



D5.1 Predicted maps of Invasive Alien Species

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Key takeaway messages

- IAS introductions are predominantly multi-pathway, requiring coordinated, sector- and taxon-specific preventive measures rather than single-pathway interventions.
- Escape from confinement was the dominant pathway, driven particularly by ornamental use and horticulture, with two main pathway clusters formed by co-occurrence: “cultivation-and-release” and “accidental-transport”.
- Major occurrence-data gaps and spatial saturation persist across Europe, particularly for invertebrates, identifying clear priorities for targeted surveillance and data mobilisation.
- A reproducible and semi-automated SDM framework delivered projections for all 120 target IAS, with strong-performing climate–habitat ensembles.
- Future IAS responses are strongly species- and scenario-dependent, with 28 species (23%) reversing their projected direction of change across scenarios, reinforcing the need for scenario-explicit risk assessment and prioritisation.
- Projected future environmental favourability shows a marked northward and upward redistribution, with increasingly divergent species responses under stronger climate and land-cover change.
- Modelled vs observed mismatches identify priority species–country combinations for horizon scanning, surveillance and early warning, supporting OneSTOP’s data-driven prioritisation approach.





Executive summary

Invasive alien species (IAS) threaten European biodiversity, economy and wellbeing, and managing them requires information on arrival routes and establishment potential. OneSTOP responds with an interoperable toolset for prevention, early detection and response. Within Work Package 5 (prioritisation, prediction, horizon scanning and early warning), Task 5.1 characterises IAS introduction pathways and projects potential distributions for 120 terrestrial IAS: 70 of Union concern under Regulation (EU) 1143/2014, including listing candidates, plus 50 nominated by OneSTOP's five Living Labs. Baseline/historical and future (2041–2070; 2071–2100) maps at ~1 km under three SSP-RCP pathways provide a reproducible, FAIR basis for downstream WP5 prioritisation and risk assessment.

Pathway data came from the EASIN, classified under the CBD framework. Models were produced with the wiSDM 2.0 semi-automated pipeline, extended by the OneSTOP fork v2.1 for user-supplied rasters, integrated cross-validation and monitored batch execution, on GBIF records (1971–2025) harmonised, cleaned and thinned to unique 1×1 km cells. wiSDM combines two hierarchical components by harmonic mean: a global climate-only model on nine CHELSA v2.1 bioclimatic variables, and a European habitat model on eleven land-cover classes taken as a 3×3 km moving window from the 1-km plant-functional-type projections of Chen et al. (2022). For each model component, ten algorithms are fitted, converted to prevalence-independent favourability (Real et al., 2006) and ranked on PC1; the five retained are combined as the pixel-wise median. Pseudo-absences (10,000) were bias-weighted by sampling effort, performance assessed by five-fold spatial block cross-validation (AUC, Boyce index, TSS) and maps binarised at training-presence percentiles (10% reported); future climate for 2070 and 2100 used a five-GCM CMIP6 ensemble average.

The analysis returned 426 introduction pathway records for 118 species. Escape from confinement dominated (38.0% of records; 72.0% of species), driven by ornamental use, horticulture and the pet trade, ahead of transport–contaminant and release in nature; co-occurrence resolved a “cultivation-and-release” cluster among plants and vertebrates and an “accidental-transport” cluster among invertebrates. Only 86 species (71.7%) were well supported by European occurrence data, with gaps concentrated in invertebrates. Maps and future projections were delivered for all 120 species (with full ensemble climate–habitat models for 96, climate-only for 24), with good-to-excellent cross-validated performance (median ensemble AUC 0.882) that outperformed both sub-models. At baseline, at least one species was favoured across 97.5% of the modelled area, averaging 24.96 species per 1-km cell and peaking in western and central Europe. Futures show northward and upward redistribution, not uniform change, with end-century mean richness reaching 25.91 species per cell under SSP1-2.6 but 22.00 under SSP5-8.5; 50 species expand and 43 contract across all futures; and 16 of 27 countries gain favourable area, led by Denmark, Finland and Sweden, against steep declines in Hungary, Bulgaria, Croatia and Italy.

The deliverable recommends a tiered workflow using semi-automated SDMs as a first-tier screen directing expert and Living Lab review; multi-pathway prevention pairing ornamental, horticultural and pet-trade controls with contaminant and stowaway biosecurity; occurrence-data gaps treated as surveillance priorities, embedding IAS in European monitoring and targeting under-represented taxa and Member States; and preparedness for redistribution, strengthening horizon scanning in northern, Baltic and montane Europe without relaxing management where favourability declines. Prioritisation should be species-specific, scenario-





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and horizon-explicit, and embedded in an adaptive cycle of detection, verification and model updating.





Non-technical summary

Invasive alien species (IAS) are plants and animals moved by people beyond their natural range, which then spread in the wild and are among the foremost threats to European biodiversity, biosecurity and socio-economic wellbeing. Preventing them is far less costly than controlling them later, which depends on knowing how they arrive and where they could live or spread. The OneSTOP project, funded by the European Union, is building a connected set of tools for prevention, early detection and rapid response. Within its work on prioritisation, prediction and early warning, Task 5.1 examines how a set of 120 invasive species of European concern arrived and maps where conditions could suit them now and in possible scenario futures later this century. These comprise 70 species listed or being considered under EU law, plus 50 nominated by the project's five Living Labs in Belgium, Finland, Portugal, Romania and the United Kingdom. Maps cover recent conditions and the middle and end of the century under three futures, from strong action on emissions to continued high emissions.

The maps come from species distribution models, which learn the environmental conditions, such as temperature, rainfall, and landscape cover, where a species is already found, then identify everywhere else offering a comparable combination. The value in these spatial models is that they highlight places a species has not yet reached, which is where prevention and early detection pay off most, and they can be re-run under future climate and land-use conditions. Two sources of evidence fed this assessment. Information on introduction routes came from the EU's official database of alien species (EASIN), grouped into standard categories such as escape from gardens or captivity, deliberate release, and accidental transport. Records of where each species has been seen worldwide came from the global biodiversity database GBIF, filtered so that only reliable, precisely located observations were used. Because no single statistical technique is dependable on its own, we ran ten for each species and merged the five most informative into one map, then tested it by withholding part of the data and checking whether the model could predict it.

Results show that introduction routes are rarely a single-route phenomenon and species are typically linked to about three routes. Escape from gardens, nurseries, collections and the pet trade was the most common, affecting nearly three-quarters of the species, whereas insects and other invertebrates mostly travel unnoticed with goods, soil and vehicles. Measures aimed at one route alone will therefore address most species only partly. Available records also showed clear gaps with only about seven species in ten were well enough recorded in Europe for the most detailed modelling, insects least of all. Maps were nonetheless delivered for all 120 species, and performed well in testing. Conditions currently suit at least one of these species across almost the whole of Europe, with the greatest overlap in Britain and Ireland, France, Belgium, the Netherlands, Germany and northern Italy. Future projections point not to more or less risk overall, but to a redistribution of species with conditions becoming more suitable further north and higher up mountains, with Denmark, Finland and Sweden gaining most, while Hungary, Bulgaria, Croatia and Italy decline most. Species respond individually rather than as groups, and for roughly one in four the future assumed decides whether they gain or lose ground, so no result should be quoted without stating which future it assumes. Comparing the maps with what has actually been reported produced a potential "watch list" composed of 225 cases where a country has favourable environmental conditions to suit a species for the first time, and 552 where conditions already suit a species but it has never been recorded there.

These maps show where a species could live, not where it is or will certainly be, since arrival and establishment also depend on how often it is transported, on chance and on what else





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lives there. Increases in suitability are therefore a firmer basis for action than decreases. The deliverable recommends using the species distribution maps as a first layer of assessment, identifying which species and places deserve closer expert study; combining prevention measures across several introduction routes at once; treating gaps in wildlife records as an explicit monitoring priority, particularly for insects and less-recorded countries; and preparing for redistribution by strengthening early warning in northern, Baltic and mountain regions, without relaxing effort where conditions are projected to become less suitable, since established populations rarely disappear unaided.





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List of abbreviations

CMIP	Coupled Model Intercomparison Project
EU	European Union
FAIR	Findable, Accessible, Interoperable, and Reusable
GADM	Database of Global Administrative Areas
GBIF	Global Biodiversity Information Facility
GCM	Global Circulation Model
IAS	Invasive Alien Species
PFT	Plant Functional Traits
RCP	Representative Concentration Pathway
SDM	Species Distribution Models
SSP	Shared Socioeconomic Pathway
WGS	World Geodetic System
WP	Work Package







1. Introduction

1.1. Task 5.1 in the context of the OneSTOP project

Invasive Alien Species (IAS) are among the foremost threats to biodiversity, ecosystem integrity, biosecurity, and socio-economic wellbeing in Europe. Their capacity to establish and spread is influenced, among other factors, by environmental conditions, including climate, land cover/land use, and habitat connectivity, and is further modulated by global change, disturbance regimes and introduction pathways. Effective IAS management requires robust information on where species could occur under current and future conditions to guide prevention, early detection, and rapid response.

The OneSTOP project aims to transform IAS management by integrating technologies, data flows, and decision-support systems across Europe. As stated in Groom et al. (2025), the overarching goal of OneSTOP is to minimise the introduction, establishment, and spread of IAS through an interoperable suite of tools, including predictive distribution modelling of species under current and future environmental scenarios.

Within this framework, Work Package 5 (WP5) is tasked with prioritisation, prediction, horizon scanning, and early warning, including modelling and scenario analysis of IAS risk. As part of this work, Task 5.1 focuses on compiling and analysing introduction pathways data, as well as generating spatially explicit maps depicting the potential distribution of terrestrial IAS of European concern under baseline/historical and future conditions. To accomplish this goal, species distribution models were developed by combining occurrence data obtained from GBIF with climatic and land-use/land-cover predictors to characterise the environmental conditions associated with species occurrence.

More specifically, the spatial-modelling component of Task 5.1 includes producing high-resolution potential distribution maps across Europe for a priority list of 70 terrestrial IAS of Union concern and 50 additional species selected by stakeholders through OneSTOP's Living Labs (WP3). These maps cover baseline/historical conditions (1981–2010) and two future periods (mid-century: 2041–2070; and end-century: 2071–2100) under three socio-climatic pathways (SSP1-2.6, SSP3-7.0, SSP5-8.5). To develop these outputs, the modelling workflow relies on the wiSDM framework (Davis et al., 2024). This framework is tailored for modelling species distributions based on environmental covariates and supports reproducibility and open science principles. Through specific modifications within the scope of Task 5.1, it integrates both climatic and land-cover projections for the same future scenarios. The framework uses ~1 km-resolution predictors from CHELSA v2.1 climate data (Karger et al., 2017, 2021) and recently developed land-cover projections from Chen et al. (2022) to estimate environmental suitability for each species across future scenarios. Model performance and prediction uncertainty were assessed separately for each species, considering the effects of modelling algorithms, data availability, and data comprehensiveness. The implementation of wiSDM was updated to version 2.0 with major upgrades supported by OneSTOP and collaborators from the EU-funded GuardIAS project (see details below in subsection 7.3.1–*Alterations to wiSDM 2.0 workflow in the OneSTOP fork* and the code repository at: <https://github.com/trias-project/risk-modelling-and-mapping>) and modified to meet the needs of OneSTOP under Task 5.1. Annex 7.3.2–*Description of wiSDM 2.0 project folders* describes the organisation of modelling outputs under wiSDM-2.0 data structures.





This deliverable presents the results of Task 5.1, including maps of the known and potential distributions of selected IAS across Europe and an analysis of their introduction pathways using EASIN data. The following sections describe data collection and preprocessing, the development of species distribution models, the evaluation of their predictive performance, and the quantification of prediction uncertainty. Together, this information supports the interpretation and evaluation of the pathway analysis and potential distribution maps and provides a basis for assessing their robustness and limitations.

Together, the pathway and potential distribution information provide an evidence base for identifying the main drivers of IAS introductions and the areas most susceptible to their establishment. These outputs are intended to support subsequent project tasks and assist stakeholders in understanding and managing IAS-related risks across Europe. Through its several developmental stages, Task 5.1 aimed to establish a robust spatial modelling foundation for WP5's downstream work, including quantifying range shifts, identifying hotspots of emerging suitability and/or invasion risk, ranking species by expansion risk, and coupling with management-oriented indicators. It also reflects the OneSTOP project's commitment to deliver FAIR, transparent, and scientifically valid outputs that align with EU-level IAS policy and management imperatives.

1.2. Species Distribution Models for IAS: core concepts and applications

Species distribution models: general notions

In a broad sense, species distribution models (SDMs; also referred to as habitat suitability models or ecological niche models) translate observations of species occurrence or abundance, environmental data and, where available, demographic and dispersal information into spatially explicit estimates of current or potential distribution (Guisan & Thuiller, 2005). This allows users to investigate and obtain spatiotemporal predictions of species distributions and species–environment relationships (Elith & Leathwick, 2009; Guisan & Zimmerman, 2000). The value of this approach lies not simply in the maps it produces, but in its capacity to integrate evidence on species distributions, environmental conditions, and invasion pathways in a structured and reproducible way to inform conservation, risk assessment, prevention, surveillance, and management.

SDMs employ a correlative and empirical approach, which means that observed species distribution data is related to environmental predictors through a 'learning' algorithm that can take many forms, such as statistical, tree-based or neural-network heuristics, to capture linear and/or non-linear aspects of species relationships with their environmental determinants. The trained model is then used to make predictions for the whole geographic and environmental space of interest (Elith et al., 2010; Elith & Leathwick, 2009). In the context of biological invasions, these maps can highlight potentially suitable areas beyond a species' currently known invaded range, reveal isolated pockets of suitability where new invasion *foci* could emerge, indicate potential invasion fronts, and assess which areas or resources are most exposed to invasion risk. Such outputs are particularly relevant for species that are not yet present or remain locally distributed (IPBES, 2023).





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Because standard SDMs do not explicitly represent dispersal, biotic interactions, genetic adaptation, or other spatial and temporal ecological dynamics, predicted suitability does not necessarily correspond to actual species occurrence Araújo and Luoto (2007). A discrepancy between the observed distribution of an IAS and the output from an SDM may be due to an invasion time lag (so range-filling will occur at some time in the future), but it may also reflect other unmodelled ecological limitations or barriers. Although SDMs are generally calibrated for a particular period, they can be projected onto reconstructed past conditions (Nogués-Bravo, 2009) or future environmental scenarios (Thuiller et al., 2011). Such projections assume environmental niches remain sufficiently stable across space and time and, therefore, the estimated relationships are transferable (Elith et al., 2010; Pearman et al., 2008).

Applications of SDMs in ecology and IAS assessments

Despite relying on simplifying assumptions about species–environment relationships, SDMs provide a flexible and reproducible framework for investigating a wide range of ecological questions and supporting management, conservation, and monitoring (Guisan et al., 2013; Honrado et al., 2016). SDMs are widely used to describe patterns, deliver spatiotemporal predictions at several scales (Elith & Leathwick, 2009) and to address fundamental questions in Ecology such as the ‘niche shift vs. conservatism’ debate (Fernández & Hamilton, 2015; Guisan et al., 2014; Pearman et al., 2008; Rödder & Lötters, 2009) or, applied questions related to the assessment of ecological impacts of climate and land-use changes (Broennimann et al., 2006; de Chazal & Rounsevell, 2009; Pecl et al., 2017).

Investigating species responses to climate change has perhaps been one of the most active areas of research in which SDMs have been applied. Bellard et al. (2012) noted that species can respond to climate change by shifting their climatic niche along three non-exclusive axes: time (e.g., phenology), space (e.g., range), and self (e.g., physiology). In this sense, SDMs, due to the spatial nature of their predictions, are particularly well equipped to investigate shifts in species ranges. For example, Thuiller et al. (2011) used SDMs to estimate the consequences of climate change on the phylogenetic diversities of plant, bird and mammal assemblages across Europe. By combining climate projections with land cover/use scenarios in SDMs, researchers were able to investigate the conjugate and often synergistic effects of expected future changes in bird (Regos et al., 2015) and amphibian species (Hof et al., 2011).

Besides these applications, SDMs have also been used for addressing other topics in applied ecological research, such as: conservation planning and reserve design selection (Cuesta et al., 2017), impact assessment and resource management (Clauzel et al., 2013; Girardet et al., 2013; Makki et al., 2013), habitat restoration and reintroduction (Angelieri et al., 2016; Frick et al., 2014; Olsson & Rogers, 2009), invasive species risk assessment (Diogo et al., 2024; Naimi et al., 2022; Vicente et al., 2013; Vicente et al., 2014), and improve species surveying and monitoring network design (Amorim et al., 2014; Carvalho et al., 2015).

