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Land-use intensity alters networks between biodiversity, ecosystem functions and services

SUPPLEMENTARY INFORMATION

Material Provided:

- **Supplementary Figures**
- **Supplementary Tables**
- **Supplementary Methods**
- **Extended Results**
- **Supplementary References**
- **Data availability**

Supplementary Figures

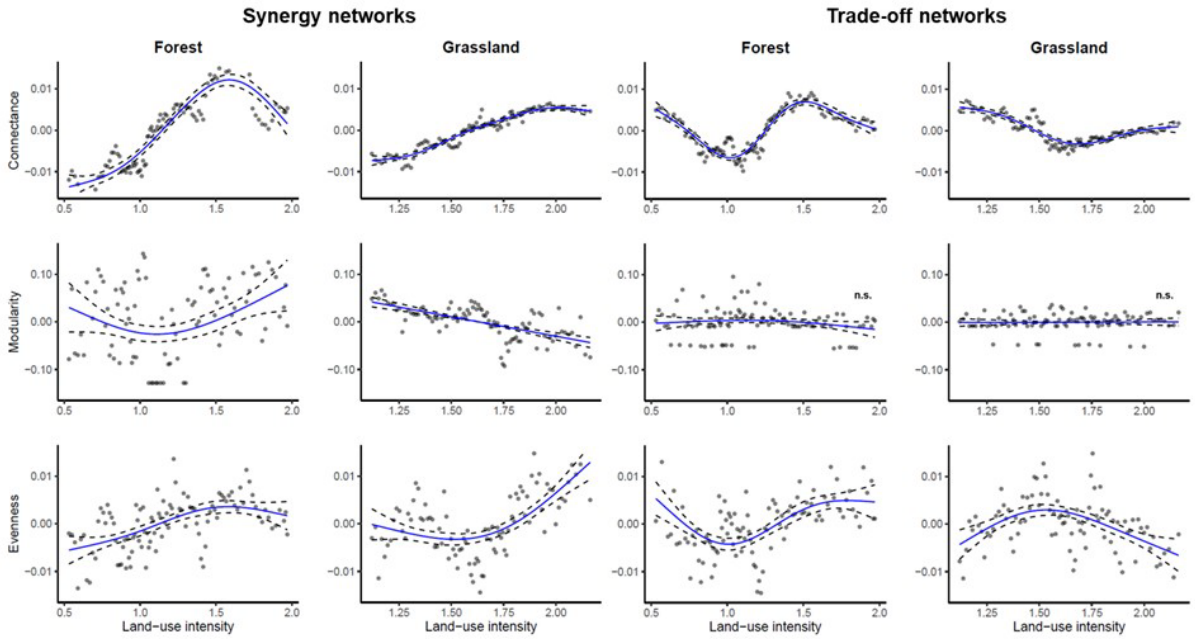

Fig. S1. Standardized effects of land-use intensity on the structure (connectance, modularity, and evenness) of synergy (positive correlation) and trade-off (negative correlation) networks in forests and grasslands. Y axes represent scaled effects (i.e. mean 0, sd 1). The 95% confidence intervals of the fitted GAMs are marked in dashed lines. X axes are based on different land use intensity indices in each habitat (see main text for details). Individual points are the metrics obtained from a correlation network based on a moving window along the land use axis including ca. 50-60 plots each. All effects are significant except indicated as n.s. (see Table S2).

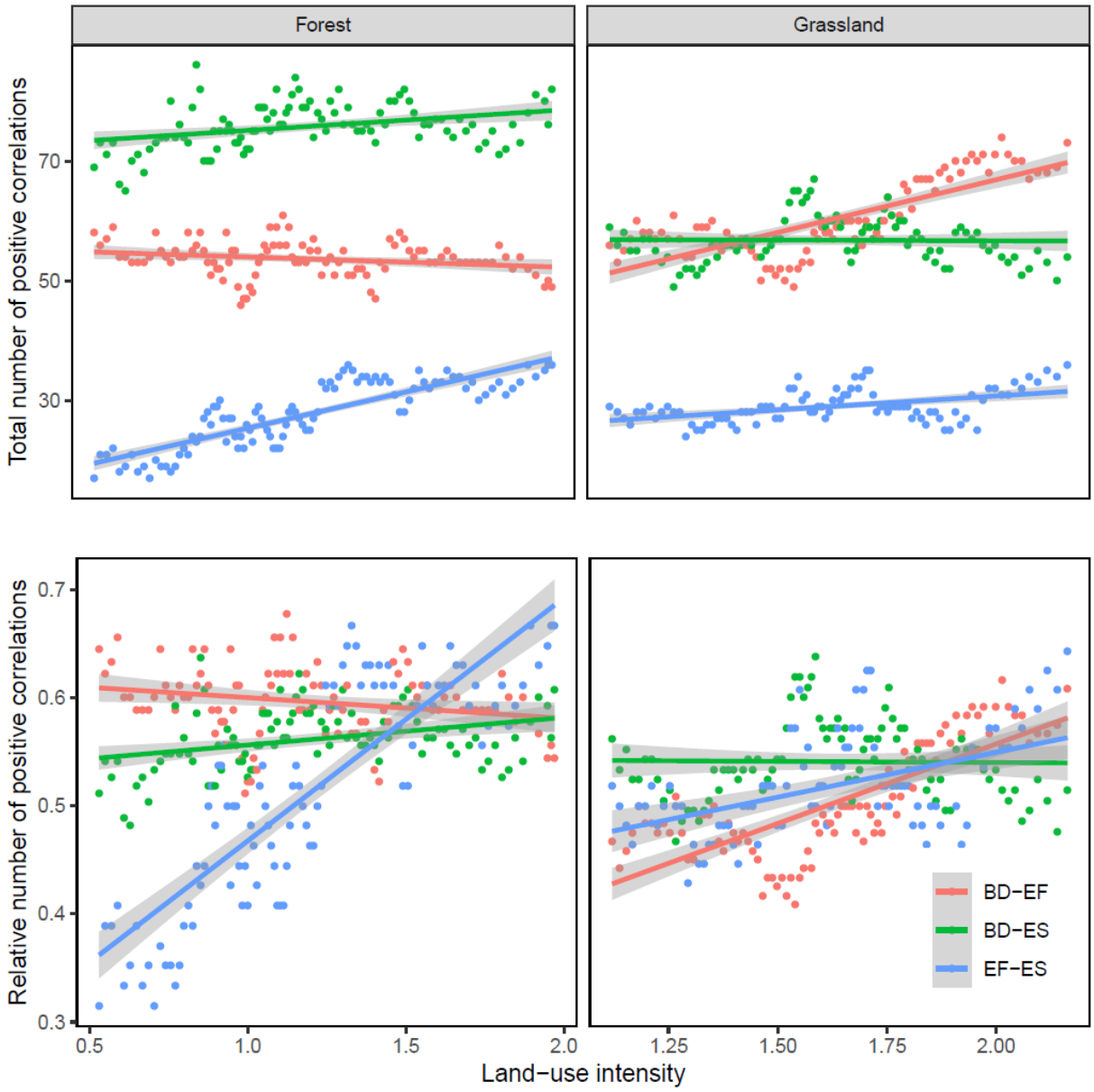

Fig. S2. Effects of land-use intensity on the total and relative number of positive correlations in forests and grasslands. Red for correlations between biodiversity and ecosystem functions, green for those between biodiversity and ecosystem services, and blue for those between ecosystem functions and ecosystem services. Note the number of negative correlations is the inverse of positive ones.

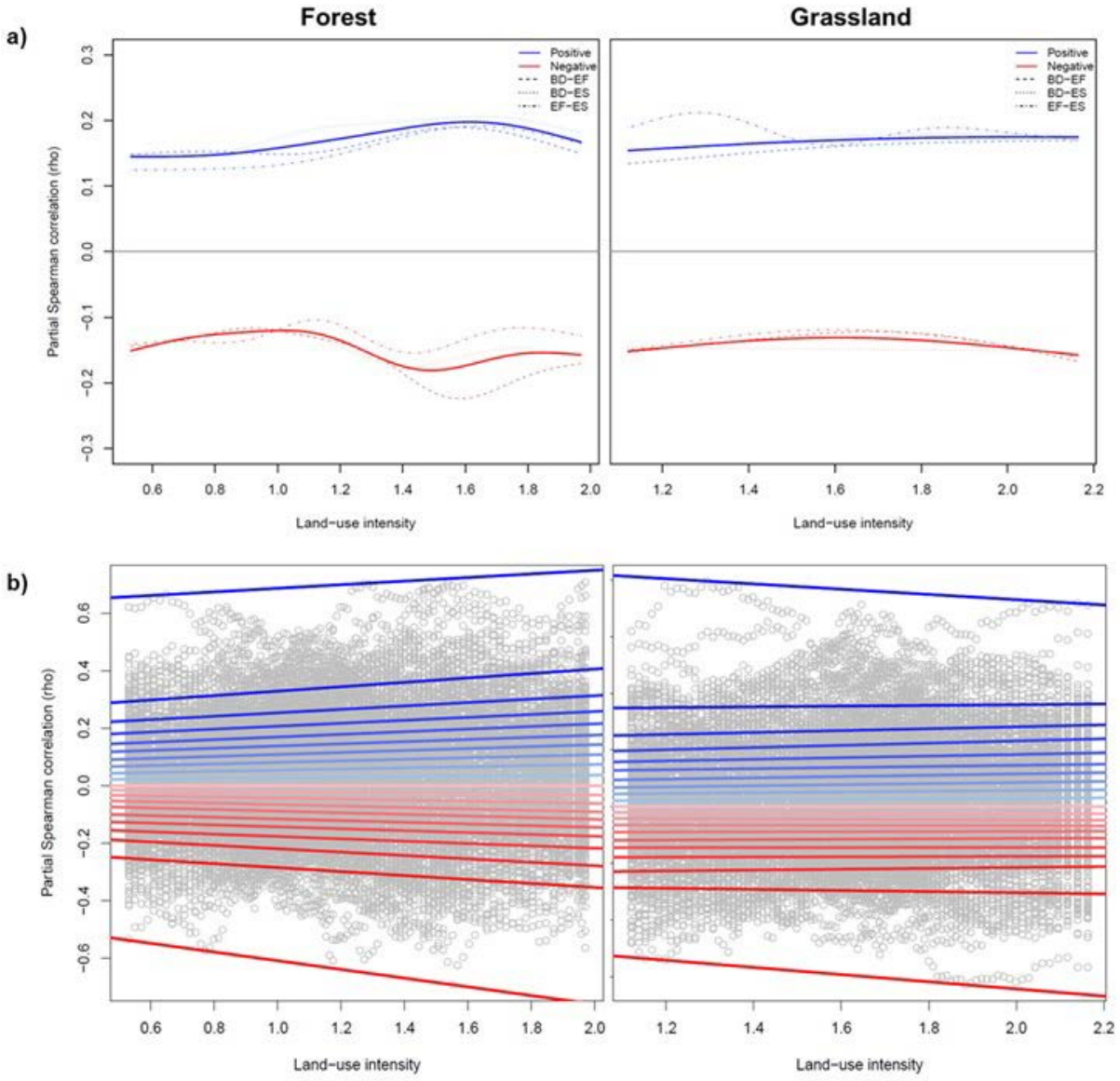

Fig. S3. Effects of land use intensity on correlation strength in forests and grasslands. Blue lines indicate positive partial Spearman correlations (synergies) and red lines negative ones (trade-offs). In a), solid lines represent overall correlations, while the dashed lines represent the correlations between biodiversity and ecosystem functions (BD-EF), biodiversity and ecosystem services (BD-ES), and ecosystem functions and ecosystem services (EF-ES). In b), lines represent quantile regressions, from quantile 0 (lightest colours) to quantile 1 (darkest colours).

