nature research

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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	*No software was used to collect the data.*
Data analysis	*R Core Team. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing Vienna, Austria, https://www.R-project.org (2017). Version R 3.4.0.* *Package "iNEXT" under R3.4.0 to estimate species richness (Hsieh T.C. and Chao A., 2016. Methods in Ecology and Evolution, 10.1111/2041-210X.12613)*

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Species, habitat and agricultural management data that support the findings of this study are available in Lüscher et al., Ecology, 97(6), 2016, doi.org/10.1890/15-1985.1. The production data (yield) that support the findings of this study are included as Supplementary Data 1.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	*Describe how sample size was determined, detailing any statistical methods used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*
Data exclusions	*Describe any data exclusions. If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Replication	*Describe the measures taken to verify the reproducibility of the experimental findings. If all attempts at replication were successful, confirm this OR if there are any findings that were not replicated or cannot be reproduced, note this and describe why.*
Randomization	*Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.*
Blinding	*Describe whether the investigators were blinded to group allocation during data collection and/or analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).*
Research sample	*State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.*
Sampling strategy	*Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.*
Data collection	*Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.*
Timing	*Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Non-participation	*State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.*

Randomization

If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description

The study is described in Lüscher et al. (2016), http://onlinelibrary.wiley.com/doi/10.1890/15-1985.1/suppinfo. We analysed a unique dataset of vascular plants, earthworms, spiders and wild bees collected on 169 farms, both organic and non-organic, across 10 regions of Europe. In each region, 12 to 20 farms, approximately half certified organic, were selected randomly. We surveyed the species richness of the four taxa in 910 semi-natural habitats and 492 production fields, using hierarchical preferential sampling and standardized protocols. Yields were estimated based on structured interviews with farmers. In each case study region, the recorded species were grouped as (i) unique to semi-natural habitats, (ii) unique to production fields or (iii) shared by both habitat categories. The use of unique species enabled the evaluation of biodiversity loss if habitats should be converted into other categories. To test for difference between the number of unique species found in semi-natural habitats and production fields, habitat type was the treatment factor and region treated as random factor (nested design). To test for difference between organic versus non organic habitats/fields, management type was the treatment factor and region treated as random factor (nested design).

Research sample

The research sample was constituted of 1402 sites (910 semi-natural habitats and 492 production fields) across 10 European regions. Vascular plants, earthworms, spiders and wild bees were observed/collected in each of the sites. Dataset is described and made public in Lüscher et al. (2016), http://onlinelibrary.wiley.com/doi/10.1890/15-1985.1/suppinfo.

Sampling strategy

After the complete area of all selected farms was mapped using the BioHab method (Bunce, R. G. H. et al., 2008, doi:10.1007/s10980-007-9173-8) habitats were distinguished in habitat types according to Raunkiær life forms, environmental conditions and management evidence. Vascular plant, earthworm, spider and bee species were sampled in one site randomly selected per habitat type occurring on each farm. This resulted in 1402 selected sites on 169 farms. In the selected sites, species were sampled during one growing season. For analysis, sites were categorized as semi-natural habitats or production fields. Species collection in such studies can rarely claim detecting all species present in a given plot, habitat or field. Lacking references concerning the sample size necessary to detect a reasonable portion of the species diversity, we decided to maximize the number of species potentially detectable by sampling one site per habitat type in each farm. Then, we analysed the dataset using species accumulation curves and compared semi-natural habitats and production fields (and organic and non organic management) for a common sample coverage (Chao et al. 2014, doi:10.1890/13-0133.1).

