metabolic rate per unit of biomass), the death rate, and the efficiency. The death rates and efficiency are based on Moore & de Ruiter (2012) as we have no found specific evidence to support other particular choices and we thus went for values widely accepted by soil food web modellers. The computer routine will return a matrix of fluxes for every links in the food web. The sum of the fluxes will equal the total flux in the food web. The units of the biomass and rates in input are such that fluxes will be returned in units of $J\ h^{-1}\ m^{-2}$ but the computer code per se does not determine the final units (the units of the input determine the units of the output).

The computer code will also return the Jacobian of the underlying population dynamics, which can be used to compute the Return Time metrics as per the methods described in the main article. Briefly, one calculate the eigenvalues of the Jacobian, extract the dominant one, and takes the real part of that one to estimate the return time. Therefore, for future applications, the user will need to estimate the biomass of the trophic species in their food web, and the metabolic loss per units of biomass (using metabolic scaling, for example). The user can then measure death rates and efficiencies or choose some of the options available in the literature from previous studies for those rates. With these parameters, and a measurement of population densities, future users can use our code to estimate energy fluxes and the Jacobian of the underlying population dynamics of the nodes in the food web.

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