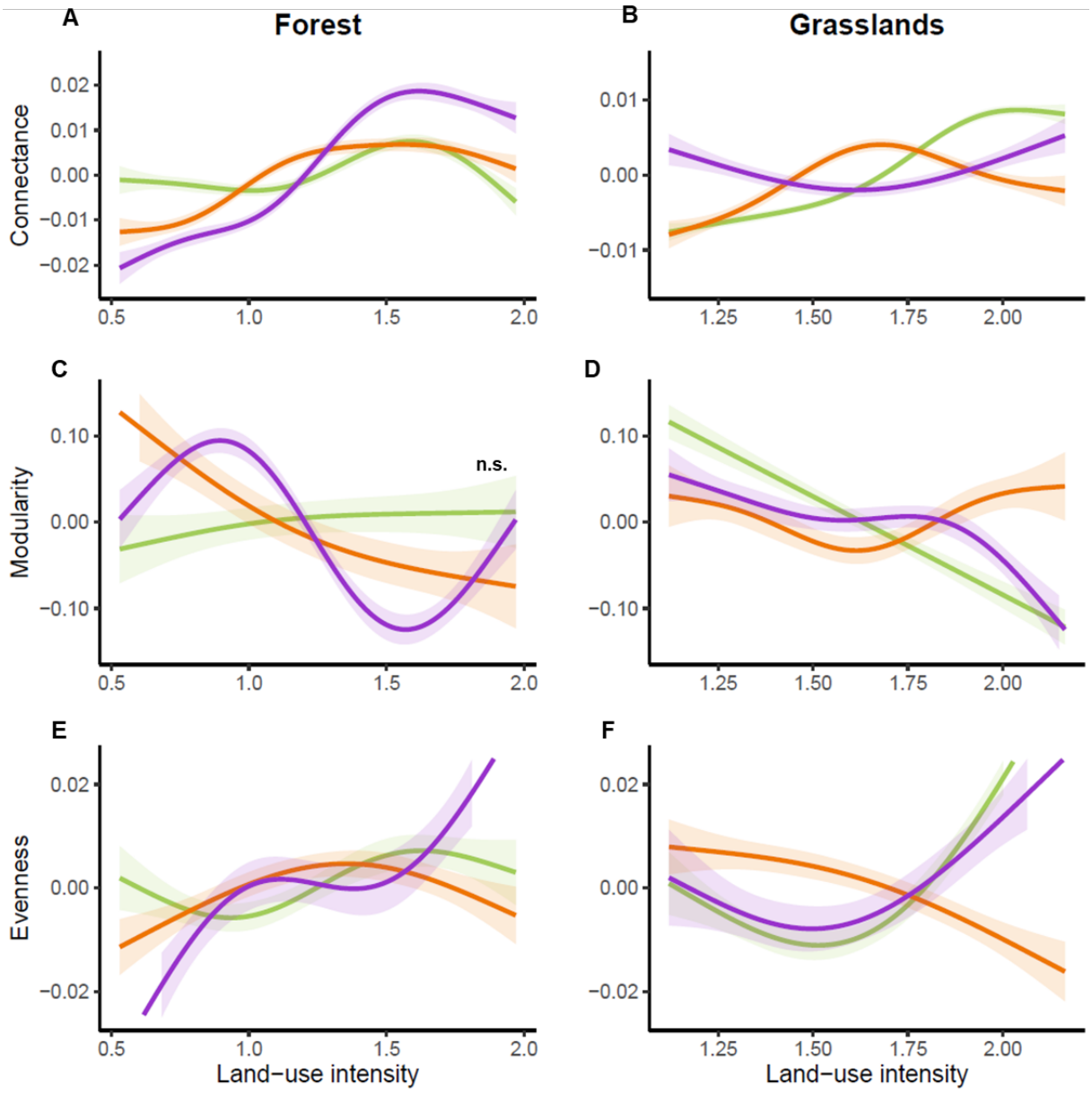

Fig. S4. Standardized effects of land-use intensity on network structure (connectance, modularity, and evenness) in forests (left) and grasslands (right). Coloured lines distinguish subsets of the networks for positive correlations between biodiversity and ecosystem functions (green), biodiversity and ecosystem services (orange), and ecosystem functions and ecosystem services (purple). Y axes represent the scaled effects (i.e. mean 0, sd 1). The 95% confidence intervals of the fitted GAMs are shadowed. All effects are significant except the ones indicated as n.s. ($p<0.001$; Table S3).

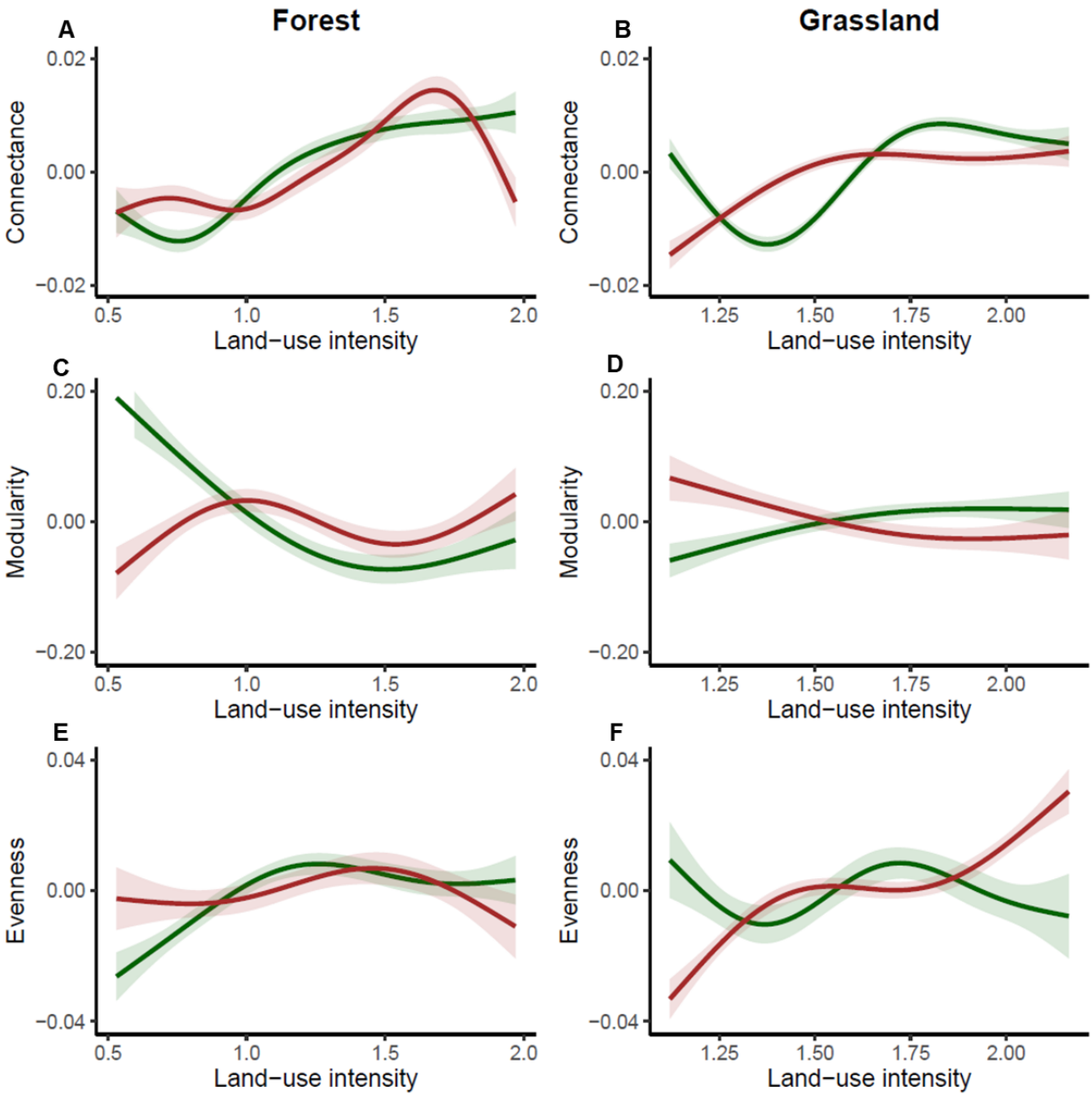

Fig. S5. Standardized effects of land-use intensity on the structure (connectance, modularity, and evenness) of aboveground (green) and belowground (brown) networks in forests (left) and grasslands (right). (See Table S1 for the components of each network). The 95% confidence intervals of the fitted GAMs are shadowed. All effects are significant (Table S4).