Ecological niche concepts and their implications for IAS distribution modelling

At its core, the ecological niche is not simply where a species occurs, but the multidimensional set of conditions and resources under which its populations can theoretically persist and reproduce. The Grinnellian-Hutchinsonian view emphasises species' environmental/abiotic requirements as defining the niche, whereas the Eltonian view focuses on species' functional





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or trophic roles. Because SDMs relate occurrences to spatial environmental predictors, they mainly describe, or approximate Hutchinson's realised niche more closely or, in more practical terms, describe the environmental niche at the scale of the data (Guisan & Thuiller, 2005; Guisan et al., 2017).

The Grinnellian fundamental niche can be described as an n -dimensional hypervolume of conditions under which a species could survive and reproduce without limiting biotic interactions. Applications of this hypervolume concept have been thriving in modelling, revealing ecological patterns and species vulnerability to climate change (Blonder et al., 2014; Blonder et al., 2018; Hespanhol et al., 2022; Rocha et al., 2022). The Hutchinson realised niche is the part expressed after this potential has been filtered by biotic interactions, dispersal, geographic accessibility, and available environments. In this regard, occupancy can often mislead, as immigration may maintain sink populations outside self-sustaining conditions, while inaccessible or uncolonised environmentally suitable sites remain empty (Guisan & Thuiller, 2005; Guisan et al., 2017; Peterson & Soberón, 2012).

This conceptual distinction between niches defines what SDMs can infer and project in space and time. Correlative SDMs associate occurrence or abundance with environmental or spatial attributes; their maps represent relative suitability (called 'favourability' in wiSDM-2.0), which can be considered as potential distribution – they do not model, not automatically occupancy, the fundamental niche or causation (Elith & Leathwick, 2009; Guisan & Thuiller, 2005). Occurrence-based models usually approximate a context-dependent portion of the realised niche and therefore, sound interpretation requires relevant predictors, appropriate grain and extent (i.e., scale matching), representative environmental gradients, a defensible accessible area or background, and explicit assessment of equilibrium status/dynamics (Elith & Leathwick, 2009; Guisan & Thuiller, 2005; Guisan et al., 2017; Peterson & Soberón, 2012).

Invasive species challenge SDM assumptions, and it is often necessary and justifiable to relax some assumptions of statistical models when the priority is accurate spatial predictions over strict inference (e.g., model parameter estimation, confidence interval estimation). For instance, distributions of IAS are highly dynamic and commonly far from equilibrium; altered dispersal barriers, enemy release, new mutualists, propagule pressure, landscape invasibility and novel climates can change which part of the niche is expressed in the recipient environment. An apparent climatic niche shift may be a realised niche shift, in which a pre-adapted species occupies a previously unavailable part of its fundamental niche, or a fundamental niche shift caused by adaptive genetic change (Bates & Bertelsmeier, 2021). Plasticity, acclimatisation and macroclimate-microclimate mismatches further complicate inference. Correlative analyses cannot distinguish these mechanisms, and the frequency of fundamental shifts remains unresolved and an ongoing matter of research and scientific discussion (Bates & Bertelsmeier, 2021; Elith & Leathwick, 2009; Guisan & Thuiller, 2005).

Accordingly, SDM-based invasion-risk modelling should treat niche stability as an empirically testable assumption rather than a default premise. Where data permit, native-only, introduced-only, and pooled-range calibrations should be compared, and niche overlap, expansion, and unfilling reported alongside environmental availability, accessibility, and non-analogue conditions. Such assessment can be highly informative for both fundamental and applied aspects of species invasions. Projections should flag extrapolation and, where possible, integrate dispersal, population processes, biotic interactions, physiological evidence and targeted experiments. The resulting maps can communicate both invasion potential and uncertainty arising from incomplete niche knowledge (Bates & Bertelsmeier, 2021; Elith & Leathwick, 2009; Guisan et al., 2017; Peterson & Soberón, 2012).





Limitations and uncertainty in SDMs

The breadth of application of SDMs makes transparent documentation of inputs, modelling decisions and associated uncertainty essential, both for communicating results effectively and for ensuring their uptake and reproducibility. On this note, it is also key that users of SDM outputs clearly understand their meaning both conceptually and in more practical terms. Often modellers fail to accurately communicate that SDM maps resulting from model spatiotemporal predictions show estimates of suitability (or favourability, as in the case of wiSDM 2.0), which indicate where environmental conditions may permit occurrence or establishment; SDM outputs do not directly demonstrate that the species is present. Conversely, an apparent absence can reflect observation processes (e.g., limited survey effort, imperfect detection), or ecological processes (e.g., dispersal barriers or a lag between introduction and establishment).

Beyond these interpretative aspects, SDMs also have relevant limitations that should be made explicit in any application and during communication to any potential user community considering applying SDM outputs in downstream assessments, including the expected uptake and downstream use in WP5 or other OneSTOP WPs. These sources of SDM uncertainty arise from multiple factors that can be summarised (non-exhaustively) as in IPBES (2023): (i) data availability and bias; (ii) scale and spatiotemporal transferability issues; (iii) non-equilibrium assumption violation and ongoing ecological change; (iv) incomplete representation of abiotic and biotic processes; and (v) single-driver future scenarios focusing more commonly on climate. These aspects should be explicitly assessed and communicated, with transparent calibration, validation and use of independent data wherever possible.

Distribution modelling as an operational basis for IAS governance

Despite their inherent limitations and uncertainty, SDMs provide a rigorous foundation to support IAS risk assessment. However, given their limitations, model outputs should be used as decision-relevant evidence rather than deterministic forecasts. When matched to the assessment objective, models can inform the probabilities of establishment and spread, identify environmental exposure of valued assets, and support the ranking of species, pathways and locations.

Methodologically robust application begins by defining the decision context, spatial and temporal extent, invasion stage, and required output. Occurrence and, where available, abundance data should be quality-controlled, screened for sampling bias and assembled from both native and invaded ranges. Predictors should be ecologically reasonable, defensible and aligned with the resolution of the biological data. In addition to climate and land cover, relevant layers may include disturbance, accessibility, propagule-pressure proxies and transport infrastructure. Algorithms and model parameterisation should be compared, and ensemble approaches, which integrate predictions from multiple models (Araújo & New, 2006), considered where appropriate. Uncertainty arising from input data, model structure, thresholds, future scenarios and extrapolation into novel environments should be explicitly mapped. Evaluation should use spatially structured cross-validation or independent data wherever possible, with particular attention to transferability given that niche change and limited native-range occurrence data can substantially reduce predictive performance in





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introduced regions (Du et al., 2024; Jiménez-Valverde et al., 2011; Liu et al., 2022; Sofaer et al., 2019; Srivastava et al., 2019). Including different modelling approaches and performing hierarchical and standardised model intercomparisons could be used to add rigour to the outputs and strengthen confidence in the resulting projections (Zurell et al., 2026).

For pathway-based assessment, environmental suitability is one component of a broader chain that also includes the association between the species and a commodity or vector, origin and volume of movements, introduction frequency, survival during transport, seasonality, detectability, post-entry movement and the probability of transfer to suitable habitat (IPBES, 2023). Evidence that climate matching, number of introduction events and road-network density influence invaded-range expansion illustrates why biophysical suitability and connectivity must be analysed jointly (Clarke et al., 2025; Du et al., 2024).

SDM outputs can also be translated directly into monitoring design. These models have increased survey efficiency when used to stratify field sampling, and iterative cycles of prediction, targeted observation, validation and refitting can progressively reduce critical data gaps (Crall et al., 2013; Sofaer et al., 2019). More recent frameworks combine suitability, known incursion locations, patch size, road networks and survey costs to identify routes that maximise the probability of early detection within operational constraints (Zhu et al., 2025). Repeated occurrence or abundance observations can then be used to update invasion fronts, evaluate changes in occupancy or population intensity, and test whether prevention, eradication, containment or control is producing the expected spatial response. Combining expert knowledge with current and future climatic suitability further enables transparent assignment of species to management categories and priority levels (Lozano et al., 2024).

Accordingly, SDMs are most powerful when embedded in an adaptive evidence cycle linking horizon scanning, risk assessment, targeted surveillance, rapid response and policy evaluation. Their value for governance derives not from eliminating uncertainty, but from making assumptions, spatial priorities and alternative futures explicit, testable and revisable. Implemented with transparent protocols, independent validation and recurrent updating, distribution and abundance models can turn heterogeneous biodiversity observations into an anticipatory intelligence system capable of directing scarce resources towards the species, pathways and sites where timely intervention will deliver the greatest benefit, while providing an auditable basis for national and EU reporting on IAS prevention and impact reduction (Lozano et al., 2024; Sofaer et al., 2019; Zhu et al., 2025).





2. Data and methods

Here, we demonstrate a reproducible workflow to create species distribution models for the 120 focal invasive species in Europe. We use global distribution data (from GBIF) to define the species' multi-dimensional niche, based on bioclimatic and land cover compositional predictors. Models trained under historical/baseline conditions were then used to obtain projections for future conditions in Europe, at fine resolution, to describe the environmental favourability and potential distribution of each species and their trajectories. This section describes the modelling workflow, including target species selection, definition of the modelling region, the input datasets and the environmental predictor variables derived from them, the data preprocessing steps implemented in the pipeline, and the generation of future projections. All figures produced used consistent, colour-vision-deficiency-safe palettes and complementary labels, ordering and facets to ensure accessibility and interpretability.

2.1. Species selection

Task 5.1 applied a structured process to identify the species to be modelled (see Supporting Table 7.1 in Annex 7.1—*Complete list of selected species and calculated indicators*). The first component focused on Invasive Alien Species of Union concern, as defined under EU Regulation 1143/2014, together with candidate species being considered for future listing. This process resulted in a priority set of 70 terrestrial taxa representing a wide range of ecological strategies, introduction pathways, and invasion histories relevant to European risk assessment. Species were classified as terrestrial when their ecological traits and habitat associations indicated that they occur and establish primarily in land-based environments. The classification criteria were refined by the project team in consultation with members of [GuardIAS](#) (DOI: [10.3030/101181413](#)), a Horizon Europe sister project responsible for assessing and modelling aquatic and freshwater IAS.

To ensure that the modelling outputs also reflected local management needs and stakeholder priorities, OneSTOP's partner Living Labs were also consulted during the species-selection process. This consultation identified 50 additional species, with each of the five Living Labs (Belgium, Finland, Portugal, Romania, and the United Kingdom) nominating 10 species of greatest national or regional concern. Together, the 70 EU-priority taxa and the 50 species selected by the Living Labs comprise the 120-species pool modelled in Task 5.1, representing both EU-level priorities and geographically specific threats.

2.2. Study area/modelling region

The spatial extent used for species distribution modelling within Task 5.1 corresponds to the set of countries belonging to the Council of Europe, supplemented by Belarus, Kosovo, and Vatican City (see detailed list of states in Table 1), totalling 49 states, to ensure complete coverage of the European region relevant to OneSTOP's IAS policy and management contributions.





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This delimitation provides a consistent geographic frame aligned with the project's European focus. National boundaries were extracted from GADM v4.1 (Global Administrative Areas dataset; URL: <https://gadm.org/index.html>), using the level-0 (country) polygons as the reference administrative units. The countries of interest were explicitly listed and verified against the GADM dataset to ensure complete correspondence, after which only the selected polygons were retained. The resulting country set was reprojected to the coordinate system of the environmental rasters (i.e., WGS 1984/Lambert Cylindrical Equal Area) and buffered by 100 km to create a modelling envelope that avoids edge effects during projection. All boundary preparation steps follow a reproducible workflow implemented in R, culminating in the creation of GeoPackage layers for selected countries ready for integration into the Species Distribution Modelling (SDM) pipeline.

For the presentation and interpretation of results, summary statistics and aggregated indicators are reported for two geographical groupings: (i) the broader set of European countries included in the assessment, as listed in Table 1; and (ii) the EU-27 Member States together with the United Kingdom. While both geographical scopes are considered throughout the analysis, greater emphasis is placed on the EU-27 and United Kingdom grouping, reflecting the geographical coverage, policy relevance and overarching objectives of the OneSTOP project (Groom et al., 2025). The geographical scope for each analysis is specified where relevant to ensure consistency and transparency in the reporting of results.

Info note

GADM (Global Administrative Areas, version 4.1) was selected as the basemap for the analyses and for displaying maps in the OneSTOP SDM Gallery [see Section 3.3.2—Species Distribution Models Map Gallery]. GADM represents national boundaries on a *de jure* basis, according to their legal status, whereas alternative datasets such as Natural Earth may use *de facto* territorial control. GADM was therefore considered the most appropriate option to ensure consistency with the institutional context of the project and current EU conventions (e.g., https://www.eeas.europa.eu/delegations/ukraine/ukraine-13th-joint-discussion-consequences-temporary-occupation-ukrainian-territories-russia_en; press communication released on: 07.07.2026).





Table 1 – List of selected countries used to define the European bounding box for modelling tasks in T5.1, including the Council of Europe countries (i.e., the 46-member intergovernmental organisation, not the European Council or the Council of the European Union) plus three additional states. Vatican City/Holy See has observer status rather than full membership; Belarus and Kosovo are not members. A cartographic representation of these countries/modelling extent for T5.1 is included in the lower right corner.

Council of Europe EU27 countries	Council of Europe (non-EU27) 19 countries	Additional countries 3 countries
Austria Belgium Bulgaria Croatia Cyprus Czechia Denmark Estonia Finland France Germany Greece Hungary Ireland Italy Latvia Lithuania Luxembourg Malta Netherlands Poland Portugal Romania Slovakia Slovenia Spain Sweden	Albania Andorra Armenia Azerbaijan Bosnia and Herzegovina Georgia Iceland Liechtenstein Moldova Monaco Montenegro North Macedonia Norway San Marino Serbia Switzerland Turkey Ukraine United Kingdom	Belarus Kosovo Vatican City



2.3. Introduction pathways data collection and analysis

General information

Introduction pathways should be treated as management-relevant data for prevention, surveillance, horizon scanning and risk prioritisation, rather than merely as historical descriptors of arrival. Their assessment should consider the frequency and volume of introductions, propagule pressure, taxa involved, pathway activity, receiving-environment vulnerability (i.e., invasibility potential), potential impact, feasibility of intervention, and





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changes over time due to trade, transport, land use, land cover change, climate change or management measures.

Overall, introduction pathways are the routes, mechanisms and associated human activities through which live alien organisms, including propagules, gametes, seeds, eggs, fragments or other viable biological material, are moved outside their natural range and into a recipient territory, thereby creating opportunities for establishment, spread and potential invasion (Saul et al., 2017). In the EU invasive alien species policy context, this definition should be interpreted consistently with Regulation (EU) No 1143/2014, which defines “introduction” as movement outside a species’ natural range as a consequence of human intervention, and “pathways” as the routes and mechanisms of the introduction and spread of invasive alien species.

Introduction pathways used the classification system proposed by the CBD pathway framework (see details in Table 2) (CBD, 2014; Harrower et al., 2018; Saul et al., 2017), which distinguishes the main mechanisms of alien species movement as importation of a commodity, arrival via a transport vector, establishment of an anthropogenic dispersal corridor, or secondary spread from a region where the species is already alien. These mechanisms are operationalised into six main categories: i) release in nature, ii) escape from confinement, iii) transport as contaminant, iv) transport as stowaway, v) corridor, and vi) unaided spread.