Data collection

All data were collected during the growing season in 2010. Vascular plant species were identified and their respective ground cover was estimated by experienced field botanists in one survey of 10 m × 10 m in the central part of the selected habitat/field. Earthworms were sampled by ecologists at three locations per selected site, which were at least 20 m apart from the border and 10 m apart from each other. A metal frame of 0.3 m × 0.3 m was placed on the soil. First, we poured a solution of allyl isothiocyanate (0.1 g/l) into the metal frame (two applications at a 5 min interval). This encouraged earthworms to move to the surface where they were collected. After 10 min, we excavated a 20 cm deep soil core of the whole frame, and hand sorted the soil for 20 min per core. The collected earthworms were stored in ethanol (80%) or formaldehyde (4%). Expert taxonomists identified the specimen to the species level in the lab. Spiders were sampled from soil surface and vegetation by ecologists at five locations per selected site. We used a modified shredder vac/blower (Stihl SH 86-D) to suck the spiders within a haphazardly placed ring of 0.357 m diameter for 30 s. The locations were at least 20 m apart from the border and at least 10 m apart from each other. Spider sampling was conducted on three dates. The exact dates depended on the region, the vegetation cover, and the weather conditions (dry and warm). Collected spiders were inverted in a zip-seal bag, stored in a cool box, and deep-frozen in the lab. Then, we separated the spiders from additional material such as sand, small pieces of vegetation, or other invertebrates and stored them in ethanol (80%). Expert taxonomists identified each specimen to the species level. Bees were sampled by ecologists in a transect walk with aerial netting for 15 min. The transect was 2 m × 100 m and crossed the middle of the vascular plant survey. If the habitat was shorter than 100 m, the transect length was divided, e.g., in two 50 m-long transects. Bees were sampled on three dates during good weather conditions, i.e. temperature higher than 15° C, sunny, and not too windy. The sampling dates depended on the region. Where identification was not possible in the field, captured bees were transferred to a killing jar, pinned, and identified by expert taxonomists in the lab. Apis mellifera individuals were not captured, but counted in the field. In the regions AT and NL, bees were sampled on only two dates. Data on agricultural management were collected in face-to-face interviews with the farmers, following a standardized questionnaire, which had been translated in the corresponding local language. In a first part of the questionnaire, the farmers provided information at farm scale. They were asked about the farming system (organic or non-organic) and its duration, about the number and types of livestock units, about fuel and electricity consumption, and about expenditures on fertilizers, crop protection and concentrate feed stuff. In a second part of the questionnaire, the farmers listed the variety of their cultivated crops and their area. Individually, for each crop under the same management, they provided information on yield, the amount and type of nitrogen input, the number of pesticide applications, the mechanical field operations, and the livestock density. Natural pesticides were included in the counts, and we distinguished between herbicides, fungicides, and insecticides. Pesticide applications were related to the cultivated crops. Mechanical field operations included soil cultivation, fertilization, pesticide application, mowing, turning, bale making, and loading. The crop specific information was then scaled up to average values for the entire production area per farm with the indicator tool DIALECTE. The duration of the interviews depended on the complexity of the farm and lasted from one to more than three hours.

Timing and spatial scale

See "sampling strategy" and Lüscher et al. (2016), http://onlinelibrary.wiley.com/doi/10.1890/15-1985.1/suppinfo.

Data exclusions

Earthworms: Juveniles, i.e. individuals without a clitellum, were excluded from the data set because not clearly identifiable.
Spiders: Juveniles were excluded from the data set because not clearly identifiable.

Reproducibility

Methods and protocols to map the habitats, collect the species data and the management data were tested by study participants and field ecologists together in training sessions to be sure that methods are used the same way.

Randomization

20 farms in each of the 10 regions were randomly selected from a panel of about 40 farms occurring, depending on the region. Sites (1 site per habitat type) in farms were also randomly selected. Sampling points in sites to collect species were situated in the middle of the site, taking into account minimum distances between two sampling points (earthworms, spiders) and from the site border.

Blinding

Blinding was only rarely possible to apply as field ecologists who sampled plants, earthworms, spiders and bees saw the habitat type – semi-natural of production fields – they were in. In contrast, field ecologists could not in all cases determine the management type – organic or non organic – of the site they were in.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions

Habitat mapping: no particular conditions.
Vegetation: no particular conditions.
Earthworms: collection done during wet weather conditions.
Spiders: dry and warm weather conditions.
Bees: temperature higher than 15° C, sunny, and not too windy weather.

Location

Data on exact location of the 10 European region are available in the supporting information of in Lüscher et al. (2016), http://onlinelibrary.wiley.com/doi/10.1890/15-1985.1/suppinfo.

Access and import/export

Sites were accessed for mapping (habitat type) and collecting species only after permission and notification of farmers. Local authorities were also notified.

Disturbance

Field ecologists were particularly made aware of respecting sites visited for data collection, asked to be the less disturbing as possible and not damaging. For the plant, bees and spider recording, a single person was on the field at each time minimizing then the possible compaction effect of accessing the field. For earthworms, due to extraction liquid to be convoyed, 2-3 persons accessed the site at a time. The excavated soil core was put back in its place after collection of earthworms.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about availability of materials

Obtaining unique materials

Describe any restrictions on the availability of unique materials OR confirm that all unique materials used are readily available from the authors or from standard commercial sources (and specify these sources).

Antibodies

Antibodies used

Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.

Validation

Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

State the source of each cell line used.

Authentication

Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.

Mycoplasma contamination	*Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.*
Commonly misidentified lines (See ICLAC register)	*Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

Palaeontology

Specimen provenance	*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).*
Specimen deposition	*Indicate where the specimens have been deposited to permit free access by other researchers.*
Dating methods	*If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	*For laboratory animals, report species, strain, sex and age OR state that the study did not involve laboratory animals.*
Wild animals	*Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*
Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*

Human research participants

Policy information about studies involving human research participants

Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*

Data quality

Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.

Software

Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.

Instrument

Identify the instrument used for data collection, specifying make and model number.

Software

Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.

Cell population abundance

Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.

Gating strategy

Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type

Indicate task or resting state; event-related or block design.

Design specifications

Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures

State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)

Specify: functional, structural, diffusion, perfusion.

Field strength

Specify in Tesla

Sequence & imaging parameters

Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.

Area of acquisition

State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software

Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).

Normalization

If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.

Normalization template

Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.

Noise and artifact removal

Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).

Volume censoring

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference
(See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.