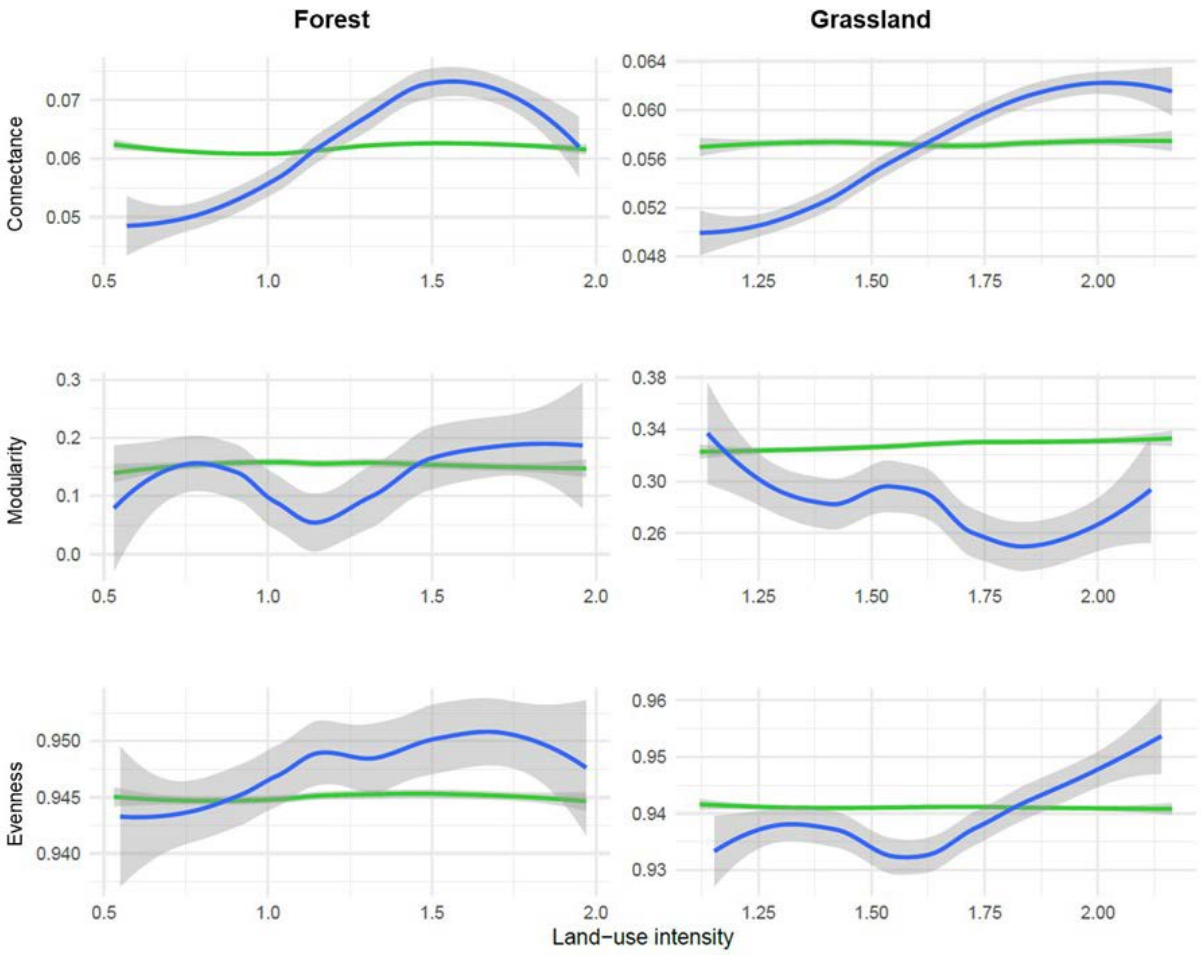

Fig. S6. Comparison between the effects of land-use intensity on the observed networks (blue lines) and on networks obtained from 100 data randomisations (green lines). 95% confidence intervals are marked in grey. Observed networks shows clearly different patterns than random data. Note that data was fitted using a 'loess' approximation and might slightly differ from the final GAM models. See *Random expectations* in Extended results for details.

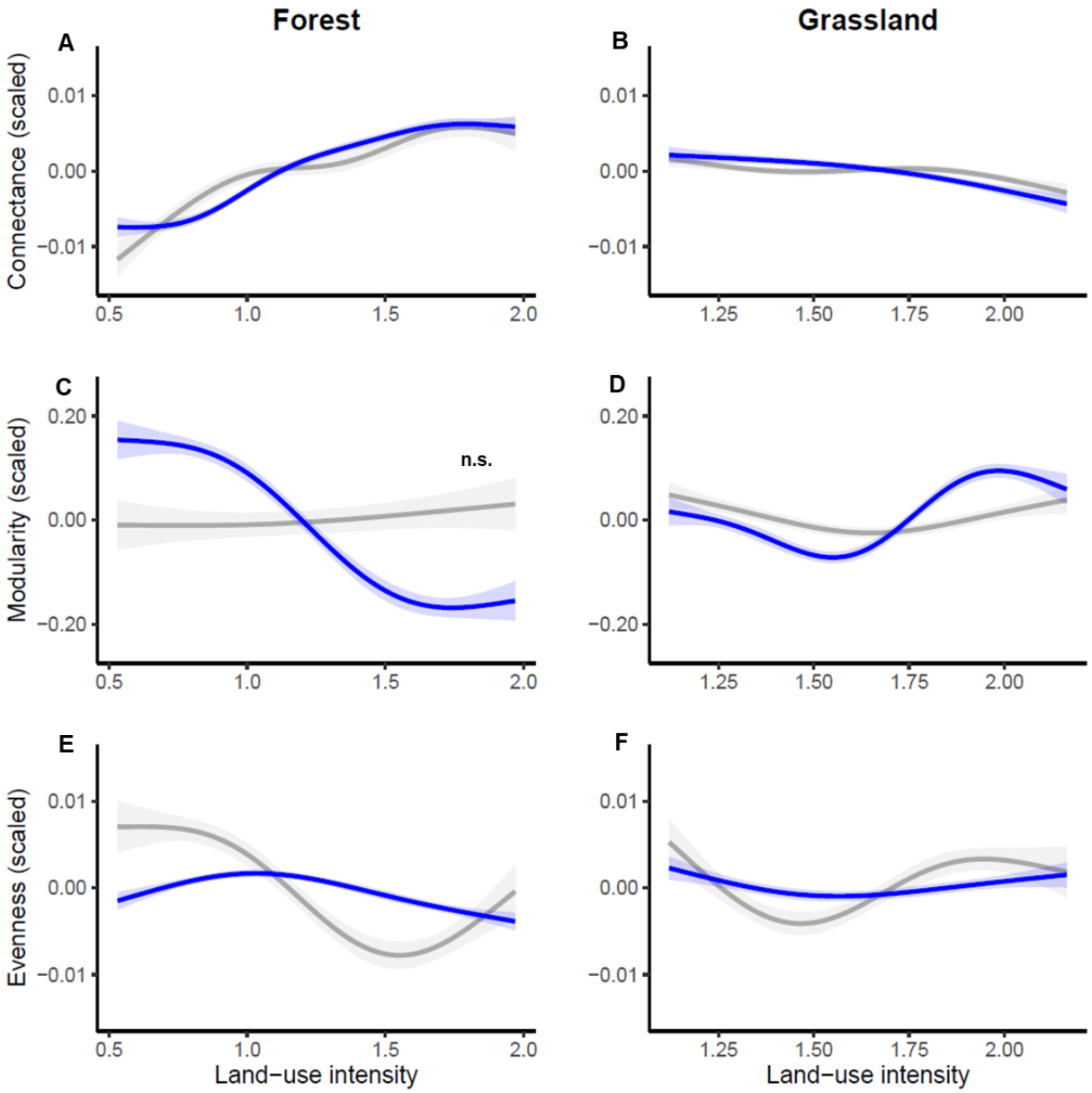

Fig. S7. Standardized effects of land-use intensity on positive network structure (connectance, modularity, and evenness) in forests (left) and grasslands (right) based on raw Spearman correlations (grey) and raw significant Spearman correlations (blue). Y axes represent scaled effects (i.e. mean 0, sd 1). Shadows represent the 95% confidence intervals of the fitted GAMs. All effects are significant ($p<0.001$) except indicated as n.s. (Table S7).

Supplementary Tables

Table S1. Nodes included in the aboveground (AG) and belowground (BG) networks per habitat (F = Forest, G = Grassland). Node types: BD = Biodiversity, EF = Ecosystem Function, ES = Ecosystem Service.

Node type	Compartment	Habitat	Variable name	Node name
BD	BG	Both	Bacteria	Bacteria
BD	BG	Both	Protist bacterivore	Protist.bacteriv
BD	BG	Both	Protist eukaryvore	Protist.eukaryv
BD	BG	Both	Protist omnivore	Protist.omniv
BD	BG	Both	Protist parasite plant	Protist.parasite.plant
BD	BG	Both	Soil fungi decomposer	Soilfungi.decomp
BD	BG	Both	Soil fungi pathotroph	Soilfungi.pathot
BD	BG	Both	Soil fungi symbiont	Soilfungi.symb
BD	AG	Both	Lichens	Lichen
BD	AG	Both	Bryophytes	Moss
BD	AG	Both	Vascular plant	Plant
BD	AG	Grassland	Plant pathogen	Plant.pathog
BD	AG	Both	Aboveground decomposer	AG.decomp
BD	AG	Both	Aboveground herbivore	AG.herb
BD	AG	Forest	Aboveground omnivore	AG.omniv
BD	AG	Both	Secondary consumer	Snd.cons
EF	BG	Grassland	Root biomass	Root.biomass
EF	BG	Both	Root decomposition	Root.decomp
EF	BG	Both	Soil C cycling	soilCflxs
EF	BG	Grassland	Nitrogen retention	NRI
EF	BG	Grassland	Soil N cycling	soilNflxs
EF	BG	Grassland	Phosphorus retention	PRI
EF	BG	Forest	N availability	N.aval
EF	BG	Forest	P availability	P.aval
EF	BG	Both	Phosphatase	Phosphatase
EF	AG	Both	Dung decomposition	Dung.decomp
ES	BG	Grassland	Infiltration	Groundwater.recharge
ES	BG	Both	Soil C stock	Soil.C.stock
ES	AG	Forest	Trees C stock	Trees.C.stock
ES	AG	Forest	Temperature regulation	Temp.reg
ES	AG	Grassland	Herbivory control	Herbivory.control
ES	AG	Forest	Pest control	Pest.control
ES	AG	Grassland	Forage quality	Forage.quality
ES	AG	Grassland	Forage biomass	Biomass
ES	AG	Forest	Timber	Timber
ES	AG	Forest	Edible fungi	Edible.fungi
ES	AG	Forest	Edible plants	Edible.plants
ES	AG	Forest	Cultural value plants	Cultural.plants
ES	AG	Grassland	Charismatic butterflies	Butterfl.abund
ES	AG	Both	Bird-watching potential	Pot.bird_watching

Table S2. Generalized Additive Model (GAM) coefficients of the effect of land-use intensity on network metrics by habitat and correlation type (k: model attribute; EDF: estimated degrees of freedom; Adj.R^2: adjusted r-squared; DE: deviance explained; N: sample size).