Table 2 – CBD categories and subcategories of pathways; see details in Harrower et al. (2018). The entries in italics (marked with an asterisk) are pathway subcategories that are suggested either for removal, in the case of the Release in nature for use, or are a new pathway suggested for addition to the scheme, in the case of the Other contaminant. The first column includes both the proposed names and “older” ones. NA – not applicable*

Category	Subcategory	Subcategory text / info
Release (Release in nature)	Biological control	Biological control
	Stabilisation & Barriers	Erosion control/dune stabilisation (wind breaks, hedges)
	Fishery in wild	Fishery in the wild
	Hunting	Hunting
	Aesthetic release	Landscape/flora/fauna “improvement” in the wild
	Conservation in wild	Introduction for conservation purposes or wildlife management
	NA	Release in nature for use (other than above, e.g. fur, transport, medical use)*
	Other release	Other intentional release
Escape (Escape from confinement)	Agriculture	Agriculture (including Biofuel feedstocks)
	Aquaculture	Aquaculture/mariculture
	Botanical gardens & Zoos	Botanical garden/zoo/aquaria (excluding domestic aquaria)
	Pet	Pet/aquarium/terrarium species (including live food for such species)
	Farmed animals	Farmed animals (including animals left under limited control)
	Forestry	Forestry (including reforestation)
	Fur farms	Fur farms
	Horticulture	Horticulture
	Ornamental	Ornamental purpose other than horticulture
	Research	Research and ex-situ breeding (in facilities)





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	Live food & live bait	Live food and live bait
	Other escape	Other escape from confinement
Contaminant (Transport – Contaminant)	Nursery material contaminant	Contaminant nursery material
	Bait contaminant	Contaminated bait
	Food contaminant	Food contaminant (including live food)
	Contaminant of animals	Contaminant on animals (except parasites, species transported by host/vector)
	Parasite of animals	Parasites on animals (including species transported by host and vector)
	Contaminant of plants	Contaminant on plants (except parasites, species transported by host/vector)
	Parasite of plants	Parasites on plants (including species transported by host and vector)
	Seed contaminant	Seed contaminant
	Timber trade contaminant	Timber trade
	Habitat material contaminant	Transportation of habitat material (soil, vegetation)
	Other contaminant*	
Stowaway (Transport – Stowaway)	Fishing equipment	Angling/fishing equipment
	Container & bulk cargo	Container/bulk
	Airplane	Hitchhikers in or on airplane
	Ship excluding ballast water or hull fouling	Hitchhikers on ship/boat (excluding ballast water and hull fouling)
	Machinery & equipment	Machinery/equipment
	People & luggage	People and their luggage/equipment (in particular tourism)
	Packing material	Organic packing material, in particular wood packaging
	Ballast water	Ship/boat ballast water
	Hull fouling	Ship/boat hull fouling
	Land vehicles	Vehicles (car, train ...)
	Other stowaway	Other means of transport
Corridor	Canals and artificial waterways	Interconnected waterways/basins/seas
	Tunnels and bridges	Tunnels and land bridges
Unaided		Natural dispersal across borders of invasive alien species that have been introduced through pathways 1 to 5

In applied assessments, an introduction pathway may comprise a geographic route, a corridor of introduction, and/or human activity that gives rise to intentional or unintentional movement. This should be distinguished from a vector, which is the physical means or agent by which organisms are transported, such as a ship, aircraft, vehicle, machinery, commodity, ballast water, soil, packaging or equipment. A species may be associated with more than one pathway, and pathways may be assigned with varying levels of certainty based on direct evidence, inference, expert judgement or analogy with documented introductions (CBD, 2014; Harrower et al., 2018; Hulme et al., 2008; Saul et al., 2017).





Additional info/glossary

Alien (= non-native) species, subspecies or lower taxon, introduced outside its natural past or present distribution by direct or indirect human action; includes any part, gametes, seeds, eggs, or propagules of such species that might survive and subsequently reproduce.

Invasive alien species (IAS) – species whose introduction and/or spread outside their natural past or present distribution threatens biodiversity, society and/or economies.

Pathway – processes that result in the introduction of an alien species from one geographical location to another.

Vector – mode of introduction, for example, a ship, cargo containers, packing materials, equipment or transport vehicles.

Primary pathway – movement of species to new regions or provinces across biogeographic barriers (oceanic, landmass or climatic barriers (i.e. trans-oceanic and intercontinental pathways).

Secondary pathways – spread and dispersal of alien species between points within or between neighbouring regions (secondary pathways often differ from the primary ones).

Stowaway – a species that uses vectors to move between locations by chance or unknowingly

Contaminant – a species that has an ecological association with, and/or dependence on, a specific organism or product.

Parasite or pathogen – organisms that live in or on a host and obtain their food from the host at a cost to the host.

Source: extracted from Harrower et al. (2018)/CBD guidance document.

Data collection

Introduction pathway-related data for the 120 species selected in OneSTOP (see section 2.1–*Species selection* and Annex 7.1–*Complete list of selected species and calculated indicators*) were obtained from the European Alien Species Information Network (EASIN), through its public Catalogue web service/API (<https://easin.jrc.ec.europa.eu/apixg/catxg>). Data were retrieved programmatically via the RESTful API. The API exposes every field presented on a factsheet, including the Convention on Biological Diversity (CBD) pathway classification. The data extraction crawler was implemented in R 4.5.2 using the *httr2*, *jsonlite*, *readxl*, *readr*, *stringi*, and *rgbif* libraries. Taxonomic name resolution and independent verification were performed against the GBIF Backbone Taxonomy (Global Biodiversity Information Facility) through the *rgbif* interface. Pathway-related data was collected from the 'CBD_Pathways' tag, and the presence info by country was compiled from the '*PresentInCountries*' tag. The code and data used to extract EASIN's pathways info are available at: https://github.com/OneSTOP-CIBIO/EASIN_pathways (DOI: 10.5281/zenodo.21852494).





Data analysis and visualisation

Pathway importance was quantified using two complementary criteria: the proportion of all deduplicated pathway records and the proportion of species associated with each pathway. The first analysis accounts for species linked to multiple introduction mechanisms, whereas the second indicates how widespread each pathway is across the species set ($n=120$). Records with unresolved attribution were retained as an explicit “unknown” category. Temporal differences in pathway composition were evaluated using the year of first European record. Because individual species may be associated with several pathways, statistical significance was assessed through species-level permutation tests rather than conventional tests assuming independent records. Multiple comparisons were controlled using the Benjamini–Hochberg procedure, while Cramér’s V was used to describe effect size. Uncertainty grades were summarised descriptively but were not used to weight frequencies because they were unavailable for most records. Results were visualised through ranked frequency plots, taxonomic-group comparisons, heatmaps, pathway-detail summaries and temporal composition trajectories.

2.4. Species occurrence data

Occurrence records were retrieved from the Global Biodiversity Information Facility (GBIF) using automated download procedures integrated into the wiSDM v.2.0 workflow. Details regarding data retrieval, data reference links, GBIF download keys, DOIs, and the number of valid records retrieved are available in Supporting Table 7.1 (Annex 7.1–*Complete list of selected species and calculated indicators*, page 119).

Species occurrence records were retrieved for 1971–2025, an extended period that encompassed the CHELSA v2.1 historical climatological data reference period (1981–2010). This was done to include a wider range of species occurrence records by capturing some past and the most recent available records, including observations associated with newly established populations, recent introductions, and actively expanding invasion fronts. By using this temporal window, we extend the period by 15 years beyond the final year of the historical climatic reference period of CHELSA v.2.1, which was set to 2010. Consequently, some recent occurrence records may be associated with climatic conditions that differ, to some extent, from those represented by the historical climate layers. Nevertheless, retaining records up to 2025 was considered the most appropriate modelling decision for IAS. Invasive alien species distributions are often highly dynamic and may change rapidly due to new introductions, secondary spread, dispersal along transport networks, and ongoing range expansion. Restricting occurrence data to 2010 would therefore risk excluding substantial portions of the contemporary invaded range and systematically underrepresenting recent invasion dynamics in a time when highly informative and precise records are available (e.g., especially the growing availability of data from citizen-science platforms and nature-related smartphone/mobile apps). Such omissions could be especially consequential for species undergoing rapid or recent expansion in Europe (e.g., *Cortaderia selloana*, *Acacia spp.*, *Vespa velutina nigrithorax*). Similarly, we allowed a slightly extended historical window to increase sample sizes and data availability.





GBIF occurrence-data processing and quality control

Global species occurrence records retrieved from GBIF between May and July 2026 were processed using a reproducible, taxon-key-based workflow. Prior to data retrieval, all target species names were matched against the GBIF taxonomic backbone. This step ensured that the occurrence search was based on standardised taxonomic concepts rather than on potentially inconsistent user-supplied names. Where a submitted name was recognised as a synonym or otherwise lacked accepted taxonomic status, the corresponding accepted GBIF usage key was used. Automated checks confirmed that every target species had been successfully matched, and the workflow was terminated if one or more taxa could not be resolved. Only georeferenced occurrence records were retrieved. Records already flagged by GBIF as presenting geospatial issues were excluded at the download stage, and records with a reported coordinate uncertainty greater than 5,000 m were also removed. Records for which coordinate uncertainty was not reported were retained, as the absence of an uncertainty estimate does not necessarily indicate poor spatial accuracy and excluding such records could disproportionately reduce data availability for less intensively documented taxa or regions.

The selected basis-of-record categories included human and machine observations, general observations, material samples, preserved specimens, occurrences of unspecified type, and records with an unknown basis of record. Fossil specimens and living specimens were excluded because their reported coordinates may refer to collection repositories, zoological or botanical institutions, captive holdings, or other locations that do not represent the species' occurrence in the environment. This filtering therefore reduced the risk of incorporating records that were geographically valid in a database sense but unsuitable for species distribution modelling.

Following retrieval, taxonomic information was further harmonised at the record level. Occurrences whose accepted taxon keys did not correspond directly to the initially resolved set of target taxon keys were treated as potentially ambiguous synonym records. Their accepted scientific names were rematched to the GBIF backbone, resolved to species level, and reassigned to the appropriate accepted scientific name and taxon key. Records that could not ultimately be reconciled with the predefined set of target taxa were excluded. This additional step reduced inconsistencies arising from alternative nomenclature, changes in taxonomic treatment, or ambiguous mappings within the downloaded GBIF data. Further quality control was applied to the identification status of individual records. Occurrences explicitly described as unverified, unvalidated, uncertain, doubtful, invalid, provisional, awaiting validation, or otherwise not conclusively confirmed were removed. The filtering accommodated several alternative expressions and languages used in the GBIF `identificationVerificationStatus` field. Records without an explicit verification-status entry were retained, because this field is not populated consistently across data providers and its absence cannot be interpreted as evidence that the identification is unreliable.

Coordinate precision was also evaluated to further confirm the data's validity for subsequent modelling processes. Records for which both latitude and longitude were reported with fewer than four decimal places were removed. At the equator, four decimal degrees correspond approximately to a spatial precision of around 10 m. This criterion was used primarily to identify strongly rounded or coarsely generalised coordinates rather than to imply equivalent positional accuracy across all records. This routine complemented, but did not replace, the filtering





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based on reported coordinate uncertainty. The remaining coordinates were screened using the *CoordinateCleaner* R package (Zizka et al., 2019) to identify common spatial artefacts in biodiversity databases. Records located within 100 m of country centroids, national capitals, biodiversity institutions, or the GBIF headquarters in Copenhagen were excluded, together with records located at or near the default zero coordinate at 0° latitude and 0° longitude. Such locations frequently arise from geocoding defaults, incomplete locality information, institutional specimen records, or data-entry errors and may otherwise generate artificial clusters in environmental space.

To support modelling components operating at different spatial requirements, namely a global climate-only component and a European habitat-only component (see details in 2.6.1–*wiSDM 2.0 general workflow/pipeline*), two cleaned occurrence datasets were produced. The principal cleaned dataset retained records with a maximum reported coordinate uncertainty of 5 km or with no reported uncertainty value. A more spatially stringent subset was additionally created for the European 1-km-resolution modelling component, retaining only records with reported coordinate uncertainty of 1,000 m or less, together with records for which uncertainty was not available. This distinction allowed the workflow to retain broader occurrence coverage for large-scale analyses while applying a closer correspondence between occurrence precision and predictor resolution in the finer-scale European models (described below).

Finally, each species name was assigned to a broad taxonomic group using its GBIF higher-level classification, including plants, birds, molluscs, amphibians, mammals, reptiles, malacostracan crustaceans, insects, and fishes, enabling the use of thinning procedures via group-specific bias layers. The processed datasets were stored together with taxonomic and download metadata, including accepted scientific names, accepted GBIF taxon keys, the temporal retrieval limits, the GBIF download DOI, and the download creation date. Importantly, these metadata provide a traceable link to the original GBIF download and facilitate reproducibility, auditing, and subsequent updating of the occurrence dataset (see details of these metadata in Supporting Table 7.1: *Annex 7.1—Complete list of selected species and calculated indicators*, page 119).

Descriptive analysis of species occurrence data adequacy and sufficiency

The occurrence records were assessed descriptively, since the number, spatial uniqueness and geographical distribution of available data determine which species can be modelled, especially for the more stringent European habitat-only model (see details in 2.6.1–*wiSDM 2.0 general workflow/pipeline*) and constrain the robustness of the resulting outputs and projections. The assessment further establishes whether record volume translates into effective spatial coverage and addresses spatial sampling saturation at the resolution used for model calibration (i.e., 1×1 km cells). To accomplish this, and based on the retrieved and filtered data, we conducted an assessment of data adequacy and sufficiency to determine the number of records after the harmonisation, tidying, and cleaning chain (i.e., fit-for-purpose or modelling-ready records). We calculated several indicators (see details in Table 3) to guide this assessment and allow us to understand which species may have more gaps or, in contrast, that have a high number of redundant records by assessing the ratio of the number of unique records at 1x1 km cells (i.e., which are functionally valid/useful for modelling) vs the total number of cleaned records. To categorise species into data availability tiers, the following classes were used: “Insufficient” (<10 unique 1x1 km records), “Marginal” (10-29 records),





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“Modellable with caution” (30-99 records), and “Well supported” (≥ 100 records). These categories deviate from wiSDM 2.0 on purpose to allow a more fine-grained analysis.

Table 3 – Calculated indices used to assess data availability and saturation based on cleaned species records obtained from GBIF.

Index name/code	Description
n_total_global	Total number of records globally available
n_total_eur	Total number of records available in countries selected for the modelling (see subsection 2.2–Study area/modelling region; Table 1) which serve as the main area
n_total_eur_bbox	Total number of records available in the bounding box plus the 100km buffer applied to selected countries, resulting in a much less strict check
n_unique_global	Number of unique 1×1 km cells globally available (i.e., “modelling-ready” or “SDM-ready” records)
n_unique_eur	Number of unique 1×1 km cells available for Europe (i.e., “modelling-ready” or “SDM-ready” records)
r_uni_global	Ratio between unique 1km cells and total record counts globally available
r_uni_eur	Ratio between unique 1km cells and total record counts globally available
r_conc_eur	Concentration ratio of unique 1km cells in Europe as the proportion between the number for Europe divided by the total globally available

i Info note

“Raw” species records are not the same as modelling-ready species records!

Raw species records are retrieved from GBIF and undergo rigorous filtering processes supported by strict criteria (e.g., existence of coordinates, coordinate precision, taxonomic checks) as well as multiple steps of harmonisation and cleaning (e.g., removal of records with coordinates bearing insufficient number of decimal places, attribution to GBIF headquarters, country or city centroids). This means that although some species may have a substantial number of records, these data do not meet the required quality for modelling applications (i.e., not fit for purpose). The subset of records that actually meet these criteria is defined as “modelling-ready” or “SDM-ready” records.





2.5. Environmental predictors

The list of post-processed datasets used for Task 5.1 modelling pipeline is available in Annex 7.2–*List of datasets used in modelling uploaded to Zenodo*, Supporting Table 7.2.

2.5.1. Climate predictors

Climatic variables were obtained from CHELSA v2.1 (URL: <https://www.chelsa-climate.org/datasets>; access date: June 2025), including a suite of bioclimatic variables characterising temperature and precipitation regimes, providing a richer representation of climatic conditions relevant to species' ecological requirements (see details in Table 4). CHELSA-bioclim is a global, kilometre-scale climate dataset generated using the CHELSA downscaling model and consists of bioclimatic variables suitable for ecological and species distribution modelling applications. The CHELSA v2.1 dataset is distributed as an active product and provides bioclimatic layers for historical/reference and future climatological periods. The modelling workflow used a targeted subset of nine CHELSA bioclimatic variables representing biologically relevant dimensions of thermal conditions, thermal variability, water availability, and precipitation seasonality (Davis et al., 2024) (see details of bioclimatic predictors in Table 4). These variables capture both average climatic conditions and limiting seasonal extremes that are ecologically relevant to species survival, establishment and potential range expansion.

Table 4 – List of bioclimatic predictors considered for modelling in Task 5.1 extracted from the CHELSA 2.1 dataset.

Variable	CHELSA v2.1 name/units	Description/ecological interpretation
BIO1	Mean annual near-surface air temperature (°C)	General thermal environment conditions and long-term temperature suitability
BIO4	Temperature seasonality (°C/100)	Intra-annual thermal variability; distinguishes stable from strongly seasonal climates
BIO5	Maximum temperature of the warmest month (°C)	Upper thermal exposure and potential heat limitation; indicates peak thermal conditions
BIO6	Minimum temperature of the coldest month (°C)	Cold-season limitation combined with overwintering potential and frost sensitivity; characterises winter cold intensity
BIO7	Annual temperature range, BIO5 – BIO6 (°C)	Annual thermal amplitude and continentality effects of climate regime
BIO12	Total annual rainfall (kg.m ⁻² .yr ⁻¹)	Overall water availability via precipitation
BIO13	Precipitation of the wettest month (kg.m ⁻² .month ⁻¹)	Maximum monthly precipitation total; peak moisture availability and wet-season conditions
BIO14	Precipitation of the driest month (kg.m ⁻² .month ⁻¹)	Minimum monthly precipitation total; drought-season constraint effects and minimum moisture availability
BIO15	Precipitation seasonality (kg.m ⁻²)	Coefficient of variation (100 × SD ÷ mean) of monthly precipitation totals; temporal concentration or variability of rainfall throughout the year



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To obtain future projections of potential range and environmental favourability change for IAS, we used the same set of bioclimatic predictors from CHELSA v2.1 CMIP6-derived climatologies for two future periods in Task 5.1 modelling workflow: 2041–2070 and 2071–2100. We considered CMIP6 Shared Socioeconomic Pathways (SSPs) scenarios that combine alternative socioeconomic trajectories with greenhouse-gas forcing levels to project future climate conditions under contrasting global-change pathways. The CHELSA 2.1 dataset includes future climatologies for 2011–2040, 2041–2070, and 2071–2100 for three Shared Socioeconomic Pathways: SSP1–2.6, SSP3–7.0, and SSP5–8.5 (see details in subsection 2.7–*Future climatic scenarios based on CMIP6-RCP/SSP*). For CHELSA 2.1, these scenario data are available for five CMIP6 Earth System Models selected on the basis of required climate-variable availability and model-performance considerations following the ISIMIP3b protocol: GFDL-ESM4, IPSL-CM6A-LR, MPI-ESM1-2-HR, MRI-ESM2-0 and UKESM1-0-LL. See details for each Global Circulation Model (GCM) in Table 5.

