

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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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

The dataset was compiled by integrating over 7 million occurrence records from major global biodiversity and biosecurity databases, primarily GBIF, EDDMapS, and GRIIS. To complement these records, ecological and distribution data for 2,038 forest pest species were sourced from the CABI Compendium and EPPO Global Database. Furthermore, global layers for ecosystem services—including timber production, biomass carbon stocks, and tree species richness—were collected from specialized repositories such as FAO, the Global Forest Resources Assessment, and the Earthstat database. All data were systematically harmonized into a standardized global grid to ensure spatial consistency.

Data analysis

All statistical analysis was conducted in R (version 4.3.2).

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](#)

All data originally used in this study are publicly available online: global Invasive and Alien Species and their Traits database (<https://doi.org/10.5281/>

zenodo.13138496), global map of forest loss drivers (<https://data.globalforestwatch.org/documents/tree-cover-loss-by-dominant-driver/about>), global map of forest management types (<https://zenodo.org/record/5879022#.ZCa9IXbMKUk>), global forest diversity (https://figshare.com/articles/dataset/The_global_map_of_tree_species_richness/17232491), global potential carbon stock (<https://doi.org/10.5281/zenodo.10021968>), forest cover 2000 (https://earthenginepartners.appspot.com/science-2013-global-forest/download_v1.7.html), travel time to urban center (https://figshare.com/articles/dataset/Travel_time_to_cities_and_ports_in_the_year_2015/7638134/3), forest fragmentation index (<https://figshare.com/s/21dbf1f50250aeb7f5a0>), forest age (<https://doi.org/10.17871/ForestAgeBGI.2021>), GDP (<https://data.worldbank.org/indicator/NY.GDP.MKTP.CD?end=2015&start=1960>), global population density (https://developers.google.com/earth-engine/datasets/catalog/CIESIN_GPWv411_GPW_Population_Density).

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

Use the terms *sex* (biological attribute) and *gender* (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, 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.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

This research investigates the global spatial patterns of forest pest richness and evaluates the resulting exposure risks to three critical ecosystem services: timber production, carbon storage, and tree biodiversity. Specifically, it seeks to identify where high concentrations of pests overlap with high-value forest resources and examines how environmental factors and forest fragmentation drive these risk distributions.

Research sample

A global dataset of 2,038 forest-pest taxa (including 1,384 fauna, 475 pathogens, and 179 flora species), supported by over 7 million occurrence records (1970–2022) and geographic range data for 1,884 species.

Sampling strategy

This research investigates the global spatial patterns of forest pest richness and evaluates the resulting exposure risks to three critical ecosystem services: timber production, carbon storage, and tree biodiversity. The research sample consists of a comprehensive global dataset of 2,038 forest-pest taxa, including fauna (1,285 insect species), pathogenic pests (fungi and bacteria), and parasitic flora, supported by over 7 million occurrence records spanning from 1970 to 2022. To ensure scientific rigor, the study employed a multi-stage systematic sampling and filtering strategy, which involved cleaning raw occurrence data for coordinate precision, aggregating records into a 100 × 100 km equal-area grid system to mitigate reporting bias, and integrating expert-validated geographic ranges for 1,884 species to accurately distinguish between native and non-native pest distributions across global forest biomes.

Data collection

The dataset was compiled by integrating over 7 million occurrence records from major global biodiversity and biosecurity databases,

primarily GBIF, EDDMapS, and GRIIS. To complement these records, ecological and distribution data for 2,038 forest pest species were sourced from the CABI Compendium and EPPO Global Database. Furthermore, global layers for ecosystem services—including timber production, biomass carbon stocks, and tree species richness—were collected from specialized repositories such as FAO, the Global Forest Resources Assessment, and the Earthstat database. All data were systematically harmonized into a standardized global grid to ensure spatial consistency.

Timing and spatial scale	The study spans a significant temporal range, utilizing pest occurrence records from 1970 to 2022 to capture long-term distribution patterns. Spatially, the research is conducted at a global scale, covering all major forested biomes. Data were processed and analyzed using a 100 × 100 km equal-area grid system (Behrmann projection) to ensure spatial consistency and to mitigate the effects of varying sampling intensities across different geographic regions.
Data exclusions	To ensure the accuracy of the spatial analysis, several exclusion criteria were applied to the raw dataset. We excluded records with high coordinate uncertainty (greater than 10 km) and those lacking specific geographic coordinates. Duplicate records and fossil remains were also removed. Furthermore, we excluded pest species that are primarily associated with agricultural crops rather than forest ecosystems. For the spatial risk assessment, any grid cells with less than 1% forest cover were excluded from the analysis to focus specifically on established forest biomes and reduce noise from non-forest land use.
Reproducibility	To ensure the reproducibility of this study, all analytical workflows were conducted using standardized R and Python scripts. The primary datasets, including the cleaned pest occurrence records and spatial risk layers, are maintained in accessible formats (e.g., CSV, GeoTIFF). Detailed descriptions of the data filtering protocols, environmental variable selection, and Random Forest modeling parameters are provided in the Methods section. Furthermore, the code for data processing and spatial mapping will be made available upon publication via a public repository (such as GitHub or Zenodo), and all underlying raw data sources are publicly accessible through platforms like GBIF and the CABI Compendium.
Randomization	Randomization was implemented at multiple stages of the statistical analysis to ensure model robustness. During the risk factor analysis, the dataset was randomly partitioned into a training set (80%) and a testing set (20%) for the Random Forest models. Furthermore, the Random Forest algorithm itself utilized bootstrap aggregating (bagging), where each decision tree was grown using a randomized subset of the data. To account for spatial sampling bias, we also employed a spatial thinning approach and generated pseudo-absence points by randomly sampling from areas outside the known distribution of specific pests, ensuring that the spatial models were not biased toward high-reporting regions.
Blinding	Blinding was not applicable to this study as it does not involve clinical trials or human/animal subjects that could be influenced by knowledge of the treatment. The research is a macroecological analysis based on objective observational data (pest occurrence records and satellite-derived environmental layers). Data processing and statistical modeling were conducted using standardized automated scripts to ensure that the investigator's expectations did not influence the quantitative results.

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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input type="checkbox"/>	<input checked="" type="checkbox"/> Plants

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	Not applicable. This study does not involve research on Laboratory animals.
Wild animals	Not applicable. This study does not involve research on regulated vertebrate animals or higher invertebrates.
Reporting on sex	Not applicable.
Field-collected samples	Not applicable. This study does not involve field collection
Ethics oversight	This study did not require ethical approval or oversight, as it did not involve human participants, live vertebrates, or higher

invertebrates.

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

Plants

Seed stocks	This study did not involve the collection of plant specimens from the field.
Novel plant genotypes	Not applicable. This study does not involve the creation, use, or field testing of novel plant genotypes, genetically modified organisms (GMOs), or gene-edited plants.
Authentication	Not applicable as no cell lines or specific antibodies were used.