Correlation	Habitat	Metric	k	EDF	F	p-value	Adj. R^2	DE	N
Positive	Grassland	Connectance	6	4.584	208.311	0.000	0.919	0.923	91
Positive	Grassland	Modularity	5	1	64.354	0.000	0.413	0.420	91
Positive	Grassland	Evenness	4	2.404	21.871	0.000	0.412	0.428	91
Positive	Forest	Connectance	6	4.314	134.594	0.000	0.866	0.872	101
Positive	Forest	Modularity	4	2.185	4.881	0.009	0.102	0.121	101
Positive	Forest	Evenness	4	2.659	14.584	0.000	0.300	0.318	101
Negative	Grassland	Connectance	6	4.305	64.944	0.000	0.776	0.787	91
Negative	Grassland	Modularity	5	1	0.021	0.886	-0.011	0.000	91
Negative	Grassland	Evenness	4	2.554	12.711	0.000	0.269	0.290	91
Negative	Forest	Connectance	6	4.888	112.908	0.000	0.849	0.857	101
Negative	Forest	Modularity	4	1.785	1.628	0.188	0.027	0.045	101
Negative	Forest	Evenness	4	2.914	16.727	0.000	0.319	0.339	101

Table S3. Generalized Additive Model (GAM) coefficients of the effect of land-use intensity on synergy network metrics by habitat and link type (k: model attribute; EDF: estimated degrees of freedom; Adj.R^2: adjusted r-squared; DE: deviance explained; N: sample size).

Habitat	Link type	Metric	k	EDF	F	p-value	Adj.R^2	DE	N
Grassland	BD-EF	Connectance	6	4.656	385.724	0.000	0.955	0.957	91
Grassland	BD-EF	Modularity	5	1	176.844	0.000	0.661	0.665	91
Grassland	BD-EF	Evenness	4	2.674	77.596	0.000	0.720	0.728	91
Grassland	BD-ES	Connectance	5	2.633	13.952	0.000	0.339	0.359	91
Grassland	BD-ES	Modularity	5	3.596	19.832	0.000	0.465	0.487	91
Grassland	BD-ES	Evenness	4	2.355	14.165	0.000	0.294	0.312	91
Grassland	EF-ES	Connectance	6	4.581	78.847	0.000	0.795	0.804	101
Grassland	EF-ES	Modularity	4	1.991	20.304	0.000	0.322	0.336	101
Grassland	EF-ES	Evenness	4	2.394	10.255	0.000	0.234	0.252	101
Forest	BD-EF	Connectance	5	3.796	65.421	0.000	0.742	0.753	91
Forest	BD-EF	Modularity	5	3.593	7.853	0.000	0.245	0.276	91
Forest	BD-EF	Evenness	4	1.967	22.021	0.000	0.364	0.377	91
Forest	BD-ES	Connectance	6	4.656	27.150	0.000	0.570	0.590	101
Forest	BD-ES	Modularity	4	1.579	1.134	0.262	0.018	0.034	101
Forest	BD-ES	Evenness	4	2.863	10.642	0.000	0.231	0.253	101
Forest	EF-ES	Connectance	6	4.656	239.408	0.000	0.922	0.926	101
Forest	EF-ES	Modularity	4	2.987	96.115	0.000	0.742	0.749	101
Forest	EF-ES	Evenness	4	2.903	23.376	0.000	0.406	0.423	101

Table S4. Generalized Additive Model (GAM) coefficients of the effect of land-use intensity on synergy network metrics by habitat and compartment (k: model attribute; EDF: estimated degrees of freedom; Adj.R^2: adjusted r-squared; DE: deviance explained; N: sample size).

Habitat	Compartment	Metric	k	EDF	F	p-value	Adj.R^2	DE	N
Grassland	Aboveground	Connectance	5	3.943	151.717	0.000	0.870	0.876	91
Grassland	Aboveground	Modularity	3	1.83	14.607	0.000	0.221	0.237	91
Grassland	Aboveground	Evenness	5	3.694	6.131	0.001	0.184	0.218	91
Grassland	Belowground	Connectance	5	3.401	60.447	0.000	0.720	0.731	91
Grassland	Belowground	Modularity	4	2.053	9.773	0.000	0.211	0.229	91
Grassland	Belowground	Evenness	5	3.7	64.602	0.000	0.738	0.749	91
Forest	Aboveground	Connectance	7	5.521	68.419	0.000	0.801	0.812	101
Forest	Aboveground	Modularity	4	2.552	45.77	0.000	0.572	0.583	101
Forest	Aboveground	Evenness	5	3.402	22.964	0.000	0.468	0.486	101
Forest	Belowground	Connectance	7	5.649	42.15	0.000	0.712	0.728	101
Forest	Belowground	Modularity	4	2.95	9.658	0.000	0.211	0.234	101
Forest	Belowground	Evenness	4	2.806	3.509	0.012	0.093	0.118	101

Table S5. Module components of the network at lowest and highest land-use intensity in grasslands and forests. To facilitate the identification of nodes, ecosystem function are in italic (blue font in Fig. 3) and ecosystem services in bold (red font in Fig. 3).

	Lowest land-use intensity		Highest land-use intensity	
Habitat	**Node name**	**Module**	**Node name**	**Module**
Grassland	Aboveground decomposers	a	Aboveground decomposers	d
Grassland	Protists eukaryvore	a	Aboveground herbivores	d
Grassland	Protists omnivore	a	Secondary consumers	d
Grassland	Protists parasite plant	a	*Nitrogen retention*	d
Grassland	Soil fungi decomposer	a	*Root decomposition*	d
Grassland	Soil fungi pathotroph	a	**Herbivory control**	d
Grassland	Soil fungi symbiont	a	**Forage biomass**	d
Grassland	*Soil N cycling*	a	**Potential bird-watching**	d
Grassland	*Soil C cycling*	a	Protists bacterivore	e
Grassland	*Nitrogen retention*	a	Protists eukaryvore	e
Grassland	*Phosphatase*	a	Protists omnivore	e
Grassland	*Phosphorus retention*	a	*Root biomass*	e
Grassland	**Soil C stock**	a	**Soil C stock**	e
Grassland	**Forage quality**	a	Bacteria	f
Grassland	**Herbivory control**	a	Protists parasite plant	f
Grassland	Bacteria	b	Soil fungi decomposer	f
Grassland	Protists bacterivore	b	Soil fungi pathotroph	f
Grassland	Plant pathogens	b	Soil fungi symbiont	f
Grassland	Secondary consumers	b	*Soil N cycling*	f
Grassland	*Root biomass*	b	*Soil C cycling*	f
Grassland	**Forage biomass**	b	*Phosphatase*	f
Grassland	Aboveground herbivores	c	**Forage quality**	f
Grassland	Lichens	c	Lichens	g
Grassland	Bryophytes	c	Bryophytes	g
Grassland	Vascular plants	c	Vascular plants	g
Grassland	*Root decomposition*	c	Plant pathogens	g
Grassland	*Dung decomposition*	c	*Phosphorus retention*	g
Grassland	**Infiltration**	c	*Dung decomposition*	g
Grassland	**Charismatic butterflies**	c	**Infiltration**	g
Grassland	**Potential bird-watching**	c	**Charismatic butterflies**	g
Forest	Protists bacterivore	a	Aboveground decomposers	e
Forest	Protists eukaryvore	a	Soil fungi symbiont	e
Forest	Soil fungi symbiont	a	*Root decomposition*	e
Forest	*Dung decomposition*	a	*N availability*	e
Forest	**Edible fungi**	a	**Potential bird-watching**	e
Forest	**Temperature regulation**	a	**Edible fungi**	e
Forest	Bacteria	b	**Trees C stock**	e
Forest	Protists omnivore	b	Aboveground herbivores	f
Forest	Protists parasite plant	b	Aboveground omnivores	f
Forest	Soil fungi decomposer	b	Bryophytes	f
Forest	Aboveground decomposers	b	Vascular plants	f
Forest	*Soil C cycling*	b	Secondary consumers	f
Forest	*N availability*	b	*P availability*	f

Forest	*Phosphatase*	b	*Dung decomposition*	f
Forest	**Potential bird-watching**	b	**Edible plants**	f
Forest	**Soil C stock**	b	**Timber**	f
Forest	Lichens	c	Bacteria	g
Forest	Bryophytes	c	Protists bacterivore	g
Forest	Soil fungi pathotroph	c	Protists eukaryvore	g
Forest	**Timber**	c	Protists omnivore	g
Forest	**Trees C stock**	c	Protists parasite plant	g
Forest	Aboveground herbivores	d	Soil fungi decomposer	g
Forest	Aboveground omnivores	d	Soil fungi pathotroph	g
Forest	Secondary consumers	d	Lichens	g
Forest	Vascular plants	d	*Phosphatase*	g
Forest	*Root decomposition*	d	*Soil C cycling*	g
Forest	*P availability*	d	**Cultural value plants**	g
Forest	**Pest control**	d	**Pest control**	g
Forest	**Cultural value plants**	d	**Soil C stock**	g
Forest	**Edible plants**	d	**Temperature regulation**	g

Table S6. Model coefficients of the effects of land-use intensity (LUI) on *D* (i.e. weighted node degree). Non-significant results are in italic grey (See Table S1 for variable acronyms).