Table 5 – List of currently available Global Circulation Models (GCMs) in future projections for the CHELSA v2.1 dataset and available summary descriptions (model sub-components, physics, resolution) from IPCC/CMIP6.

CMIP6 GCMs used in CHELSA	Data provider/institution	Brief description and approximate native resolution
GFDL-ESM4	NOAA Geophysical Fluid Dynamics Laboratory, Princeton, USA	A coupled Earth system model from GFDL, including interactive aerosols, atmospheric chemistry, land, ocean, ocean biogeochemistry and sea ice components. The CMIP6 metadata lists AM4.1 atmosphere, LM4.1 land, OM4p5/MOM6 ocean, COBALTv2 ocean biogeochemistry and SIS2 sea ice components. GFDL's ESM4.1 documentation describes it as a coupled chemistry-carbon-climate model that emphasises Earth-system interactions, carbon cycling, chemistry, and ecosystem comprehensiveness. Nominal CMIP6 metadata: atmosphere/land/aerosol/chemistry at ~100 km; ocean, ocean biogeochemistry and sea ice at ~50 km.
UKESM1-0-LL	Met Office Hadley Centre, Exeter, United Kingdom	The first version of the UK Earth System Model. It uses HadGEM3-GC31-LL as its physical climate core and includes interactively coupled terrestrial carbon and nitrogen cycles, dynamic vegetation, agricultural land-use change, ocean biogeochemistry, and unified troposphere–stratosphere chemistry coupled to aerosol processes. Nominal CMIP6 metadata: atmosphere, land, aerosols and atmospheric chemistry at ~250 km; ocean, ocean biogeochemistry and sea ice at ~100 km.
MPI-ESM1-2-HR	Max Planck Institute for Meteorology, Hamburg, Germany	A high-resolution configuration of the Max Planck Institute Earth System Model version 1.2. The model is based on the ECHAM6.3 atmosphere, JSBACH land, MPIOM ocean, and HAMOCC ocean biogeochemistry, with coupling of energy, momentum, water, and CO ₂ between components. The HighResMIP description emphasises its use for assessing effects of increased atmospheric and oceanic resolution on climate mean states and ocean–atmosphere dynamics. Nominal CMIP6 metadata: atmosphere and land at ~100 km; ocean, ocean biogeochemistry and sea ice at ~50 km.
IPSL-CM6A-LR	Institut Pierre-Simon Laplace, Paris, France	The sixth version of the IPSL coupled climate model in low-resolution configuration. It couples the LMDZ atmosphere, ORCHIDEE land surface, NEMO ocean, PISCES ocean biogeochemistry and LIM3 sea ice components. The model documentation describes IPSL-CM6A-LR as developed for CMIP6 to study natural climate variability and climate response to natural and anthropogenic forcings. Nominal CMIP6 metadata: atmosphere and land at ~250 km; ocean, ocean biogeochemistry and sea ice at ~100 km.





MRI-ESM2-0	Meteorological Research Institute, Tsukuba, Ibaraki, Japan	The second-generation MRI Earth System Model. The published model description states that MRI-ESM2.0 was developed from earlier MRI-CGCM3 and MRI-ESM1 models, with improvements to physical components, cloud representation, radiation, vertical atmospheric resolution and climate reproducibility. The model uses MRI-AGCM for the atmosphere/land and MRI.COM for ocean and sea ice components. Nominal CMIP6 metadata: atmosphere and land at ~100 km; aerosols and atmospheric chemistry at ~250 km; ocean, ocean biogeochemistry and sea ice at ~100 km.
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For each time period and SSP/RCP scenario, future SDM projections were generated using an unweighted, cell-wise average of the five CHELSA v2.1 CMIP6 global climate models available for the selected SSP/RCP combinations, producing a single multi-model ensemble climate surface for each bioclimatic variable. This multi-model mean provides an estimate of the central climate response and avoids making projected IAS suitability dependent on the particular sensitivities, parameterisations or regional biases of any single GCM. Multi-model means commonly reproduce broad-scale observed climate more reliably than individual models because model-specific errors may partly cancel, although this advantage is not uniform across variables and regions (IPCC, 2007). The approach ensured that all species were projected against a common and internally consistent set of future predictors, thereby supporting both methodological consistency and computational efficiency across the modelling workflow. This was particularly advantageous for a continental-scale analysis involving 120 species, ten modelling algorithms, two future periods and three emissions pathways, as the use of a harmonised predictor set avoided unnecessary replication of projections across five separate GCMs and substantially streamlined computation, storage and post-processing. The adopted strategy was therefore considered proportionate to the principal objective of producing harmonised, comparable European-scale estimates of future climatic suitability rather than fully probabilistic estimates of climate-model uncertainty.

Descriptive climate data analysis across periods, scenarios and EU27 countries

The bioclimatic predictors were examined descriptively before modelling, since the magnitude, direction, and spatial structure of projected change determine the extent of species distributional change in future projections and provide the basis for understanding modelled shifts in favourability to specific climatic drivers. To achieve this, CHELSA 2.1 bioclimatic data were summarised at country level for the historical baseline and for each combination of future period and SSP/RCP scenario. The analysis considered nine temperature- and precipitation-related indices, using country means as the principal summary while retaining additional statistics describing within-country spatial variation. Change was quantified as the absolute difference from baseline for temperature variables and as percentage change for precipitation variables. To allow comparison among variables with different units, changes were also standardised by the cross-country standard deviation of baseline conditions. An overall measure of bioclimatic displacement was then calculated for each country, period and scenario as the standardised Euclidean distance across all nine indices, alongside separate temperature and precipitation components and identification of the dominant contributing variable. Results were visualised through country rankings, scenario ranges, variable-level heatmaps, temperature–precipitation response plots and cross-country distributions, thereby supporting comparison of the magnitude, direction and spatial consistency of projected climatic change relevant to future IAS trajectories.





2.5.2. Land-cover predictors

Our projection of SDM outputs into the future requires us to consider land use change as well as climatic change, providing a more comprehensive assessment of potential IAS distributions by capturing the combined influence of climatic and land-cover dynamics. This is even more challenging than climatic predictions. Here, land-cover data were obtained from the global high-resolution 1-km Plant Functional Type (PFT) projections of Chen et al. (2022), which provide harmonised historical and future land-cover projections under socio-climatic scenarios. The dataset offers global 1-km land-cover projections from 2015 to 2100, subdivided into 20 Plant Functional Types (PFTs), and was selected because it meets all required criteria in terms of spatial resolution, thematic detail, accuracy (OA = 0.929; Kappa = 0.864; FoM = 0.102), and alignment with CMIP6 SSP-RCP scenarios.

This dataset combines top-down land-use demands from the Land-Use Harmonization 2 (LUH2) dataset with bottom-up spatial simulations based on the Future Land Use Simulation (FLUS) model, a cellular-automata and machine-learning hybrid widely used in global land-change studies (Figure 1). FLUS estimates land-type suitability using artificial neural networks informed by a suite of socioeconomic drivers (GDP, population density, proximity to urban centres, road networks) and environmental drivers (temperature, precipitation, topography, soil quality), and then allocates land cover types competitively through probabilistic simulation using Cellular Automata dynamics. The resulting land-cover projections are consistent with CMIP6 Tier-1 and Tier-2 SSP-RCP scenario trajectories and capture spatially explicit transitions at a resolution suitable for ecological modelling, thereby substantially improving upon coarser LUH2 products. These characteristics make the Chen et al. (2022) dataset particularly well-suited for integration into SDMs, enabling OneSTOP to incorporate scenario-consistent, ~1km resolution fine-scale land-cover change at the global level alongside climate projections in assessments of invasive species' potential distributions.

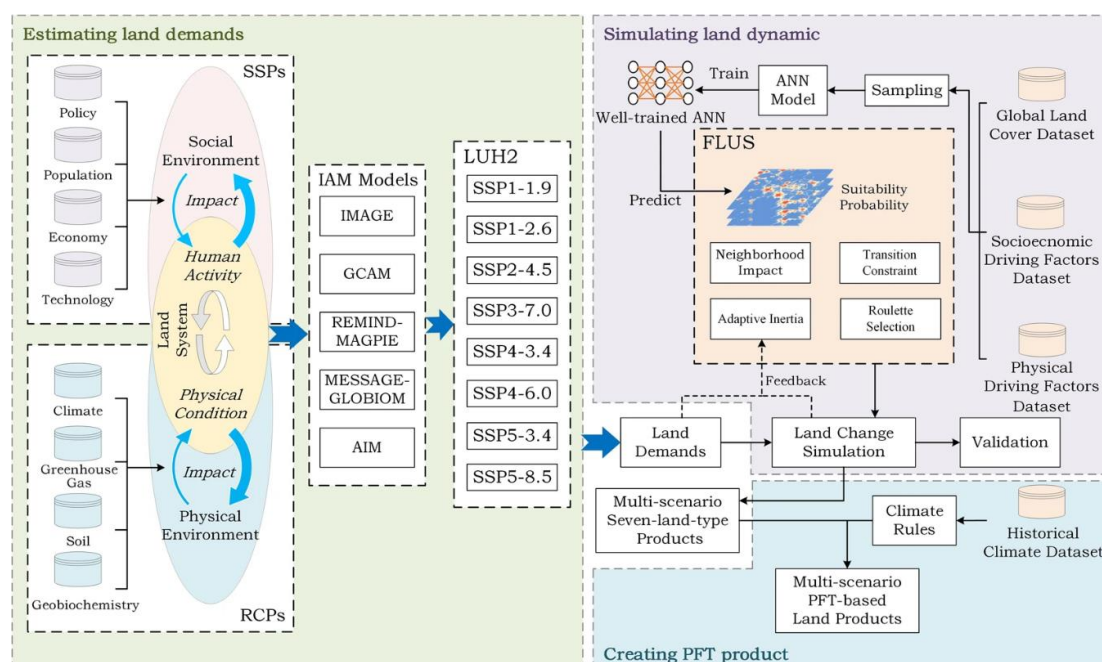


Figure 1 – Process used to generate future global land-cover datasets at 1-km resolution under SSP-RCP scenario conditions (image reproduced from Chen et al. 2022; <https://www.nature.com/articles/s41597-022-01208-6>; CC BY 4.0).





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To integrate land cover data into the modelling workflow, the original dataset's detailed Plant Functional Type classes were simplified via reclassification. The original scheme, while ecologically detailed, included numerous subclasses (e.g., C3/C4 grasslands, macro-climatic forest types) that would unnecessarily increase model complexity and computational demand for projections for Europe. To streamline model development and ensure compatibility across historical and scenario-based projections, a harmonised categorical scheme was developed by aggregating related PFT classes into a reduced set of broad land-cover categories (e.g., forests, shrublands, grasslands, croplands, urban). This reclassification (Table 6) preserved the ecological categories potentially relevant to IAS establishment in Europe while enabling stable and reproducible inclusion of land-cover predictors in the wiSDM-based modelling pipeline.

Table 6 – Proposed crosswalk reclassification scheme of the original PFT/ land cover classes of Chen et al. (2022).

Original code	Original class	New code	New class
1	Water	1	Water
2	Broadleaf evergreen tree, tropical	2	Broadleaf evergreen forest
3	Broadleaf evergreen tree, temperate		
4	Broadleaf deciduous tree, tropical		
5	Broadleaf deciduous tree, temperate	3	Broadleaf deciduous forest
6	Broadleaf deciduous tree, boreal		
7	Needleleaf evergreen tree, temperate	4	Needleleaf evergreen forest
8	Needleleaf evergreen tree, boreal		
9	Needleleaf deciduous tree	5	Needleleaf deciduous forest
10	Broadleaf evergreen shrub, temperate	6	Broadleaf evergreen shrubland
11	Broadleaf deciduous shrub, temperate	7	Broadleaf deciduous shrubland
12	Broadleaf deciduous shrub, boreal		
13	C3 grass, arctic	8	Grasslands
14	C3 grass		
15	C4 grass		
16	Mixed C3/C4 grass		
17	Barren	9	Barren
18	Cropland	10	Cropland
19	Urban	11	Urban
20	Permanent snow and ice	12	Permanent snow and ice



D5.1 Predicted maps of Invasive Alien Species

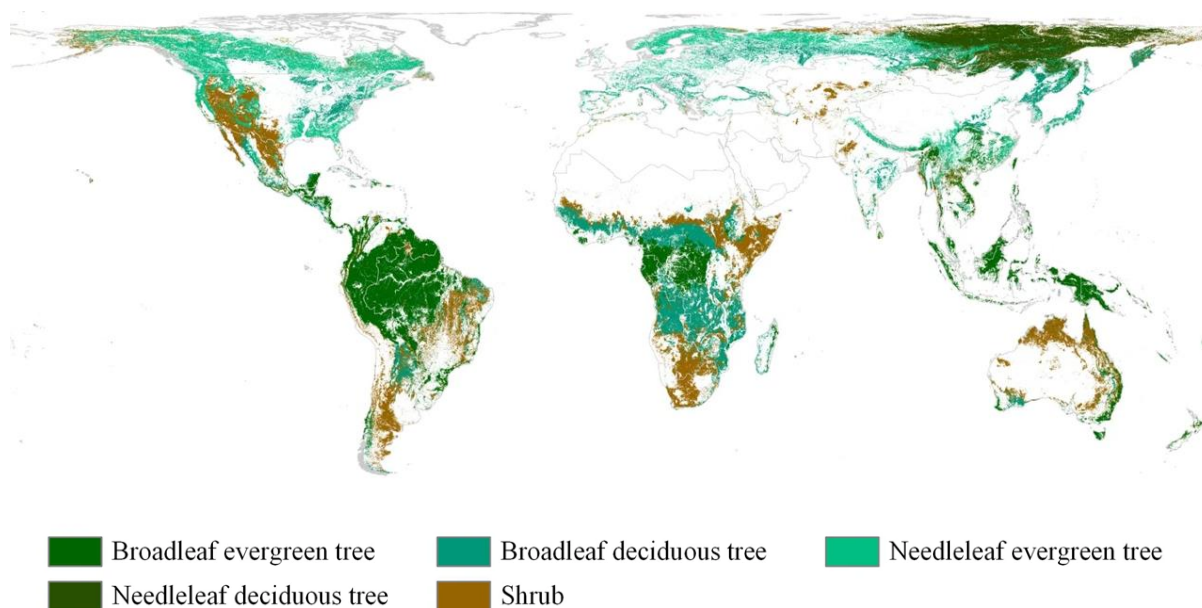


Figure 2 – Distribution of forest-type PFTs in ESA-CCI in 2015 (image reproduced from Chen et al. 2022; <https://www.nature.com/articles/s41597-022-01208-6>; CC BY 4.0).

