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Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the 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
☐	☒	A statement on 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 statistical parameters 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

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	This study did not involve new instrument-based data collection. Climate forcing inputs were obtained from the NOAA Monthly U.S. Climate Division dataset (1895-2022) via NCEI, cited in the manuscript as: Vose, R. S. et al. Improved Historical Temperature and Precipitation Time Series for U.S. Climate Divisions. J. Appl. Meteorol. Climatol. 53, 1232–1251 (2014).
Data analysis	Code for analyzing model outputs, including the multilayer network routines that compute GE, CD, BC, and WLOCOP and for generating all figures is available on GitHub at https://github.com/shubhamrt/connectivity-based-early-warning. Editors and reviewers have unrestricted access. (The underlying model is archived on Zenodo and is cited in the manuscript).

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Precipitation data used in this study are from the NOAA Monthly U.S. Climate Division dataset, which is publicly available at https://www.ncei.noaa.gov/. Model outputs were produced using a modified version of the ecogeomorphic model developed by Stewart et al. (2014), with all modifications detailed in the supplementary document (Section S1). The model code is openly available in the Zenodo repository (https://doi.org/10.5281/zenodo.16104933). Analysis code for processing model outputs and generating figures is available on GitHub: https://github.com/shubhamrt/connectivity-based-early-warning

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	This study did not involve human participants; no sex or gender information was collected.
Reporting on race, ethnicity, or other socially relevant groupings	No human participants or human data were included.
Population characteristics	No human participants were included in this study.
Recruitment	No recruitment was conducted because the study did not involve human participants.
Ethics oversight	Ethics review was not required because the study did not involve human participants, human data or human biological materials.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

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

Study description	Computational ecohydrology study coupling a spatially explicit, process-based ecogeomorphic model with multilayer graph analysis to test how aridity, grazing intensity and wind direction reorganize connectivity and drive grassland to shrubland regime shifts. We quantify structural and functional connectivity of water and nitrogen and evaluate connectivity-based early-warning indicators (4-6 years lead).
Research sample	A simulated hillslope landscape of 120 × 120 m at 1 m² resolution (uniform 2° slope). Results are summarized over the inner 100 m × 100 m to avoid edge effects. Initial state is grass-dominated (mean 31.1 g m⁻², random) with a uniform shrub seed bank (5 g m⁻²).
Sampling strategy	No statistical sampling. We analyze the entire landscape for each pre-specified scenario. 1. Climate endmembers from NOAA Climate Divisions: Southwest Arizona (Mean Annual Rainfall (MAR) 132.1 mm; CoV 38.1%) and Northern Plateau New Mexico (MAR 286.2 mm; CoV 22.8%), plus two modified-variability scenarios that swap CoV while holding MAR constant. 2. Grazing: 1 g m⁻² yr⁻¹ (native herbivores) and 30/45/60% removal of available grass; actual consumption scales with availability (density-dependent). 3. Wind direction: downslope (aligned with overland flow) vs upslope (counter to flow).
Data collection	Forcing inputs are historical precipitation from the NOAA Monthly U.S. Climate Division dataset (1895-2022), cited as Vose et al. 2014, JAMC 53:1232–1251. The model generates annual vegetation biomass and year-specific water/nitrogen connectivity networks from which GE, CD, BC, WLOCOP are computed; we then calculate lagged correlations (0, 2, 4, 8, 16 years) among rainfall, biomass, and connectivity metrics.

Timing and spatial scale	Temporal: simulations 1895-2022 with a 45-year spin-up using mean rainfall before the main runs. Spatial: 120 × 120 m (1 m² cells), 2° slope; reporting over inner 100 × 100 m.
Data exclusions	None; full time series for all scenarios were analyzed (figures and matrices report every lag and intensity).
Reproducibility	Workflow is deterministic given fixed inputs. Code and all modelled outputs (biomass, connectivity matrices, figure source data) are openly archived (Zenodo DOI: 10.5281/zenodo.16104933) with environment files and run scripts to reproduce figure and statistic.
Randomization	Not used; scenario factors (climate/variability, grazing, wind) are defined a priori and applied deterministically.
Blinding	Not applicable; no observers or subjects, analyses are scripted and automated.

Did the study involve field work? ☐ Yes ☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks	All analyses are in silico, using public climate data and a documented ecogeomorphic model; no plants, live organisms, tissues, clinical data, hazardous agents, or wet-lab methods were involved, so the items above are not applicable.
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*