Habitat	Variable	Estimate	Std. Error	t value	Pr(>|t|)	Significance
Grassland	LUI	*-0.008*	*0.062*	*-0.123*	*0.902*	
Grassland	AG.herb	-1.074	0.144	-7.468	0.000	***
Grassland	Bacteria	-1.488	0.144	-10.345	0.000	***
Grassland	Biomass	2.073	0.144	14.413	0.000	***
Grassland	Butterfl.abund	*-0.015*	*0.144*	*-0.104*	*0.917*	
Grassland	Dung.decomp	0.498	0.144	3.466	0.001	***
Grassland	Forage.quality	0.434	0.144	3.015	0.003	**
Grassland	Groundwater.recharge	0.670	0.144	4.658	0.000	***
Grassland	Herbivory.control	*-0.085*	*0.144*	*-0.593*	*0.553*	
Grassland	Lichen	*-0.097*	*0.144*	*-0.674*	*0.500*	
Grassland	Moss	-0.472	0.144	-3.282	0.001	**
Grassland	NRI	-1.057	0.144	-7.353	0.000	***
Grassland	Phosphatase	2.151	0.144	14.955	0.000	***
Grassland	Plant	*0.260*	*0.144*	*1.808*	*0.071*	
Grassland	Plant.pathog	-0.514	0.144	-3.576	0.000	***
Grassland	Pot.bird_watching	*-0.236*	*0.144*	*-1.639*	*0.101*	
Grassland	PRI	-1.814	0.144	-12.611	0.000	***
Grassland	Protist.bacteriv	0.846	0.144	5.887	0.000	***
Grassland	Protist.eukaryv	0.735	0.144	5.111	0.000	***
Grassland	Protist.omniv	1.097	0.144	7.625	0.000	***
Grassland	Protist.parasite.plant	*0.226*	*0.144*	*1.574*	*0.116*	
Grassland	Root.biomass	-1.629	0.144	-11.325	0.000	***
Grassland	Root.decomp	*0.011*	*0.144*	*0.075*	*0.940*	
Grassland	Snd.cons	-0.937	0.144	-6.513	0.000	***
Grassland	Soil.C.stock	*0.049*	*0.144*	*0.341*	*0.733*	
Grassland	soilCflxs	*0.133*	*0.144*	*0.927*	*0.354*	
Grassland	Soilfungi.decomp	*-0.060*	*0.144*	*-0.414*	*0.679*	
Grassland	Soilfungi.pathot	-0.367	0.144	-2.554	0.011	*
Grassland	Soilfungi.symb	*0.208*	*0.144*	*1.444*	*0.149*	
Grassland	soilNflxs	1.091	0.144	7.588	0.000	***
Grassland	LUI:AG.herb	0.726	0.087	8.344	0.000	***
Grassland	LUI:Bacteria	1.029	0.087	11.825	0.000	***
Grassland	LUI:Biomass	-0.956	0.087	-10.988	0.000	***
Grassland	LUI:Butterfl.abund	0.295	0.087	3.387	0.001	***
Grassland	LUI:Dung.decomp	*-0.056*	*0.087*	*-0.646*	*0.518*	
Grassland	LUI:Forage.quality	0.348	0.087	4.001	0.000	***
Grassland	LUI:Groundwater.recharge	*-0.074*	*0.087*	*-0.856*	*0.392*	
Grassland	LUI:Herbivory.control	*0.148*	*0.087*	*1.704*	*0.089*	
Grassland	LUI:Lichen	*0.091*	*0.087*	*1.045*	*0.296*	
Grassland	LUI:Moss	0.371	0.087	4.265	0.000	***
Grassland	LUI:NRI	0.691	0.087	7.942	0.000	***
Grassland	LUI:Phosphatase	-1.018	0.087	-11.707	0.000	***
Grassland	LUI:Plant	*-0.132*	*0.087*	*-1.521*	*0.128*	

Grassland	LUI:Plant.pathog	0.483	0.087	5.556	0.000	***
Grassland	LUI:Pot.bird_watching	0.627	0.087	7.203	0.000	***
Grassland	LUI:PRI	1.392	0.087	15.998	0.000	***
Grassland	LUI:Protist.bacteriv	-0.319	0.087	-3.666	0.000	***
Grassland	LUI:Protist.eukaryv	-0.258	0.087	-2.963	0.003	**
Grassland	LUI:Protist.omniv	-0.454	0.087	-5.216	0.000	***
Grassland	LUI:Protist.parasite.plant	*0.108*	*0.087*	*1.241*	*0.215*	
Grassland	LUI:Root.biomass	1.488	0.087	17.111	0.000	***
Grassland	LUI:Root.decomp	*0.108*	*0.087*	*1.244*	*0.214*	
Grassland	LUI:Snd.cons	0.618	0.087	7.103	0.000	***
Grassland	LUI:Soil.C.stock	1.134	0.087	13.033	0.000	***
Grassland	LUI:soilCflxs	0.554	0.087	6.363	0.000	***
Grassland	LUI:Soilfungi.decomp	*0.166*	*0.087*	*1.912*	*0.056*	
Grassland	LUI:Soilfungi.pathot	0.401	0.087	4.613	0.000	***
Grassland	LUI:Soilfungi.symb	-0.209	0.087	-2.403	0.016	*
Grassland	LUI:soilNflxs	*0.079*	*0.087*	*0.909*	*0.364*	
Forest	LUI	0.369	0.078	4.756	0.000	***
Forest	AG.herb	*-0.158*	*0.138*	*-1.143*	*0.253*	
Forest	AG.omniv	*0.019*	*0.138*	*0.136*	*0.892*	
Forest	Bacteria	0.381	0.138	2.751	0.006	**
Forest	Cultural.plants	-0.291	0.138	-2.103	0.036	*
Forest	Dung.decomp	*0.051*	*0.138*	*0.369*	*0.712*	
Forest	Edible.fungi	1.084	0.138	7.833	0.000	***
Forest	Edible.plants	*0.031*	*0.138*	*0.225*	*0.822*	
Forest	Lichen	0.394	0.138	2.845	0.004	**
Forest	Moss	0.403	0.138	2.913	0.004	**
Forest	N.aval	0.406	0.138	2.937	0.003	**
Forest	P.aval	*0.055*	*0.138*	*0.399*	*0.690*	
Forest	Pest.control	0.338	0.138	2.440	0.015	*
Forest	Phosphatase	-1.063	0.138	-7.683	0.000	***
Forest	Plant	*0.232*	*0.138*	*1.678*	*0.093*	
Forest	Pot.bird_watching	1.150	0.138	8.313	0.000	***
Forest	Protist.bacteriv	0.635	0.138	4.586	0.000	***
Forest	Protist.eukaryv	0.673	0.138	4.864	0.000	***
Forest	Protist.omniv	0.876	0.138	6.331	0.000	***
Forest	Protist.parasite.plant	*0.253*	*0.138*	*1.827*	*0.068*	
Forest	Root.decomp	2.383	0.138	17.221	0.000	***
Forest	Snd.cons	*-0.044*	*0.138*	*-0.315*	*0.753*	
Forest	Soil.C.stock	*0.089*	*0.138*	*0.646*	*0.518*	
Forest	soilCflxs	0.926	0.138	6.688	0.000	***
Forest	Soilfungi.decomp	*0.221*	*0.138*	*1.594*	*0.111*	
Forest	Soilfungi.pathot	0.436	0.138	3.148	0.002	**
Forest	Soilfungi.symb	0.406	0.138	2.936	0.003	**
Forest	Temp.reg	*0.210*	*0.138*	*1.516*	*0.130*	
Forest	Timber	-0.563	0.138	-4.067	0.000	***
Forest	Trees.C.stock	0.665	0.138	4.808	0.000	***
Forest	LUI:AG.herb	0.301	0.110	2.749	0.006	**

Forest	LUI:AG.omniv	*0.174*	*0.110*	*1.588*	*0.112*	
Forest	LUI:Bacteria	-0.420	0.110	-3.830	0.000	***
Forest	LUI:Cultural.plants	1.253	0.110	11.431	0.000	***
Forest	LUI:Dung.decomp	*0.158*	*0.110*	*1.438*	*0.151*	
Forest	LUI:Edible.fungi	-0.408	0.110	-3.719	0.000	***
Forest	LUI:Edible.plants	0.499	0.110	4.556	0.000	***
Forest	LUI:Lichen	-0.366	0.110	-3.338	0.001	***
Forest	LUI:Moss	-0.366	0.110	-3.337	0.001	***
Forest	LUI:N.aval	-0.333	0.110	-3.037	0.002	**
Forest	LUI:P.aval	0.423	0.110	3.861	0.000	***
Forest	LUI:Pest.control	-0.399	0.110	-3.637	0.000	***
Forest	LUI:Phosphatase	1.930	0.110	17.607	0.000	***
Forest	LUI:Plant	0.250	0.110	2.282	0.023	*
Forest	LUI:Pot.bird_watching	*-0.083*	*0.110*	*-0.756*	*0.449*	
Forest	LUI:Protist.bacteriv	-0.607	0.110	-5.540	0.000	***
Forest	LUI:Protist.eukaryv	-0.522	0.110	-4.760	0.000	***
Forest	LUI:Protist.omniv	-0.722	0.110	-6.583	0.000	***
Forest	LUI:Protist.parasite.plant	-0.272	0.110	-2.478	0.013	*
Forest	LUI:Root.decomp	-1.326	0.110	-12.099	0.000	***
Forest	LUI:Snd.cons	*0.094*	*0.110*	*0.856*	*0.392*	
Forest	LUI:Soil.C.stock	0.455	0.110	4.151	0.000	***
Forest	LUI:soilCflxs	0.248	0.110	2.263	0.024	*
Forest	LUI:Soilfungi.decomp	*-0.180*	*0.110*	*-1.646*	*0.100*	
Forest	LUI:Soilfungi.pathot	-0.308	0.110	-2.808	0.005	**
Forest	LUI:Soilfungi.symb	-0.500	0.110	-4.563	0.000	***
Forest	LUI:Temp.reg	-0.335	0.110	-3.054	0.002	**
Forest	LUI:Timber	0.787	0.110	7.184	0.000	***
Forest	LUI:Trees.C.stock	-0.493	0.110	-4.495	0.000	***

Table S7. Generalized Additive Model (GAM) coefficients of the effect of land-use intensity on synergy network metrics by habitat and correlation type. (Raw: raw Spearman correlations; Sign: raw significant Spearman correlations; k: model attribute; EDF: estimated degrees of freedom; Adj. R^2: adjusted r-squared; DE: deviance explained; N: sample size).