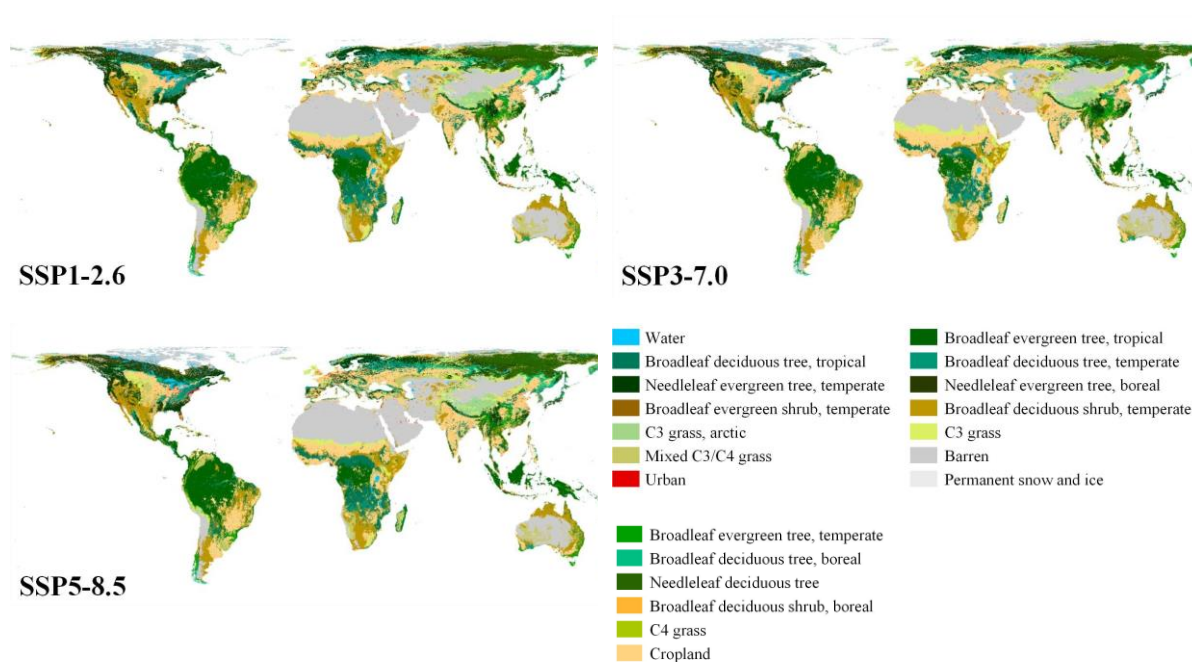


Figure 3 – Future scenarios for 2100 and the three SSP/RCP scenarios used in modelling (image reproduced from Chen et al. 2022; <https://www.nature.com/articles/s41597-022-01208-6>; CC BY 4.0).

In a subsequent step, the land-cover dataset was transformed from categorical classes into measures of local landscape composition, using a moving-window approach. This was done





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to better capture the proportional availability of different habitat types surrounding each grid cell, rather than assigning a single dominant class. Such compositional metrics are more ecologically meaningful across a broad range of taxa, as they reflect habitat availability within the immediate landscape context while avoiding assumptions about species-specific ecological responses to spatial configuration. A focal moving window of 3×3 cells (corresponding to a 3 km × 3 km neighbourhood at the native 1-km resolution) was applied across the European land-cover rasters of Chen et al. (2022). Within each window, the proportion of each land-cover class was calculated as the percentage of valid cells belonging to that class relative to the total number of valid cells in the window. Cells with missing data were excluded from the denominator to avoid bias in edge and masked regions.

The resulting output consists of multi-band raster layers, where each band represents the percentage cover of a single land-cover class within the local neighbourhood. Per cent values were stored as scaled integers (per cent × 100) to preserve precision while maintaining efficient storage. A consistent NoData value (–32768) was used across all outputs.

Eleven aggregated land-cover classes (out of the 12 resulting from the legend crosswalk) were retained for species distribution modelling, eliminating category “Permanent snow and ice” due to the very high number of zeros, which would inflate issues of near-zero variance predictors. These categories represent the major land cover/PFT/habitat types (Table 6) and were subsequently used as predictors in the European-scale habitat models.

A detailed description and hypothesised relationship between each land-cover class and its predictive effect are displayed in Table 7, which also establishes associations with potential introduction pathways, ecological dynamics, and abiotic conditions.

Warning note

A few insular territories (e.g., Isle of Man, Guernsey, Jersey) and one insular state (Malta) are not included in the Chen et al. (2022) dataset for both baseline conditions and future scenarios. Consequently, these areas could not be included in the models or the resulting distribution projections. The WP5 Team reached out to the authors for clarification and a possible solution but has not received a response as of this report.

Table 7 – Land cover predictor variables used in SDM development and their tentative ecological relevance and potential interpretation in SDM development/interpretation.

Land-cover predictor	Ecological interpretation and relevance (as % cover in 3 × 3 km moving window)
Water	Continuous estimate of the local proportion of water-covered surfaces. In IAS models, this can represent proximity to aquatic habitats, riparian zones, wetlands, reservoirs, coastal margins or dispersal corridors/pathways. Because water is treated as static in the source dataset, it should be interpreted mainly as baseline aquatic landscape context, not as future hydrological change.
Broadleaf evergreen forest	Represents the percentage of the local landscape occupied by evergreen broadleaf forest. Higher values indicate persistent woody canopy cover, relatively stable year-round structural habitat, and, depending on the region, warmer or more humid forest conditions that may favour shade-tolerant, forest-associated, or edge-colonising invasive species.
Broadleaf deciduous forest	Represents the local proportion of deciduous broadleaf forest. As a continuous neighbourhood variable, it captures woodland availability and canopy-related structure, forest-edge density and potential understorey habitats. It may be relevant for invasive species associated with



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	woodlands of distinct ecoregions, land use/management types, forest margins or disturbed deciduous forest landscapes.
Needleleaf evergreen forest	Represents the proportion of evergreen coniferous forest in the local 3 × 3 km neighbourhood. Higher values may indicate cooler, shaded, acidic or plantation-influenced environments, and may help identify species responses to conifer-dominated forest matrices, forest continuity or management-associated disturbance.
Needleleaf deciduous forest	Represents the percentage cover of deciduous coniferous forest in the surrounding landscape. This class is likely spatially limited in Europe but can help distinguish specific cold-climate or high-latitude forest conditions in which seasonal needleleaf canopy dynamics affect light availability, microclimate, and ecosystem structure and habitat availability.
Broadleaf evergreen shrubland	Represents the local proportion of evergreen shrub-dominated vegetation. In ecological models, higher values may indicate Mediterranean-type shrublands, semi-natural woody vegetation, dryland vegetation, or fire- or disturbance-associated landscapes. As a percentage-cover predictor, it captures the degree of local shrubland dominance rather than the presence of a single categorical class.
Broadleaf deciduous shrubland	Represents the percentage of deciduous shrubland within the local neighbourhood. Higher values may reflect regenerating vegetation, transitional habitats, forest edges, scrub encroachment, semi-natural shrub mosaics or disturbed landscapes. This can be important for invasive species adapted to open-canopy woody vegetation or early-successional habitats.
Grasslands	Represents the local proportion of herbaceous open vegetation. In invasive species models, this can capture open, light-rich habitat availability, grazing or mowing-associated disturbance, low canopy competition and potential suitability for herbaceous invaders. Because the predictor is continuous, it reflects a grassland-dominated landscape gradient rather than a binary grassland/non-grassland classification.
Barren	Represents the local proportion of sparsely vegetated or unvegetated land. Higher values may indicate exposed soils, rock, dunes, drylands or disturbed substrates. For invasive species, this predictor may capture low-competition environments, abiotic stress, disturbance exposure (e.g., wildfires in sparsely vegetated areas) or, potentially, early-colonisation opportunities.
Cropland	Represents the percentage of agricultural land within the 3×3 km window. Higher values may indicate frequent disturbance, nutrient enrichment, irrigation, soil movement, machinery use, crop transport and other anthropogenic introduction pathways. It is therefore both a habitat-composition variable and a proxy for propagule pressure or human-mediated dispersal for many invasive species.
Urban	Represents the local proportion of built-up or artificial surfaces and associated pathways located in these areas. It encompasses highly heterogeneous densities. For invasive species models, urban cover can serve as a proxy for human population density, transport infrastructure, ornamental planting (e.g., gardens, parks), disturbed habitats (e.g., peri-urban sites, industrial/post-industrial areas), microclimatic/heat island effects, and high propagule pressure. As a moving-window percentage, it captures the intensity of urban influence around each grid cell rather than simply whether the focal cell is urban.

Descriptive analysis of land cover data across periods, scenarios and EU27 countries

The land-cover projections were examined descriptively before modelling, since baseline conditions strongly influence model outcomes and the magnitude, direction, and scenario dependence of projected habitat change condition the interpretation of combined climate–habitat projections. This assessment also establishes whether the future climatic and land-cover scenarios are consistent across pathways, a prerequisite for understanding how projected shifts in favourability relate to environmental drivers. To achieve this, land-cover projections were summarised from 1-km cell-frequency data for each country, land-cover class, period and SSP/RCP scenario. Missing class-country combinations were completed with zero values (coalesced), and class frequencies were converted to proportions of national area to ensure that land-cover composition summed consistently to 100%. Change was quantified as the difference from the 2015 baseline in both percentage points and absolute area (km²). Overall land-cover reallocation was measured using a turnover index, defined as the proportion of national territory redistributed among classes. The results were visualised through country rankings, scenario ranges, class-level heatmaps, gain vs loss profiles, and





D5.1 Predicted maps of Invasive Alien Species

area-weighted EU aggregates, thereby supporting comparisons among countries, future periods, and scenarios.

2.6. Modelling Framework

2.6.1. wiSDM 2.0 general workflow/pipeline

All modelling outputs were produced using the wiSDM v2.0 (Figure 4) semi-automated multi-purpose modelling pipeline/workflow, available from the TRIAS risk modelling and mapping repository: <https://github.com/trias-project/risk-modelling-and-mapping>. For this work, we used a slightly modified implementation based on CIBIO's wiSDM v2.1, available at <https://github.com/OneSTOP-CIBIO/risk-modelling-and-mapping> (DOI: 10.5281/zenodo.21880434; URL: <https://zenodo.org/records/21880434>; see also Annex 7.3.1–*Alterations to wiSDM 2.0 workflow in the OneSTOP fork*). This implementation preserves the original modelling pipeline while incorporating improvements and a new framework for parallelising model runs and monitoring their execution.

In summary, wiSDM v2.0 implements an ensemble modelling approach using ten algorithms: generalised linear models (GLM), generalised additive models GAM, environmental envelopes (BIOCLIM), boosted regression trees BRT, random forest, polynomial GLM, multivariate adaptive regression splines (MARS), maximum entropy (MaxEnt), flexible discriminant analysis (FDA) and classification and regression trees (CART). It also combines these ensemble models trained at two hierarchical levels: first, a global climate model, and second, a continental European habitat model based on land-cover data. The resulting climate and habitat ensembles are integrated using the harmonic mean to produce a final estimate of environmental favourability under current and future scenarios. The first modelling component is a global, climate-only model fitted at 1-km resolution using CHELSA v2.1 climate layers and global presence data. This model estimates the climatic favourability of each species across the global calibration area. Such a global-scale procedure is critical to avoid niche truncation when projecting future scenarios. The second modelling component is a continental European habitat model fitted at 1-km resolution using land-cover predictors and European presence data. This model estimates habitat, or perhaps better framed, land-cover-based species favourability within Europe. Throughout this report, the terms “habitat” and “land cover” are used interchangeably for brevity and to remain consistent with the wiSDM v2.0 terminology, where the term “habitat” is used. Although habitat and land cover are ecologically distinct concepts, land-cover information represents the best available spatial proxy for habitat at the spatial scale and resolution considered here.



D5.1 Predicted maps of Invasive Alien Species

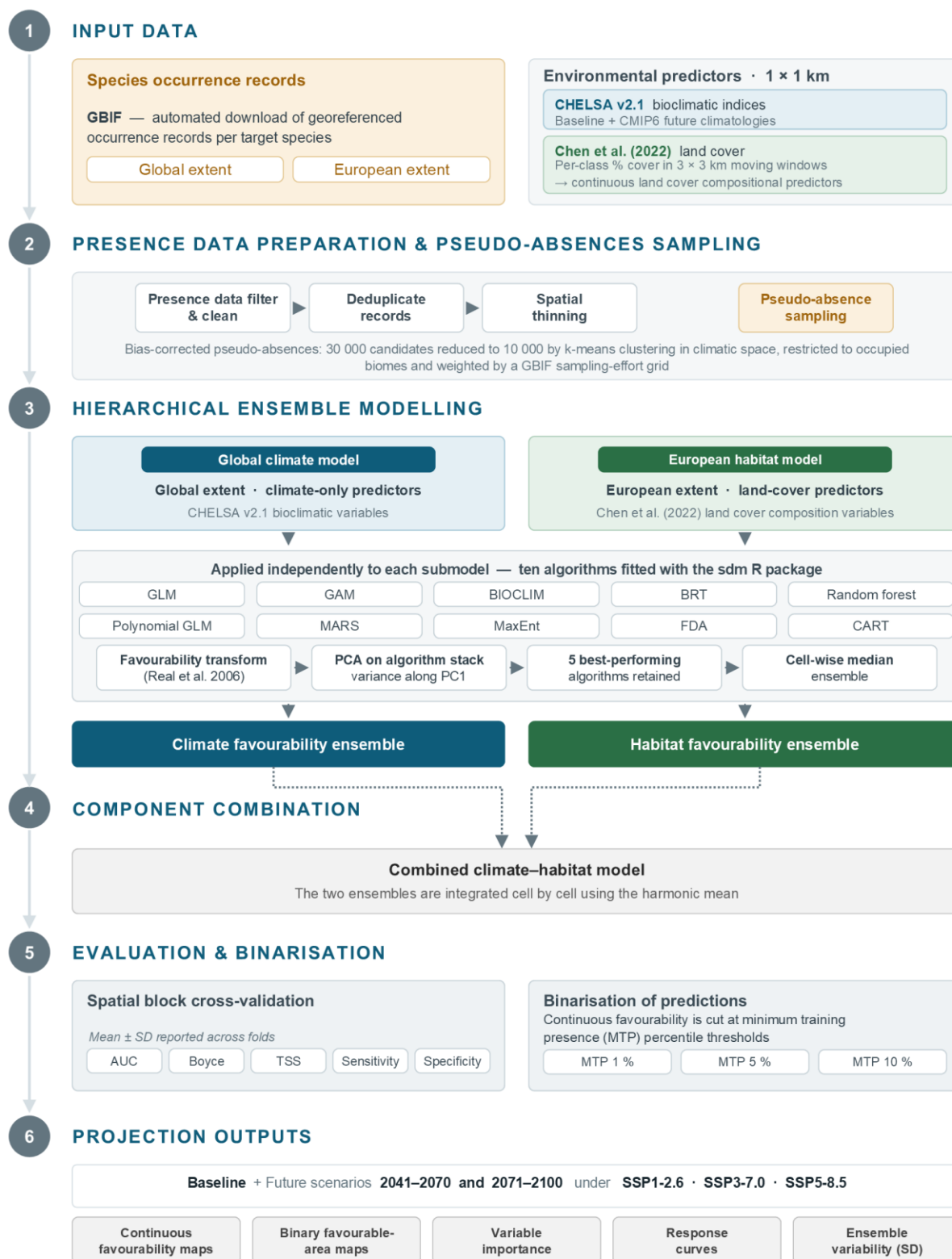


Figure 4 – wiSDM-2.0 semi-automated hierarchical ensemble modelling workflow.





D5.1 Predicted maps of Invasive Alien Species

Climate and habitat ensembles were produced for current conditions and for future periods, including 2041–2070 and 2071–2100, under SSP1-2.6, SSP3-7.0, and SSP5-8.5. For each future scenario, the combined favourability maps were obtained by pairing the projected climate favourability with the corresponding projected habitat favourability, and then integrating both components using the harmonic mean. The full list of file outputs from wiSDM-2.0 and the naming conventions are detailed in Annex 7.3.2–*Description of wiSDM 2.0* project folders.

2.6.2. Pseudo-absence sampling and sampling bias

Biodiversity databases such as GBIF are overwhelmingly presence-only, since occurrence records document where a species was observed but not where it was sought and not found. Reliable absences are therefore scarce, constraining SDM algorithms that require a binary presence–absence response. To overcome this limitation, pseudo-absences are used. These are modeller-generated locations lacking species records (e.g., drawn by random sampling within the study area) that are treated as absences, enabling SDM algorithms that require a binary presence–absence response to contrast occupied sites with the range of conditions available in the study region.

Pseudo-absences were sampled from climatically valid cells within biomes containing at least one retained occurrence. Cells containing any known occurrence, including records removed during thinning, were excluded. Eligible cells were weighted using taxon-specific sampling-effort grids from (Delva et al., 2025), derived from GBIF records collected between 1974 and 2024 and aggregated at 1° resolution. Grid values were log-transformed and rescaled from 1 to 20, making well-sampled cells up to 20 times more likely to be selected. When no suitable bias grid was available, as for flatworms, all cells were weighted equally.

Using a fixed seed, wiSDM drew 30,000 candidate pseudo-absences, generally from an approximately 5-km grid, and reduced these to a final set of 10,000. Under the k-means method, candidates were clustered in climatic space, and one was selected from each cluster, with any shortfall filled randomly. This approach accounts for geographic variation in recording effort while representing the range of climatic conditions within the occupied biomes.

The number of pseudo-absences was fixed rather than matched to the number of presences. Bias-grid values affected only where pseudo-absences were selected; they were not used as observation weights during model fitting.