Correlation	Habitat	Metric	k	EDF	F	p-value	Adj. R^2	DE	N
Raw	Grassland	Connectance	4	2.879	9.644	0.000	0.236	0.261	91
Raw	Grassland	Modularity	5	3.013	13.405	0.000	0.346	0.368	91
Raw	Grassland	Evenness	4	2.953	19.305	0.000	0.379	0.399	91
Raw	Forest	Connectance	6	4.428	53.433	0.000	0.719	0.731	101
Raw	Forest	Modularity	4	1.393	1.362	0.357	0.009	0.023	101
Raw	Forest	Evenness	4	2.954	57.072	0.000	0.631	0.642	101
Sign	Grassland	Connectance	4	2.151	34.483	0.000	0.495	0.507	91
Sign	Grassland	Modularity	5	3.945	75.780	0.000	0.771	0.781	91
Sign	Grassland	Evenness	4	2.548	8.498	0.000	0.190	0.213	91
Sign	Forest	Connectance	6	4.702	222.685	0.000	0.917	0.921	101
Sign	Forest	Modularity	4	2.964	187.044	0.000	0.848	0.853	101
Sign	Forest	Evenness	4	2.951	48.304	0.000	0.585	0.598	101

Supplementary Methods

Details of the soil sampling procedure

Joint soil sampling campaigns were performed in May 2011, 2014 and 2016, each one collecting 14 samples of the upper 10 cm of the mineral soil in each of 300 plots using a split tube sampler with a diameter of 5 cm. Cores were taken along two transects of 20 m in grasslands and 40 m in forests, which were selected always in the same relationship to the overall plot. The cores were cut at a section representing a fixed sampling depth of 0 to 10 cm. Aboveground portions of plants were removed. Composite samples were prepared by mixing the material selected from the 14 cores.

Biodiversity

Bacteria (ID 19526). Soil samples from the 2011 joint soil-sampling campaign (see above) were processed using pyrosequencing-derived partial 16S rRNA gene sequences with the QIIME software package. Following the extraction of raw data, reads shorter than 300 bp, of bad quality, with long homopolymer stretches (>8 bp), or primer mismatches (>3) were removed. Subsequently, sequences were denoised employing Acacia (1). Cutadapt (2) was employed to remove remaining primer sequences. Chimera-checking was performed using the most recent versions of USEARCH and the SILVA SSURef 123 NR database as reference (3, 4). Processed sequences were clustered in operational taxonomic units (OTUs) at 3% and 20% genetic distance representing species and phylum level, respectively. Taxonomic assignment was performed using the QIIME assign_taxonomy.py script, performing a BLAST alignment against the most recent SILVA database.

Protists (bacterivores, eukarivores, omnivores and plant parasites from phyla Cercozoa and Endomyxa; ID 24426). Soil samples from the 2011 joint soil-sampling campaign (see above) were processed using high-throughput Illumina sequencing of the V4 region of the small subunit rRNA gene (5). Taxonomic and trophic group assignment procedures were described previously in (6).

Soil fungi (decomposers, pathotrophs and symbionts; ID 25446-25448). Soil samples were collected in each of the 300 plots during the joint soil-sampling campaign in May 2011 (see above). From each plot, the pooled soil sample was stored at -80°C and DNA was extracted twice from a 0.5 g subsample of each sample using MoBio Power Soil DNA isolation kits (MoBio Laboratories, Carlsbad, CA, USA) following the manufacturer's recommendations. Afterwards, we used a PCR approach to amplify fungal rDNA (c), purified and cleaned the products and sequenced the ITS2 region by using 454 pyrosequencing (7). Quality filtering and analysis of the sequences was performed in a sequential analysis using MOTHUR (8) as described in (9). Initially, a filtering step was performed to discard sequences with ambiguous bases, homo-polymers and primer differences of more than eight bases. Simultaneously all primer and barcode sequences were removed. At the same time, sequence reads with a quality score lower than 20 and a read length of less than 300 bp were removed, using the keepfirst 300 bp command and thereby chopping at least 50 bp of the sequence end to remove sequencing noise. This resulted in a sequence read fragment of 300 bp length covering the ITS2 region. Sequences were checked for chimeric sequences using the UCHIME algorithm (4) implemented in MOTHUR. The remaining, non-chimeric, sequences were clustered into operational taxonomic units (OTUs) using cd-hit-est (10) at a threshold of 97% pairwise identity. The dataset was then normalized to the smallest sample size by random removal using the subsample command as implemented in MOTHUR. Taxonomic assignment of the representative sequences for the OTUs was done with the classify.seq command of MOTHUR applied to the UNITE fungal ITS reference database version 7.1 (11). To improve the taxonomical resolution, those OTUs that had been identified only down to the family

level were then subjected to a BLASTn search (e.g. (12) against the NCBI GenBank database (13). Finally, representative sequences of the fungal OTUs that had been assigned at the genus level were attributed to ecological trophic groups on the basis of sequence similarity using the default parameters of the GAST algorithm (14) against the reference dataset (15). Thereby, fungi for which functional information is available were assigned to the trophic groups: symbiotroph, pathotroph or saprotroph. We selected only OTUs for which we had information on functional type. The final dataset had 2254 OTUs corresponding to 688 putative species. Since the total number of arbuscular mycorrhizae species in the forest plots was very low (n=5), we included them in a soil symbionts category, along with ectomycorrhizae.

Lichens (ID 4460) and *Bryophytes (ID 4141)* were recorded in 20 m × 20 m subplots in forests and 4 m × 4 m subplots in grasslands during 2007 and 2008. All lichen and bryophyte species were identified and recorded separately for each of the four substrate categories: bark (corticolous species, up to 2.5 m height on tree trunks and branches of shrubs), rocks (saxicolous species), deadwood (lignicolous species), and soil (terricolous species) (16–19).

Vascular plants (ID 16506 in forests; ID 14326 in grasslands) were recorded in 20 m × 20 m subplots in forests and 4 m × 4 m subplots in grasslands in 2011. In forests, the vegetation was sampled in spring and summer of the same year. Cover was estimated across four different vegetation layers (herbs, shrubs <5m, trees 5–10 m, trees >10 m). To assess the diversity and correct the cover values of vascular plant species per plot, the spring and summer records were combined, using the higher cover value for each species (20). In grasslands, vascular plant species and their cover were sampled once in early summer (21).

Plant pathogens (ID 18546; grasslands only). We performed four transects (i.e. 25 m × 1 m relevés) of foliar fungal pathogens in each grassland plot (including rust fungi, powdery mildews, downy mildews, and smut fungi), and estimated the richness of foliar fungal pathogen species richness in each plot.

Arthropods (aboveground decomposers (Coleoptera: ID 16866; plus Dictyoptera: ID 16886, Hemiptera: ID 16867 and Hymenoptera: ID 16906 in forests), herbivores (Coleoptera; Hemiptera; Orthoptera: ID 16886; plus Hymenoptera in forests), omnivores (Coleoptera, Hemiptera, Hymenoptera, Dermaptera, Opiliones: ID 16887, Mecoptera ID: 16869, Orthoptera in forests only) and secondary consumers (Araneae: ID16868; Neuroptera: ID 16869; Hemiptera; Orthoptera; plus Myriapoda: ID 20146 in grasslands and Coleoptera, Opiliones, Pseudoscorpiones, Hymenoptera, and Raphidioptera in forests). Arthropods were sampled with two methods during the entire growing season from mid-April to mid-October 2008. In forests, ground-dwelling arthropods were sampled with pitfall traps (funnel traps with a diameter of 15 cm, (22, 23). Flying arthropods were sampled with flight-interception traps in the understory (1.5 m height) and mid-canopy (24). These traps consisted of two crossed transparent plastic shields (40 cm × 60 cm) with smooth plastic funnels attached to the bottom and to the top. At the end of both funnels, sampling jars were mounted. Three traps of each type (pitfall, flight-interception understory, flight-interception mid-canopy) were installed in three randomly chosen corners of each of the 150 plots and emptied monthly. 3% copper sulphate solution with a drop of detergent solution was used for all trap types and samples were subsequently transferred to 70% ethanol until laboratory identification. Of the three samples taken each month on each plot, two samples were chosen randomly for further processing. In cases where one trap was found not functional or destroyed, the other two traps were selected. In grasslands, 12 pitfall traps were installed. Three pitfall traps were placed at each of the four sides of the 50 m × 50 m plot. The traps were placed along the edges of the plots at 12.5 m, 25 m and 37.5 m from the corners. Plastic cups

with a diameter of 7 cm were put in to the soil and filled with a solution of water, salt and soap (200 g salt, 1 ml liquid soap per liter of water). The content of traps was collected three days after the installation (25).

Ecosystem functions

Root biomass (ID 14448; in grasslands only). We took soil samples from the 2011 joint soil-sampling campaign (see above). From the composite soil sample, roots were removed and cleaned from the adhering soil particles with distilled water in a 500 micrometer sieve. Fine roots were sorted according to a diameter size class of < 2 mm. Samples were dried at 40°C to constant weight in a force-air oven. The biomass of the fine roots was weighed after drying.

Root decomposition (ID 16666). In October 2011 three litterbags per plot containing 0.5 g of beech fine root litter (< 2 mm in diameter) were distributed vertically into a 10 cm deep slit in the mineral soil. The litterbags were made of a 100 µm polyester mesh screening to allow micro-faunal decomposition and had a size of 10 cm × 10 cm. In April 2012, after 6 months of decomposition, the litterbags were collected from the grassland plots and transported to the laboratory where the ingrown material was gently removed and the fine root-litter was cleaned from adherent soil particles. After drying at 40°C, average fine root decomposition rates (mass loss in %) were calculated. In forests, the litterbags were harvested after 12 months (in October 2012) and we followed the same lab protocol. We used the percentage of root litter mass loss as a proxy of decomposition (26).

Soil C cycling (ID 20246). We took soil samples from the 2011 joint soil-sampling campaign (see above). The enzymatic activities β-Glucosidase, Xylosidase (Xylanase in forests), N-Acetyl-β- Glucosaminidase were determined according to (27) as described in detail in (28), using fluorescent 4-methylumbelliferone substrates (4-MUF; Sigma-Aldrich, St. Louis, USA) and a buffered solution (pH 6.1). We calculated a combined measure of the enzymatic activities to estimate overall functioning of the soil C cycling using the *multidiv* function available at https://github.com/eric-allan/multidiversity.

Soil N cycling (ID 20246; in grasslands only). We took soil samples from the 2011, 2014 and 2016 joint soil-sampling campaign (see above) and analyzed several enzymatic activities related to nitrogen (N) cycling, including denitrification enzyme activity (DEA), urease, potential nitrification, *nifH* gene abundance, abundance of *amoA* genes in ammonia-oxidizing bacteria and archaea, abundance of *nxrA* gene for *Nitrobacter* nitrite-oxidizing bacteria and 16S rRNA gene for *Nitrospira* nitrite-oxidizing bacteria (NOB). We calculated a combined measure of these enzymatic activities to estimate overall functioning of the soil N cycling using the *multidiv* function available at https://github.com/eric-allan/multidiversity. *Denitrification enzyme activity* (DEA) was measured according to (29, 30). *Urease* activity was measured photometrically after (31), using 1 g of fresh soil that was incubated for 2 h at 37 °C with 1.5 ml 0.08M urea solution. To estimate *potential nitrification* (*ID 13986*; mean of 2011 and 2014), 10mM ammonium sulphate solution was supplied as substrate to 2.5 g of soil composite samples following (32). 1.5M sodium chlorate was added to prevent the turnover of nitrite to nitrate. After incubation for 5 h at 25°C, 2M potassium chloride was used to stop the reaction, followed by 20 min incubation and a centrifugation step. After addition of ammonium chloride buffer and a reagent for nitrite determination to the supernatant, the color reaction was measured with the spectrometer. Potential nitrification rates were calculated as the production of nitrite per gram of dry soil per hour (33). The abundance of different functional genes (*nifH*, *amoA, ID 13986*; mean of 2011 and 2016) was quantified via real-time qPCR analysis according to (34, 35). *Nitrite-oxidizing bacteria* (*ID 21546* and *ID 21547*) were targeted by primer sets for 16S rRNA genes for *Nitrospira* and nxrA genes specific for *Nitrobacter* (36).

Phosphatase (*ID 20246)*. We took soil samples from the 2011 joint soil-sampling campaign (see above). Soil enzymatic activities were determined according to (27) as described in detail in (28), using fluorescent 4-methylumbelliferone substrates (4-MUF; Sigma-Aldrich, St. Louis, USA) and a buffered solution (pH 6.1).

Phosphorus retention (ID 21688; in grasslands only). An index for phosphorus (P) retention (PRI) was calculated as the ratio between the sum of P in vascular plants and microbes related to the sum of plant-available P in soil, P in vascular plants and P in microbes, following (37). Plant samples were digested with concentrated HNO_3 in a microwave oven. In the extracts, P_i concentrations were determined with a continuous flow analyzer (Bran+Luebbe, Norderstedt, Germany) using the molybdenum blue method (38). To determine the microbial biomass P, we used a combination of methods proposed by (39, 40). We used hexanol instead of chloroform as fumigation agent. Plant-available P concentrations in soil were determined using a slightly modified $NaHCO_3$ method (41). 0.5 g of air-dried soil was extracted with 0.2 l of a 0.5 M $NaHCO_3$ solution (adjusted to pH 8.5 with 1M NaOH).

P availability (ID 19286; in forests only). Soil samples were collected in the 2014 joint campaign as described above. Available P was extracted with 0.5M NaHCO3 (pH = 8.5) following the Olsen methodology (42) and measured with Inductively Coupled Plasma/Optical Emission Spectrometry (ICP-OES, PerkinElmer Optima 5300 DV, S10 auto sampler).

Nitrogen retention (in grasslands only). An index for nitrogen (N) retention (NRI) was calculated as the ratio between N in vascular plants and microbes related to the sum of N in soil, N in vascular plants and N in microbes, adapted from (37). Plant samples were dried at 80°C for 48h, weighed and pulverized using a cyclone mill. Samples of 2-3 g were analyzed with a NIR spectrometer. The reflectance spectrum of each pulverized biomass sample was recorded between 1250 and 2350 nm at 1 nm intervals; with each scan consisting of 24 single measurements averaged to one spectrum. Calibration models that were used to predict N, P and K concentrations were derived from previously established calibration models; accuracy of model prediction was checked by applying an external validation process (ID 21087) (43, 44). Chloroform-fumigation-extraction method (45, 46), was used to determine microbial biomass nitrogen. N was extracted from each fumigated and non-fumigated replicate (5 g) with 40 ml 0.5M K_2SO_4. The suspension was horizontally shaken (30 Min, 150 rpm) and centrifuged (30 Min, 4400 x g). Fumigated sample replicates were incubated with $CHCl_3$ for 24 hours. N concentrations in dissolved (1:4, extract:deion. H_2O) extracts were measured with a TOC/TN analyzer (Multi N/C 2100S, Analytik Jena AG, Jena, Germany) (*ID 20251*). Ammonium (NH_4) and nitrate (NO_3) analyzed in the 2011 soil campaign (see above) were used to estimate N in soil (*ID 19847*). After extraction of soil samples with 0.01 M CaCl2 at a soil-to-liquid ratio of 1:3, ammonium and nitrate concentrations were determined by continuous flow analysis with a photometric autoanalyzer (CFA-SAN Plus; Skalar Analytik, Germany) according to (34).

N availability (ID 19847; in forests only). We investigated the nitrification process in forest soils in terms of potential nitrification activity associated with N availability. Soil samples were collected in the 2014 joint soil-sampling campaign (see above). Potential nitrification measures were derived from the abundance of nitrifying bacteria following (32) and were used as a proxy of soil N availability (37, 47).

Dung removal (ID 21206). We installed five dung piles (cow, sheep, horse, wild boar, red deer) in each of the 300 plots and collected the remaining dung after 48 hours. The average percentage of dung dry mass removed (mostly by tunneling dung beetles) was used as indicator of dung removal rates (48).

Ecosystem services

Provisioning services

Forage biomass (ID 16209). Aboveground grassland biomass was harvested as peak standing crop by clipping the vegetation 3 cm above ground in four randomly placed quadrates of 0.5 m × 0.5 m in each plot (i.e. 1 m^2 per plot) between mid-May and mid-June from 2008–2017. The plant biomass was dried at 80°C for 48 hours, weighed and summed over the four quadrates, and averaged across years. Temporary fences prevented biomass removal by livestock before our sampling.

Forage quality. Index based on crude protein concentration and relative forage value. Total nitrogen concentrations in ground samples of aboveground biomass were collected in 2009 and determined using an elemental auto-analyzer (NA1500, CarloErba, Milan, Italy). Neutral detergent fibre (NDF) and acid detergent fibre (ADF) contents were measured gravimetrically according to (49) (Fibertec 2010, Foss, Höganäs, Sweden). Further details can be found in (43, 44).

Timber production (ID 22868). We calculated the mean annual increment (MAI) across rotation (i.e. culmination of MAI) for even-aged forests and the periodic annual increment (PAI) between two forest inventories for uneven-aged and unmanaged forests. MAI was estimated based on site class or site maps of forest administrations. Culmination of MAI is estimated on 70 years to 100 years for *Picea abies*, 70 years to 90 years for *Pinus sylvestris*, 110 years to 130 for *Quercus* sp., and 160 years for *Fagus sylvatica*. PAI was estimated as the difference between the increment measured during the first forest inventory (2008–2011) and the second forest inventory (2015–2016) of our plots divided by the time span in years. All values are given as volume above bark (> 7 cm in diameter) in $m^3\ ha^{-1}\ a^{-1}$ as in (50).

Regulating services

Herbivory control (ID 18566). In spring 2013, a rectangular metal frame (10 cm × 45 cm × 3 cm height) was placed at two random sampling points on the ground in each 150 grassland plots. We then cut the vegetation at the height of the frame edge. Each vegetation sample was separated into grasses and forbs. A total of 100 leaves were drawn from grasses and forbs relative to their estimated proportion of biomass in the vegetation sample. The proportions were noted and leaves were stored separated for both functional groups in plastic bags with moist cloths and transported in a cooler to a laboratory. Herbivory damage (damaged surface area of a leaf in mm^2) was estimated by eye using a series of circular and square templates ranging in size from 1 mm^2 to 500 mm^2. Four damage types, i.e. chewing, sap sucking, leaf mining and rasping, were included in the estimates and damaged leaf area was summed over all individual leaves in a sample. The leaf area of all leaves in a sample (i.e. the area that left after feeding of the herbivores including petioles) was then measured using a LI-COR area meter. Herbivory rate, i.e. the proportion of leaf area damaged, was calculated by dividing the area damaged by herbivores by the sum of the leaf area measured and the damaged area to account for the fact, that the leaf area meter underestimates the original leaf area by the amount of chewing damage. This calculation yields conservative estimates of herbivory rates. To estimate the service "herbivory control", we took the inverse logarithm so larger values represent larger supply of the service; i.e. log (1/herbivory).

Soil C stock (ID 17086). Based on the joint 2011 soil sampling campaign (see above), each composite sample was weighed, air-dried, sieved (<2 mm) and a subsample homogenized and ground with a ball mill (RETSCH MM200, Retsch, Haan, Germany). Total carbon (TC) contents were analyzed on ground subsamples by dry combustion in a CN analyzer "Vario Max" (Elementar Analysensysteme GmbH,

Hanau, Germany). Inorganic carbon (IC) was determined after combustion of organic carbon in a muffle furnace (450°C for 16 h). The soil organic carbon (SOC) equals the difference between TC and IC. The total soil mass was calculated based on the weight of the dry fine-soil (105°C) and its volume. Organic carbon stocks were determined by multiplying SOC concentrations with the total soil mass (0-10 cm) per unit area (<2 mm) per m^2 at each site.

Infiltration (ID 22746; in grasslands only). We used a soil water balance model, developed to calculate vertical soil water fluxes (in mm = L m^{-2}) from the 0–0.15 m soil layer in grassland (51–53), based on (54). The model is based on the soil water balance equation: P + UF = DF + ETa + ΔS; where P is precipitation, UF is upward flux (via capillary rise), DF is downward flux, ETa is actual evapotranspiration, and ΔS is the change in soil water storage between two subsequent observation dates (ΔS = St2 − St1). As input data for the model, we used biweekly precipitation, and climate data (soil moisture, air temperature, relative humidity) per plot. The model output comprised biweekly actual evapotranspiration, downward water flux and upward water flux. The net flux from the 0–0.15 m soil layer to deeper soil was calculated as the difference between downward water flux and upward water flux in 14-day resolution and then aggregated to annual resolution for the years 2010 to 2016 (51). Then, we used the average values of the net flux per plot; i.e., the net flux between the 0–0.15 m soil layer and deeper soil in mm as an estimate of infiltration rate.