2.6.3. Favourability transformation and multi-algorithm model combination

The wiSDM v2.0 workflow uses an ensemble approach to produce outputs, which is guided by a Principal Component Analysis (PCA) of the individual model outputs. For each modelling component, namely the global climate model and the European habitat model, ten statistical or machine-learning algorithms were fitted using the `sdm` R package. Each algorithm produced a continuous prediction surface. Based on these raw model predictions, expressed either as occurrence probability or habitat suitability, they were post-transformed into environmental favourability using the function proposed by Real et al. (2006). This means that predicted occurrence probability/suitability is converted into environmental favourability to separate the fitted response to predictors from sample prevalence (Acevedo & Real, 2012;





D5.1 Predicted maps of Invasive Alien Species

Real et al., 2006). Raw probabilities reflect both local predictor effects and the overall balance between presences and absences; hence, comparable environmental responses can yield lower probabilities for rare species and higher probabilities for widespread species (Acevedo & Real, 2012; Real et al., 2006). For a cell with predicted probability (P), favourability (F) will be calculated as:

$$F = \frac{P/(1 - P)}{n_1/n_0 + P/(1 - P)}, 0 \leq F \leq 1$$

where (n_1) and (n_0) are the numbers of presences and absences in the analysed dataset (Acevedo & Real, 2012; Real et al., 2006). The favourability transformation can be applied to calibrated probability outputs from logistic regression or other modelling approaches (Acevedo & Real, 2012). In other words, this transformation adjusts predictions for species prevalence in the calibration/training data, specifically the relative number of presences and absences. As a result, the final favourability values are less dependent on sample prevalence and are more directly comparable among species, datasets, and modelling components. Ecologically, F measures whether local conditions increase or decrease occurrence odds relative to the prevalence expected across the study domain, rather than estimating occurrence probability itself. The neutral value, $F=0.5$ occurs when P equals sample prevalence; larger values towards one denote favourable conditions and smaller values towards zero denote detrimental conditions (Acevedo & Real, 2012; Real et al., 2006). When presences and absences are balanced, $F=P$; for rarer presences, $F>P$, and the reverse when presences predominate (Real et al., 2006). The calculation of favourability therefore changes the question from "*how probable is occurrence here?*" to "*how strongly do conditions favour occurrence relative to the sampled baseline?*" (Acevedo & Real, 2012; Real et al., 2006). The common prevalence-referenced scale permits comparison or combination of surfaces for species with different prevalence values (Acevedo & Real, 2012; Real et al., 2006). Also, it is key to note that favourability is not an alternative occupancy probability and remains conditional on study design. As such, changing the spatial extent or background may change prevalence and thus (F), so comparisons should use a consistent domain and sampling frame (Acevedo & Real, 2012).

After transformation, the stack of algorithm-specific favourability predictions is summarised using principal components analysis (PCA). Algorithms were ranked according to the spatial variance of their predictions for each grid cell, projected onto the first principal component (PC1), which captures the dominant spatial signal among models. The five algorithms with the highest variance along PC1 were retained, i.e. the ensemble captured a range of variation from the models, and the ensemble prediction was calculated as the pixel-wise median of these five selected algorithms. For each species and each presence-data configuration, the workflow therefore produced climate-only, habitat-only, and combined climate-habitat favourability maps at 1-km resolution for current conditions and for the selected future periods and scenarios.

2.6.4. Model evaluation and spatial cross-validation

The predictive performance of models was evaluated using spatial block cross-validation. The default wiSDM v2.0 procedure applies five-fold spatial block cross-validation, dividing the modelling area into spatially balanced folds. Evaluation metrics were computed for the Climate/Global model, the Climate/Europe component where relevant, the Habitat/Europe





D5.1 Predicted maps of Invasive Alien Species

model, and the final Combined Climate-Habitat/Europe model. For each model, performance was summarised using the mean and standard deviation across cross-validation folds. The following metrics were calculated: area under the receiver operating characteristic curve, AUC; continuous Boyce index; true skill statistic, TSS; sensitivity; and specificity.

wiSDM v2.0 procedure assigns spatial blocks randomly to training and testing folds over 200 iterations using a distance threshold of 100 km. For range-restricted species, this procedure can generate folds with no presence records, which would make model training or evaluation invalid. Therefore, these distance criteria were later adapted, with softer incremental steps for each species according to the number and spatial distribution of presences, ensuring that all folds contained presence records. Another adaptation concerned algorithm selection during validation. In the standard wiSDM v2.0 workflow, model validation uses the five top-performing algorithms selected during the full model calibration through the PCA-based assessment of variance along PC1. However, because cross-validation models are trained on subsets of the full dataset, some algorithms can fail for particular folds, especially for spatially clustered or range-restricted species. To address this, only successfully fitted algorithms were retained for model testing and validation within each fold. Where spatial cross-validation was applied, models were trained on k minus one spatial blocks and evaluated on the held-out block. This process was repeated until each block had been used for testing, and performance was then averaged across folds. Evaluation metrics were computed separately for the global climate model, the European habitat model, and the final combined climate-habitat model. In very specific cases (usually related to low sample sizes or uneven/irregular distribution of sampling records across spatial blocks), the evaluation stage used (as a last fallback) non-spatial k -fold cross-validation with the same k value.

2.6.5. Model output binarisation into favourable and unfavourable areas

Continuous model projections were converted into binary maps of favourable and unfavourable areas using training-presence percentile thresholds of 1%, 5%, and 10%. For each threshold, the favourability values predicted at the training-presence localities were ranked, and the corresponding percentile was selected as the cut-off. Grid cells with favourability values equal to or above the selected cut-off were classified as favourable, while grid cells below the cut-off were classified as unfavourable.

This approach permits the omission of the 1%, 5%, or 10% of training occurrences with the lowest predicted favourability. It therefore reduces sensitivity to potentially erroneous records, spatial inaccuracies, or observations located in marginal environments. Higher percentile thresholds produce progressively more restrictive estimates of favourable area. Strictly speaking, the minimum training-presence threshold corresponds to 0% omission, whereas the thresholds used here represent percentile-based extensions of that rule.





2.6.6. Additional outputs exported by the wiSDM 2.0 modelling pipeline

Model variability across algorithms

To quantify disagreement among algorithms, wiSDM applied an unstandardised PCA to their favourability predictions, using up to 100,000 raster cells. The five algorithms contributing most strongly to the first principal component were retained for the ensemble. Ensemble favourability was calculated as the cell-wise median of their predictions, while variability was measured as the population standard deviation across the available predictions. This metric indicates relative disagreement among algorithms; it does not represent confidence intervals, prediction error or uncertainty around the ensemble median.

Variable-importance measures

Variable importance is calculated separately for each of the five selected algorithms using ``sdm::getVarImp()`` (Naimi & Araújo, 2016). Because models are fitted without a resampling or independent-test specification, the implemented default mode of calculating predictor importance uses training records. For each model and predictor, ``sdm`` permutes that predictor among records five times, leaving the other predictors unchanged (usually at their mean value). Larger values (towards one) indicate that permutation changes predictions more strongly or causes a larger loss of AUC. In turn, near-zero values indicate little predictive importance in SDM training. These model- and dataset-specific measures quantify predictive dependence, not effect direction, causation, or independent contribution.

Response curves

Response curves are generated for every successful model in the five selected algorithms using ``sdm::getResponseCurve()`` (Naimi & Araújo, 2016). For each continuous predictor, the function creates 100 equally spaced values from its training-data minimum to maximum. It varies that predictor while holding other continuous predictors at their mean among training presences and categorical predictors at their most frequent presence class. The fitted algorithm is evaluated for each combination. The response is therefore the original ``sdm`` prediction (generally a probability or algorithm-specific suitability score), not the prevalence-adjusted favourability used for ensemble mapping. These plots, devised by the `sdm` package, are one-at-a-time response profiles, or partial-dependence-type curves. These differ from a classical partial dependence plot, which averages over the empirical distribution of remaining predictors. wiSDM instead fixes them at presence-based reference values. The curves show the modelled functional form for species-environment relationships, enabling checking/comparison of nonlinearities, thresholds and algorithm disagreement. They are not causal, and edge-of-range patterns require caution because constructed combinations may be environmentally rare.

2.7. Future climatic scenarios based on CMIP6-RCP/SSP

Projecting future environmental favourability and potential species distributions under contrasting environmental-change pathways is a core objective of OneSTOP Task 5.1, as it enables assessment of how invasion risk may shift spatially under plausible future conditions





D5.1 Predicted maps of Invasive Alien Species

and provides an evidence base for anticipatory prioritisation and management. To achieve this, species distribution models trained under baseline environmental conditions were then projected onto a harmonised set of scenario-based future environmental layers for the OneSTOP European modelling extent. Climate predictors were based on the CHELSA v2.1 dataset, which provides high-resolution, terrain-informed climate layers at approximately 30 arc-second (kilometre-scale) resolution. CHELSA v2.1 applies mechanistic downscaling procedures to future climatic layers that account for topographic effects on temperature and precipitation, including lapse-rate corrections, orographic uplift, leeward drying and valley effects, making the dataset particularly suitable for spatial ecological modelling in topographically heterogeneous regions such as Europe.

Future projections from CHELSA 2.1 are available for two 30-year periods, 2041–2070 and 2071–2100, using the CMIP6 scenario combinations currently available: SSP1-2.6, SSP3-7.0 and SSP5-8.5. CHELSA provides these future climatologies for five CMIP6 Global Circulation Models (GCMs) or Earth System Models: GFDL-ESM4, IPSL-CM6A-LR, MPI-ESM1-2-HR, MRI-ESM2-0 and UKESM1-0-LL (see more info in Table 5) downscaled to 30 arc-second resolution using a delta-change approach. The SSP-RCP scenarios used here for SDM projections should be interpreted as combined socioeconomic-climate forcing scenarios rather than predictions. In the CMIP6 Scenario MIP framework, each scenario combines a Shared Socioeconomic Pathway (SSP), describing alternative assumptions about population, economic development, technology, land use, governance and environmental policy, with an approximate end-century radiative forcing level (i.e., RCP). The forcing numbers are expressed in the scenario names and include the following values: 2.6, 7.0 and 8.5 W.m⁻². These values are then used as nominal identifiers and should not be interpreted as exact realised forcing values in every model simulation.

Regarding the land cover scenario projections, Chen et al. (2022) dataset simulates global land-use and land-cover change from 2015 to 2100 at 5-year steps under the same CMIP6 SSP–RCP socio-climatic scenarios. Because these data are organised in 5-year steps, we used 2055 to represent the mid-century future projection period (2041-2070) and 2085 to represent the late-century period (2071-2100).

Table 8 – General description of baseline/historical conditions as well as SSP/RCP CMIP-6 future scenarios for obtaining model projections for selected species.

Scenario name/code	Main description
Historical / reference baseline	Baseline projections describe areas climatically and environmentally suitable under the reference conditions used to train or calibrate the species models. They provide the comparator for assessing future gains, losses or shifts in potential suitability.
SSP1–2.6	Used as a low-emissions, sustainability-oriented scenario. It represents a future with relatively strong mitigation, lower resource intensity and reduced end-century climate forcing. In the context of invasive species projections, this scenario provides a conservative estimate of future climate-driven changes in potential suitability.
SSP3–7.0	Considered as a high-emissions, regional-fragmentation scenario. It represents a future with weak international cooperation, high challenges to mitigation and adaptation, substantial land-use pressure and strong end-century climate forcing. For invasive species, it provides a stress-test scenario for climate-driven expansion, contraction or redistribution of suitable areas under great environmental change.





SSP5–8.5

Used as a very high-emissions, fossil-fuelled development scenario. It represents a future with rapid economic growth, high energy demand and continued fossil-fuel dependence, producing very strong end-century radiative forcing. For invasive species projections, it provides an upper-end estimate of climate-driven change in potential environmental suitability.

For each species, projections were produced at approximately 1 km resolution across the European extent adopted by OneSTOP. The final outputs include binary suitability maps for all species across seven temporal/scenario combinations: the historical or reference baseline, plus SSP1-2.6, SSP3-7.0 and SSP5-8.5 for 2041–2070 and 2071–2100. These maps represent potential environmental favourability driven by the predictors.





3. Results and discussion

3.1. Introduction pathways

3.1.1. Analysis of EASIN-CBD introduction pathways

KEY HIGHLIGHTS

- Broad pathway coverage: the analysis identified 426 species–pathway records for 118 of the 120 OneSTOP target species (median = 3 pathways per species), showcasing that species introduction processes tend to be by multiple pathways.
- Dominance of escape-related pathways: escape from confinement was the most prevalent pathway, accounting for ~38% of all records and affecting ~72% of species, followed by transport–contaminant and release in nature categories.
- Key underlying mechanisms: ornamental use, horticulture, the pet and aquarium trade, and the transport of habitat or plant material emerged as some of the major mechanisms contributing to introductions across the Task 5.1 120 species pool.
- Strong taxonomic differentiation: escape and intentional release predominated among vascular plants and vertebrates, whereas contaminant and stowaway transport pathways were particularly important for invertebrates.
- Effective prevention will often require coordinated measures addressing several introduction mechanisms simultaneously.
- Two main pathway clusters: pathway co-occurrence patterns revealed a “cultivation-and-release” cluster and an “accidental-transport” cluster, providing an operational basis for designing more targeted, sector- and taxon-specific biosecurity responses.
- Temporal patterns and evidence gaps: no statistically robust change in the overall pathway composition was detected, but the post-1950 species indicate pronounced increases in transport–contaminant pathways and declines in escape from confinement. These trends should be interpreted cautiously because of the limited number of species in recent periods, while the significant increase in “Unknown” attributions and the incomplete documentation of uncertainty further emphasise the need to strengthen the evidence base for pathway assessment and prioritisation.

This subsection presents an assessment of introduction pathways for the OneSTOP’s (Task 5.1) 120 species pool under the CBD pathway framework (CBD, 2014; Harrower et al., 2018; Hulme et al., 2008) retrieved from EASIN. The results presented below examine both the frequency and species coverage of the principal CBD pathway categories. The main unit of





D5.1 Predicted maps of Invasive Alien Species

analysis is the species-pathway pair, with species typically having more than one pathway listed. In total, 426 deduplicated pathway records across 118 species were retrieved (two of the 120 species, *Apis florea* and *Fagus orientalis*, have no EASIN pathway record). Collectively, the 120 target species span 42 of the 45 pathway subcategories of the CBD classification scheme (93 %), leaving only research and ex-situ breeding, other contaminants, and tunnels and land bridges unrepresented.

Pathway frequencies (Figure 5) are given against two denominators: (i) % of records (weights a species by how many pathways it uses) and (ii) % of species (share of species using a pathway at least once; these do not sum to 100%). Results show that the “Escape from confinement” category dominates both denominators, with 38.0% of records and 72.0% of species, meaning that nearly three-quarters of the target species have at some point escaped cultivation or captivity (or any other form of containment). This category is followed by the “Transport–contaminant” (20.9% of records and 44.1% of species) and “Release in nature” (16.4%; 43.2%), then “Transport–stowaway” (13.6%; 28.8%), “Unaided” (6.3%; 19.5%), and finally the “Corridor” (1.2%; 4.2%). Results also show that the unattributed “Unknown” (3.5% / 12.7%) is present. Around 3.5% / 12.7% of the species are unattributed and therefore labelled as “Unknown”. The gap between the two denominators itself is informative. For instance, “Release in nature” reaches 43% of species while accounting for only 16% of records, meaning it is a widespread driver but rarely a species' sole pathway. (We note that these data only inform about the presence of the pathway, not its frequency.) For biosecurity, this may help frame intervention priorities, as the ornamental use, horticulture, and pet trade subcategories behind the “escape” main category are the single largest drivers and “escape” together with “release in nature” are the two most species-rich pathways, encompassing most of the target list between them.