Pest control (ID 20035; in forest only). Predator-prey ratios have been frequently used as measure of pest control potential in different systems (55–57). We assessed the abundance of potential pest species on ambrosia beetles (i.e. bark beetles, an important pest in forests (58)), together with their antagonists. We selected ambrosia beetles within the tribe Xyleborini because they comprise generalist species that are all found in conifer as well as broadleaved forests with some showing preference either for broadleaved (e.g. *Trypodendron domesticum (L. 1758)*) or conifer (e.g. *Trypodendron lineatum (Oliv. 1795)*) trees. All species share antagonists among predators and parasitoids. We assessed bark beetle and antagonist abundances by pheromone traps using a bottle trap. Lineatin lures and ethanol were used as attractants for bark beetles and their antagonists. Traps were emptied every second day during the main flight activity of the beetles and in weekly to monthly intervals afterwards. We standardized the data based on the method proposed by (59). We only considered bark beetles that are attracted by lineatin or ethanol (i.e. species within the tribe Xyleborini) and predators and parasitoids that are mentioned as antagonists of Xyleborini in the literature (60). The ratio between the sum of predators and parasitoids *vs*. bark beetles was used as a proxy of pest control (i.e. (Predators + Parasitoids) / (Bark beetles)).

Temperature regulation (ID 19007; in forests only). Data on air temperature 2 m above ground was collected from climatic stations installed in each of the 150 forest plots. Diurnal temperature ranges (DTR) were calculated as differences between daily maximum and minimum temperature values (61). Missing data was interpolated from surrounding stations. The inverse value of the average DTR per plot (DTR^{-1}) was used as indicator to facilitate the interpretation of the results, i.e. higher values indicate mean higher temperature regulation (62).

Tree C stock (ID 16466). To assess the amount of carbon stored in trees, we estimated the living tree volume in each of the 150 forest plots (63). Dry biomass was estimated using the conversion factor of 0.43 for plots dominated by Norway spruce, 0.49 for plots dominated by Scots pine, 0.66 for plots dominated by oak species and 0.68 for plots dominated by European beech, according to (64). The carbon stored in trees is approximately 50% of its dry biomass (65).

<u>Cultural services</u> *(Note that these are indicators of potential supply of ecosystem services)*

Bird-watching potential (ID 21688). Both forests and grasslands provide excellent recreational opportunities for those interested in bird-watching (66–68). Therefore, we included bird species richness as a proxy of bird-watching potential. Five bird surveys were performed during breeding times from March to June 2011, counting the number of individuals seen or heard during 5 minutes from the center of each plot (69) as in (50).

Charismatic butterflies (in grasslands only). Butterflies are highly appreciated by people (https://butterfly-conservation.org/butterflies/why-butterflies-matter), in particular butterflies aesthetic traits and charismatic butterflies such the Monarch butterfly, have been extensively researched as cultural service indicators (70, 71). We used four traits to define charismatic butterfly species. For each trait we scored the charisma level from 0–2: (A) size of forewing (>40 mm: 2 points; >30 mm: 1 point), (B) color of wing upper side (three or more contrasting colors: 2 points; similar, but one of these colors not conspicuous: 1 point), (C) shiny wing upper side (conspicuously shiny: 2 points; shiny, but not conspicuous: 1 point), and (D) shape of wings (with long tails or conspicuously curved margin: 2 points; similar, but not conspicuous: 1 point). Species with three or more points were considered to be charismatic species. We use the abundance of charismatic butterfly species as an indicator.

Edible fungi (in forests only). We estimated the potential of 150 forest plots to harbor edible fungi by analyzing fungal species pools in forest soils, following the abovementioned description of the joint soil-sampling campaign. Edible fungi were identified following the criteria of the German Mycological Society, excluding those species with inconsistent edible value (72). We used species richness of the edible fungi as a proxy of potential observation of edible fungi as in (50).

Wild edible vascular plants (in forests only). Plants were sampled as described above for *Vascular plants*. Based on expert knowledge, we identified wild edible vascular plant species known to be collected in forests. Total cover of these species in each plot was used as a proxy of potential gathering of wild edible plants as in (50).

Vascular plants of cultural value (in forests only). Forests harbor a great variety of vascular plants, many of which are of special interest for botanists and educators, such as the forest specialists *Helleborus spp., Asarum europaeum,* or *Galium odoratum* (73), or are species blooming in early spring appreciated for their aesthetic value (74), such as *Anemone nemorosa* and *Gagea lutea*. We recorded all vascular plant species following the abovementioned method. Vascular plant species of special interest for the general public or for botanists were identified by botanists from the Botanical Society of Bern (Bernische Botanische Gesellschaft) with knowledge of people's preferences. Total cover of these species in each plot was used as a proxy of potential plant cultural value as in (50).

Environmental factors

Location. Each of the three regions covered by the Biodiversity Exploratories. This factor includes regional effects of climate, land-use history and soil texture, amongst others.

Elevation (ID 11603). Height above sea level; average over plot area.

Soil type (ID 20907). Soil type after Deutsche Bodensystematik (75).

Soil depth. We determined soil depth by sampling a soil core in the center of all 150 plots in 2009. We used a motor-driven soil-column cylinder with a diameter of 8.3 cm for the soil sampling (Eijkelkamp, Giesbeek, Netherlands). The combined thickness of all topsoil and subsoil horizons was used as a proxy of soil depth.

Soil pH (ID 14447). We collected soil samples following the abovementioned description of the 2011 joint soil-sampling campaign. pH was determined as the average value of two measurements based on 0.01M $CaCl_2$ with a soil solution ratio of 1:2.5.

Topographic wetness index (TWI). Data was obtained from a digital terrain model with a cell size of 25 m for all grasslands plots using ArcGIS following (76, 77). TWI combines both upslope contributing area (determining the amount of water received from upslope areas) and slope (determining the loss of water from the site to downslope areas). Therefore, sites with a high TWI are likely to have wet soils that accumulate soil material via rainfall erosion and solifluction.

Extended results

Random expectations

We tested whether the effect of land-use intensity on network metrics differed from random expectations by randomizing the diversities, ecosystem functions, and ecosystem services along the land-use intensity gradient. In this way, the data collected in each plot is maintained but we randomized the land-use intensity level assigned to each plot (and therefore, its position in the correlation matrix). This procedure removes the effect of land-use intensity on each variable and allows us to test whether the observed changes are driven by land-use intensity or by chance. We then compared the network metrics from the observed network versus 100 data randomizations and observed clear differences in trends (see Fig. S6).

Above- and belowground comparison

The overall changes in connectance, evenness and modularity with land-use intensity could be driven by distinct responses above- and belowground (78). Therefore, we analyzed aboveground and belowground networks separately (see details in Table S1). Above- and belowground networks displayed significant but generally distinct responses to land-use intensity (Table S4). Connectance increased up to intermediate levels of land-use intensity in both habitats and compartments, showing a further decrease in belowground forest networks, while aboveground networks showed an initial decrease in both habitats. Modularity and evenness showed opposite responses to land-use intensity in each habitat and compartment, although similar values of modularity were found at high land-use intensity levels for both compartments and habitats (Fig. S5). Belowground networks in grasslands showed a very similar pattern to the overall grassland network, suggesting that the belowground compartment may drive the overall response to land-use intensity in grasslands. This can be explained by the fact that most soil processes are linked via nutrient and carbon cycling, i.e. the turnover of soil organic matter (79, 80), while aboveground processes are driven by specific trophic-function relationships, such as those involved in pollination and predation (81, 82). In contrast, above- and belowground patterns in forests were more similar.

Significant correlations

In order to assess the potential effect of excluding non-significant correlations, we repeated all the analyses for both synergy and trade-off networks with raw Spearman ranks and significant Spearman ranks ($p \leq 0.05$) using the R package Hmisc (83). We did not find major differences between the approaches, except for the non-significant effect of land-use intensity in forests' modularity when using raw positive correlations (Fig. S7). Note that we did not use partial correlations for this comparison, as the partial correlation approach is very conservative and we already accounted for the strength of the correlations to weight all network metrics. Therefore, we used a continuous approach based on partial correlations for the main analyses, as it could be considered superior than selecting an arbitrary significance threshold (84).

Changes in module composition

Three modules were differentiated in the grasslands' lowest land-use intensity network (Table S5). Module **a** was driven by soil microbes (protists, soil fungi) and aboveground decomposers (e.g. Coleoptera) and was associated to nutrient cycling and forage quality (Fig. 3*A*a); module **b** comprised productive functions and services (i.e. root and forage biomass); and module **c** comprised some soil functions (i.e. root and dung decomposition) and was associated to aboveground organisms (lichens,

bryophytes, vascular plants and aboveground herbivores) and cultural ecosystem services (Fig. 3*A*). In the highest land-use intensity network, four modules were differentiated. The two larger modules maintained a similar composition: module **c** (mostly associated to cultural services) was very similar in composition to module **g**, and half of module **a** (associated to nutrient regulation) turned into module **f**. A separate module (**e**) contained soil C stock as the only ecosystem service, and another module comprised a mixture of services (Fig. 3*A***d**).

In forests we identified three clear modules in the lowest land-use intensity network, while the role of the fourth module (**a**) was poorly defined (Table S5). Module **b** was associated to nutrient cycling, module **c** to old growth forests combining tree C storage and low timber production, and module **d** to open forest glades and plant-related services. In the highest land-use intensity network, the modules were completely rearranged. The smallest module could be associated to less intensive forest stands combining tree C stocks with some cultural services (Fig. 3*B***e**), another module aggregated nodes associated to intensive plantations, such as timber production, phosphorus availability, edible plants and aboveground arthropods (Fig. 3*B***f**), while the larger module was related to soil organisms and functions, and some cultural services too (Fig. 3*B***g**).

Supplementary References

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Data availability

The individual datasets used in the analyses can be accessed via https://www.bexis.uni-jena.de/PublicData/SearchPublicData.aspx , using the ID provided in brackets in the Supplementary Methods. Note that some datasets might be subject to an embargo period.

The R script used to analyze the data and produce all figures is available in GitHub https://github.com/MariaFelipe-Lucia/biodiversity-function-services_networks.