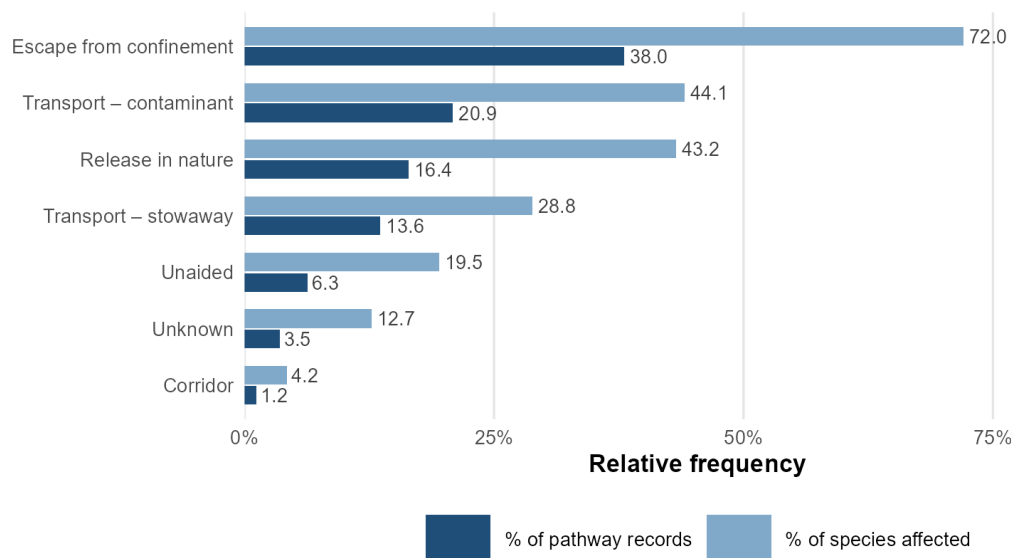


Figure 5 – Introduction pathways of the OneSTOP target species described as the relative frequency of the CBD pathway categories, under two denominators: % of pathway records (i.e., the % based on the total of species-pathway statements which sum up to 100%) and %species affected (i.e., for a given pathway category, what is the share of species affected by it; do not sum up 100%). Records (n = 426) are deduplicated species-pathway statements; species (n = 118) are the target species carrying pathway data. A species may use several pathways, so species percentages do not sum to 100.



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Within-group pathway profiles (Figure 6) show that the headline ranking is a blend of strongly taxon-specific signatures. Escape and release categories are frequent for vascular plants, and together they dominate herbaceous plants, trees, mammals, and birds (potentially linked to a broad set of ornamental, forestry, game, and pet-traded species). The transport pathways mainly seem to dominate accidentally carried species, especially (but not exclusively) in the invertebrates. The transport contaminant category dominates for flatworms, gastropods, and arachnids, while transport stowaway dominates for insects. The heatmap re-reads the same shares across groups and adds the raw record counts, making the volume behind each profile easier to read (Figure 7). Herbaceous plants carry most instances in the escape (n=50) and contaminant (n=30) categories; insects the most stowaway (n=24) and contaminant (n=18); mammals the most escape (n=23) and release (n=21). The heatmap also shows the sparse, low-count cells (single-species groups like Arachnid, Gastropod) that should not be over-interpreted.

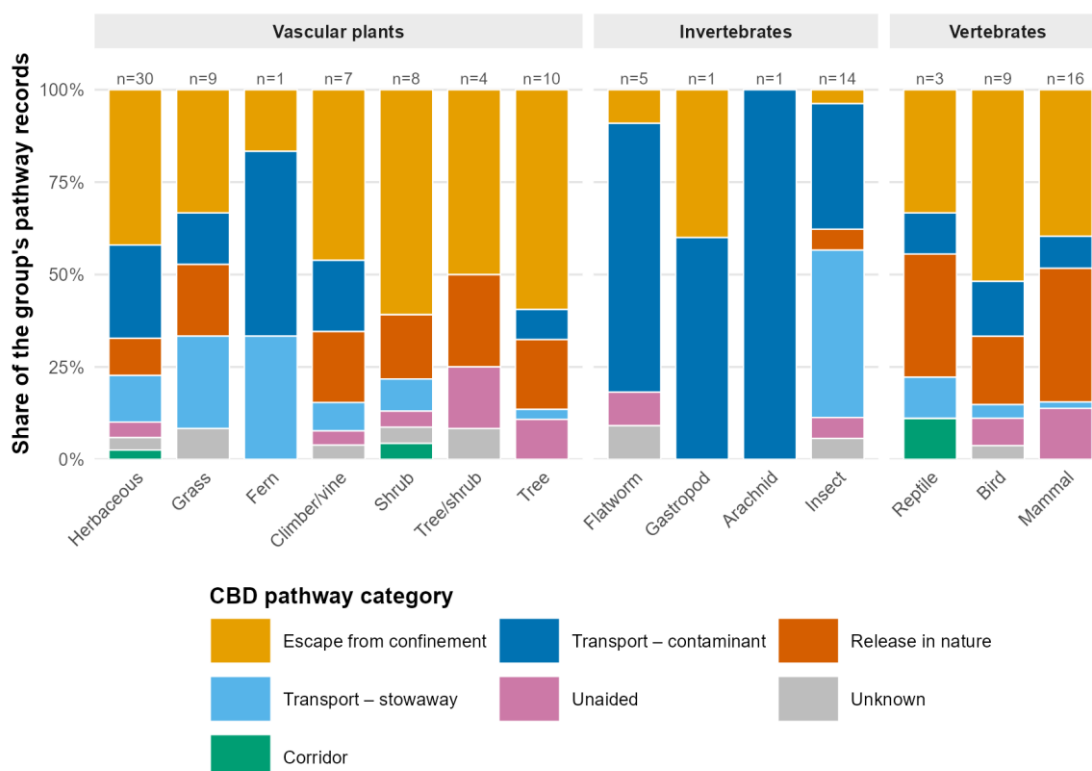


Figure 6 – Pathway composition by taxonomic group as the share of each group's pathway records; groups ordered by growth form and phylogeny, n = species per group. Percentages are within-group: the groups differ roughly 30-fold in species number, so raw counts would merely re-plot the taxonomic composition of the species selection.



D5.1 Predicted maps of Invasive Alien Species

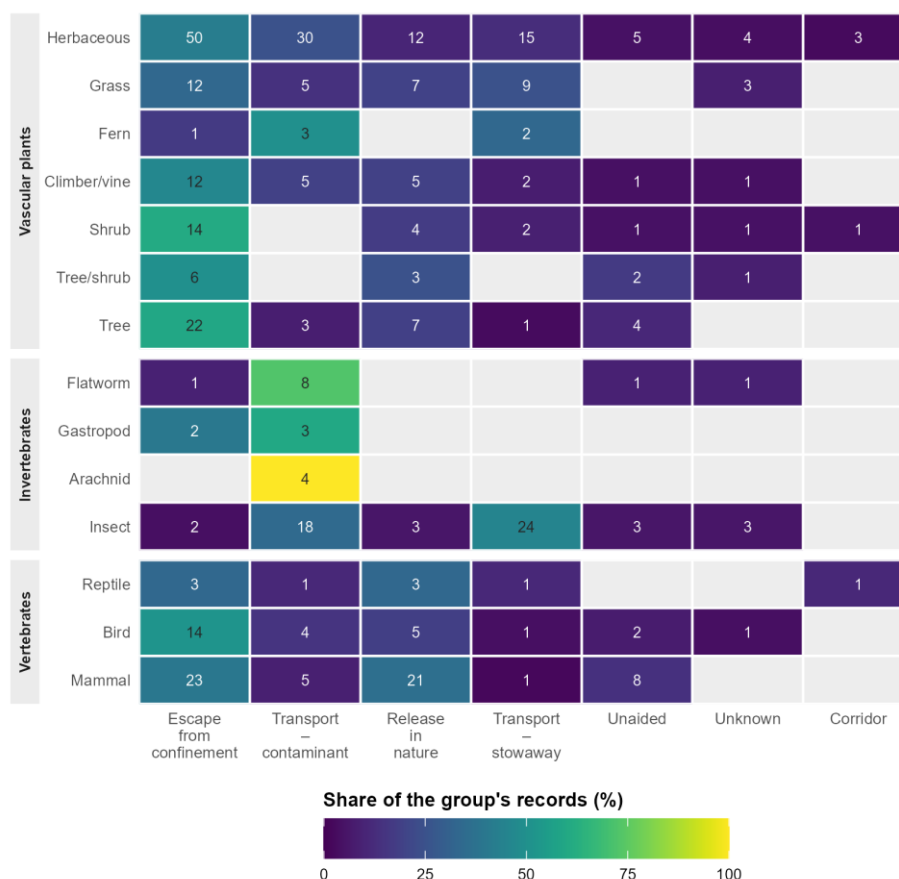


Figure 7 – Pathway use across taxonomic groups. The cell shade colour shows the share of that group's pathway records, while the cell label equals the record count.

Moving from broad pathway categories to the specific CBD subcategories enables the mechanisms underlying the dominant pathways to be identified, thereby potentially increasing the assessment's value for management and intervention planning. Escape from confinement resolves into ornamental use other than horticulture (48), horticulture (38), botanical garden/zoo/aquaria (24) and pet/aquarium species (19), forming a connected cluster of ornamental-and-pet-trade activities that largely drive introduction mechanisms. Transport–contaminant is led by transportation of habitat material (29) and seed/plant contaminants; Release in nature by other intentional release (22), erosion control/dune stabilisation (15) and landscape “improvement” (12); Transport–stowaway by vehicles (13), machinery and ship hitchhikers; Unaided is almost entirely natural dispersal across borders (27). Despite the absence of information on the relative importance and usage frequency of each pathway for each species, these details allow us to convert the pathway rankings into more operational targets, in which the horticultural and ornamental trades are the dominant introduction mechanism for OneSTOP selected species.



D5.1 Predicted maps of Invasive Alien Species

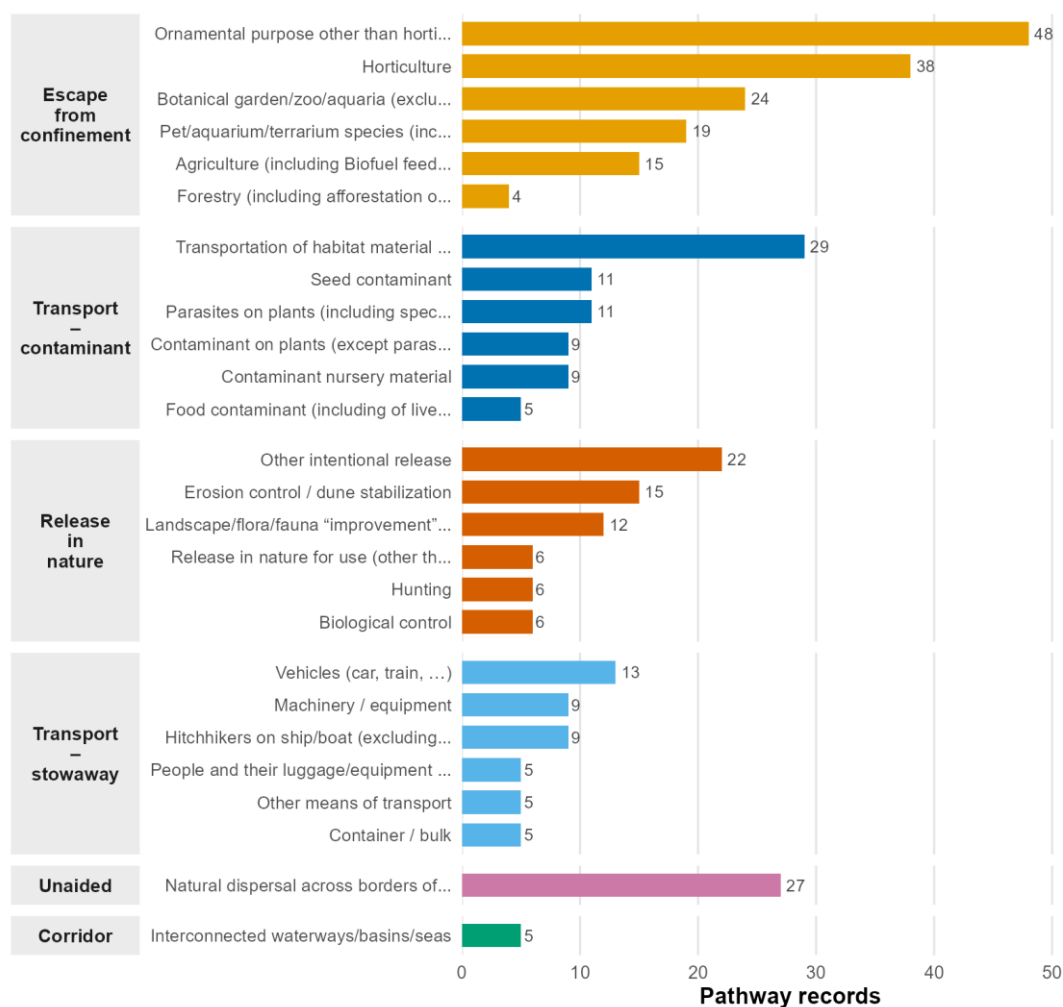


Figure 8 – Dominant pathway details/sub-categories within each CBD category. Up to the 6 commonest CBD pathway sub-categories per category. Labels are truncated at 38 characters. A shared x-axis is used so that detail counts remain comparable between categories.

Most species are not strictly linked to one specific pathway (although escape is the dominant primary driver) and, in fact, have multiple mechanisms (Figure 9). The median number of pathways attributed per species is three (up to a maximum of 13), and only 14% rely on just one. Escape from confinement remains the dominant primary driver (recorded for 72% of species), but it typically operates alongside other mechanisms. Frequency by taxonomic group (see distinct colours across Figure 9 bars) shows that vertebrates cluster at the low end (often 1 to 3), while vascular plants carry the long right tail (>5 pathways despite prevalence).

A key message from these results is that species associated with several independent introduction pathways may be unlikely to be effectively addressed through measures targeting a single pathway. For most species, prevention may therefore require a coordinated, multi-pathway approach, while species linked to numerous pathways may be particularly difficult to manage through interception measures alone.



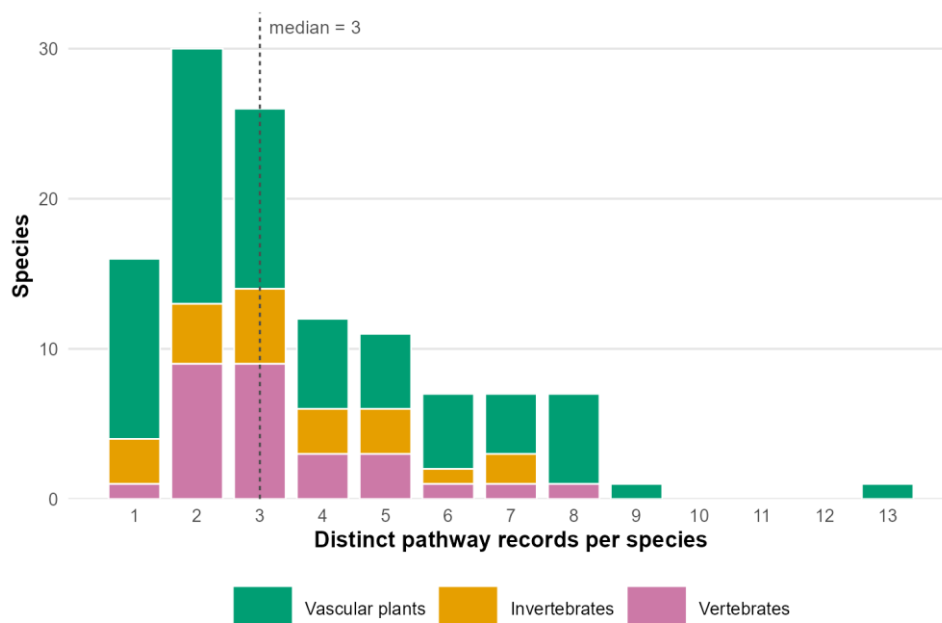


Figure 9 – Histogram depicting the number of distinct pathway records per species, coloured by taxonomic group.

Considering that species typically use multiple introduction pathways (Figure 9), we assessed which pathways co-occur most often (Figure 10). The strongest associations are Escape from confinement × Release in nature (with 45 shared species, highest Jaccard value), suggesting that species brought in for ornamental or game use are both liable to escape cultivation in different settings (from privately owned gardens or horticulture) and to be released or applied on purpose for distinct reasons/purposes. The second most common association is Transport–contaminant × Transport–stowaway (with 24 shared species), which relates the two commodity- and vehicle-borne transport pathways. The practical implication is that the introduction pathways fall into two empirical clusters that can be considered as: (i) a “cultivation-and-release” cluster and an “accidental-transport” cluster. A potential consequence of this association pattern is that prevention measures aimed at one member of a cluster often address a correlated second, whereas the two distinct clusters need specific prevention/containment measures and instruments. Importantly, this grouping emerges directly from the observed co-occurrence patterns among the OneSTOP target species pathway data, rather than being defined a priori on the basis of existing classifications or previous literature.



D5.1 Predicted maps of Invasive Alien Species

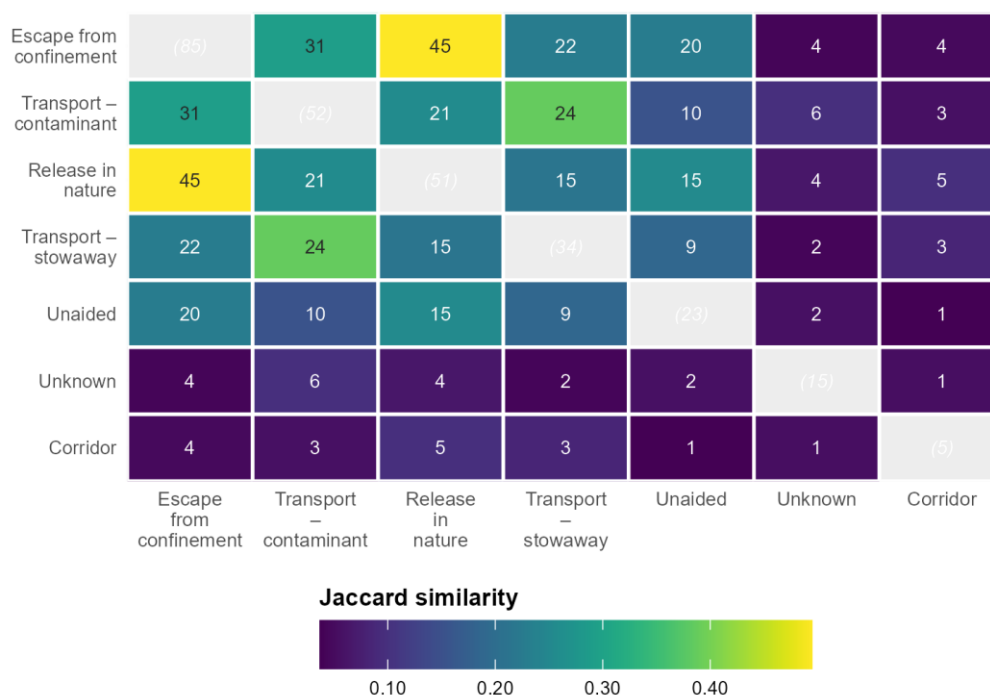


Figure 10 – Two-way contingency table depicting which introduction pathways associate. Species sharing both categories (cell label) shaded by Jaccard similarity. Jaccard (shared species/species using either) corrects for the very unequal prevalence of the categories, so a large raw overlap with a common pathway is not mistaken for a strong association. The values are identical either side of the diagonal.

A temporal assessment of introduction pathways and their frequency through recent history based on EASIN's data allowed further investigation of the recent trends (Figure 11 and Figure 12). Binning species by the period of their first European record shows most falling in the earliest bins (pre-1800, 1800–1899), which is likely a property of the OneSTOP species selection of established, and relatively well-studied invaders. As such, these results must not be read as a decline in introductions since the bars are counts over periods of unequal length and not rates.

Despite some slight differences, results in Figure 11 signal that the relative frequency of pathways through time did not change much. Results from the formal permutation test show that the pathway mix did not change detectably over time since the period × pathway table is not distinguishable from independence ($\chi^2 = 30.1$, permutation $p = 0.054$, Cramér's $V = 0.15$, a small effect, although close to significance at $p < 0.05$). Nonetheless, in Figure 12 we can see growth in the “Unknown” (in grey; the only class that shifted significantly after Benjamini-Hochberg correction; $p = 0.029$). This increase in the “unknown” category suggests that the completeness and quality of pathway attribution are decreasing, with recent arrivals being less completely attributed. These results do not provide an ecological reading of the temporal profile of pathways, but rather indicate the need to improve these attribution processes and to conduct further research and assessments.

Results also show that “Transport–contaminant” clearly rises after 1950–1979, while, in contrast “Escape from confinement” decreases from that period forward. However, neither category's shift survives statistical correction, and the three recent periods hold only 36 species.



D5.1 Predicted maps of Invasive Alien Species

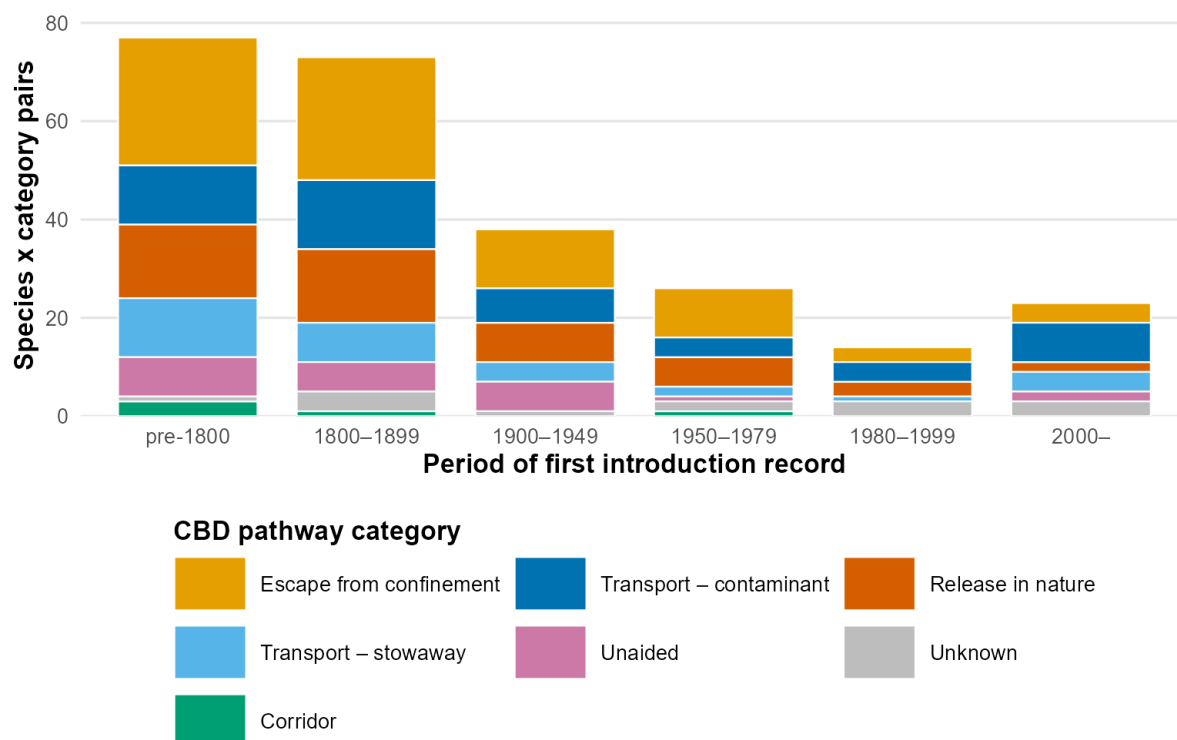


Figure 11 – Pathway composition by period of first European record. Species counted once per pathway category, binned by the year of their first introduction record. The 'first_introduction_year' is a species-level attribute, not a date for the individual pathway, so this shows when the species using a pathway arrived, but it cannot date the pathway itself. 14 species x category pairs lack a year and are excluded.

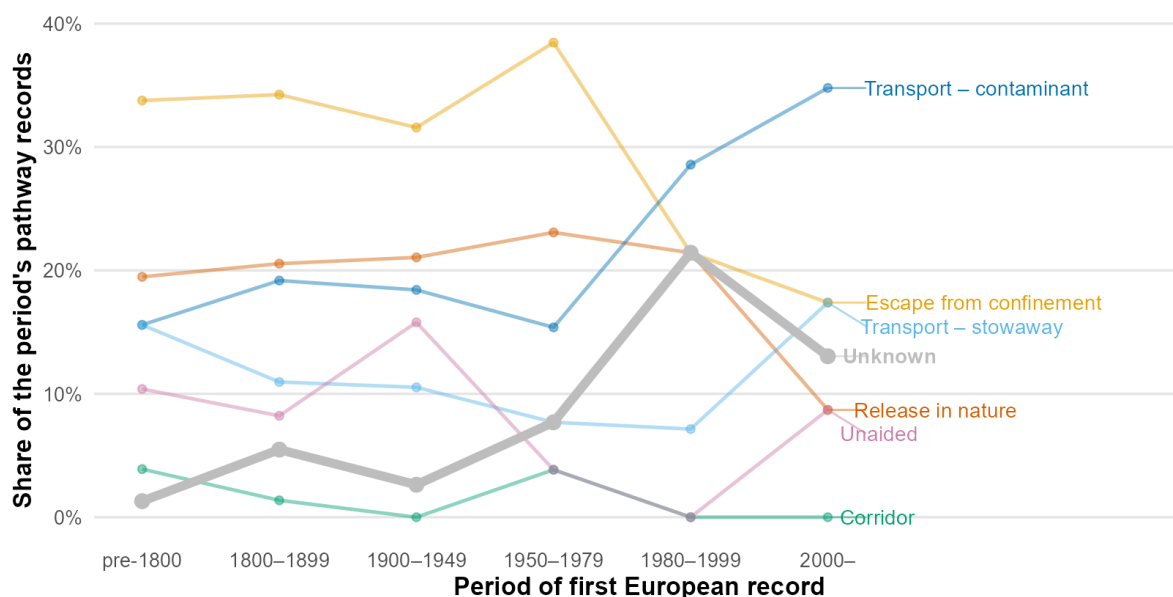


Figure 12 – Temporal plot showing how much the mix of introduction pathways has changed over time. The temporal profiling shows minimal change, with the period x pathway table not distinguishable from independence (chi-square = 30.1, permutation p = 0.054, Cramer's V = 0.15). Each line is a CBD pathway category's share of the period's records. Bold series lines shift significantly in composition after Benjamini-Hochberg correction, whereas the regular, fainter series do not. Periods are permuted across species, each carrying its whole pathway set, because records are clustered within species.





D5.1 Predicted maps of Invasive Alien Species

Regarding the quality of pathway attributions, we found that only 42% of records carry a source-uncertainty grade, so "Not available" (grey; Figure 13) is the largest band in every category and across the "Corridor" category. Where grades actually exist, they lean toward low uncertainty, but the coverage is highly incomplete across categories. These results show that the pathway attributions are usable and relatively well-structured, but their per-record confidence is mostly undocumented in the source. This issue warrants further attention and effort in the future. Research that explicitly assesses the confidence, certainty and reliability of pathway attributions is essential for strengthening inference and enabling analyses that weight pathway records according to their evidential support.

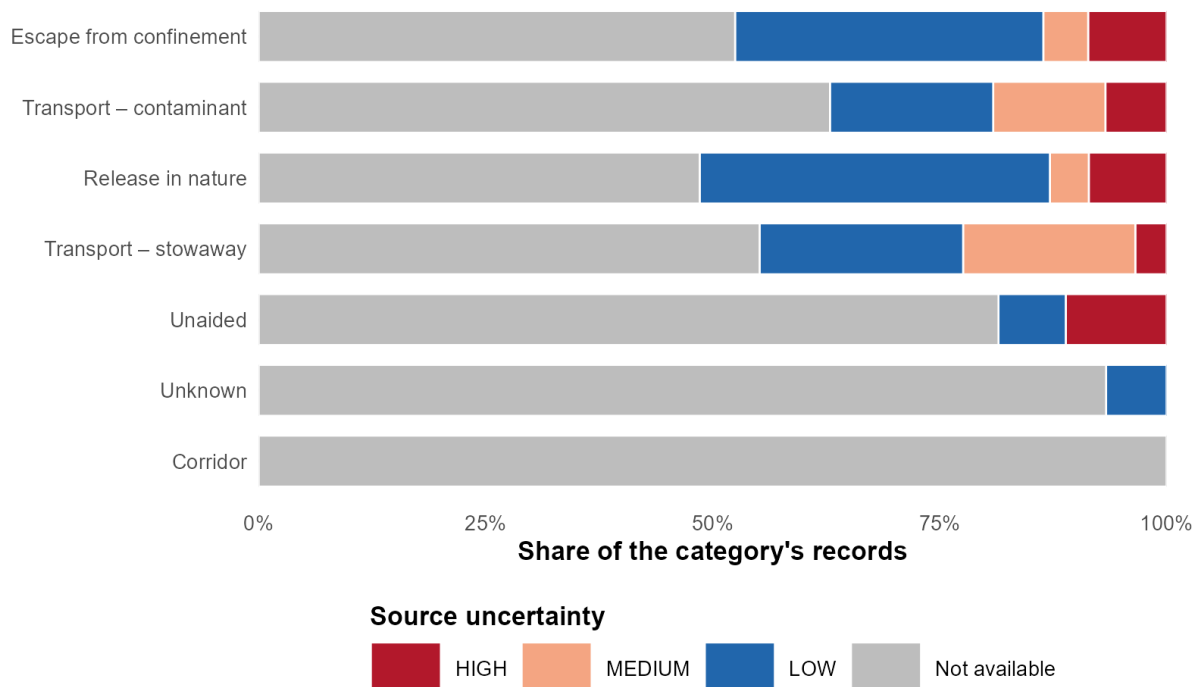


Figure 13 – Bar plot showing the evidence quality behind the pathway attributions. The 'Not available' category is retained rather than filtered given the size of the attribution gap is itself considered a result.

Drawing these findings together, the assessment of introduction pathways provides an essential basis for translating these data into targeted prevention and for defining policy and management priorities. By showing that most species are associated with multiple introduction pathways, identifying two prominent mechanism clusters associated with the OneSTOP species pool, and distinguishing primary introductions from subsequent spread, this analysis supports more coordinated, taxon- and sector-specific biosecurity responses. At the same time, the results should be interpreted as evidence of pathway occurrence rather than pathway intensity, given the absence of propagule-pressure data and the incomplete documentation of attribution uncertainty.





3.2. Descriptive analysis and trend assessment of input data used in modelling

3.2.1. Species occurrence data

KEY HIGHLIGHTS

- Overall data availability: all 120 OneSTOP target species had sufficient global GBIF occurrence data to support climate-model calibration; however, applying the stricter quality, spatial-precision and deduplication requirements for European SDMs substantially reduced the number of unique usable records at 1×1km modelling cells: 86 species (71.7%) were well supported for European modelling, while 8 (6.7%) were modellable with caution, 7 (5.8%) were marginal and 19 (15.8%) had insufficient data. In total, 26 species fell below the ≥30 unique 1km cells minimum threshold.
- Taxonomically uneven data gaps: occurrence-data limitations were concentrated disproportionately among invertebrates, particularly insects, whereas most vascular plants and vertebrates were comparatively well represented. This pattern identifies invertebrate taxa as a priority for targeted surveying and data mobilisation.
- Priority species-level deficits: the composite gap assessment identified substantial mismatches between global and European data coverage. Five species had no European records meeting the full SDM-readiness criteria, despite having extensive global occurrence datasets.
- Record volume does not ensure spatial representativeness: increasing numbers of GBIF records were generally associated with greater concentration in already sampled 1km grid cells. This shows that raw counts alone can overstate the effective information available for modelling.
- Marked geographic imbalance: SDM-ready records were strongly concentrated in a small number of countries, with the United Kingdom, Germany and France jointly accounting for approximately 46% of all unique cells. By contrast, several Baltic, Mediterranean and smaller Member States showed substantially lower coverage, likely reflecting differences in monitoring intensity, reporting capacity and data-mobilisation initiatives.
- Persistent country-level modelling gaps: fewer than half of the species documented by EASIN as present in the EU-27 plus the United Kingdom were supported by sufficient cleaned GBIF data for country-level modelling (i.e., ≥30 cells threshold). Across 1,514 documented species–country presences, 219 cases (14.5%) had no cleaned GBIF record in the relevant country, highlighting a clear need for targeted, non-redundant data collection and mobilisation.





The analysis of GBIF species occurrence records focuses on georeferenced data between 1971 and 2025. For modelling, we used 1x1km “modelling-ready” or “SDM-ready” cells, by using an incremental set of filters and more stringent criteria were applied to go from “raw” records (i.e., unfiltered geo-referenceable records from GBIF at global and the continental levels) up to filtered, cleaned, harmonised, and deduplicated occurrences at the spatial unit used for modelling. Crucially, every metric in this subsection describes data availability, and not species occupancy: a low European record count means a species is poorly recorded here, not that it is absent or rare; hence, these results relate to observation, recording and data accumulation processes through space and time, not distribution.

Of the 120 target species, 117 were matched to EU-27 presence records in EASIN, while *Solenopsis richteri* was matched taxonomically but had no associated country-level records, and *Apis florea* and *Fagus orientalis* could not be matched in the database.

Based on this preliminary descriptive analysis, we found that all 120 OneSTOP species have enough records to train the global climate model; with only five species having <1000 global records (post cleaned counts): *Australoplane sanguinea* (404/349), *Solenopsis richteri* (682/110), *Ambrosia tenuifolia* (688/503), *Baccharis spicata* (740/570); from this we also found that only three species have <300 unique 1×1 km records at the global level: *Solenopsis richteri*, *Varroa destructor*, and *Australoplane sanguinea*. Following this broad evaluation, we assessed the occurrence records against the more stringent filtering, cleaning, and deduplication criteria required to produce “SDM-ready” data for European bounds (see subsection 2.2—*Study area/modelling region for details*), resulting in a substantial reduction in the number of usable records. In Figure 14, we present the descriptive results for SDM-ready counts across four tiers, which enabled us to make a diagnostic assessment of data sufficiency. Based on this assessment, we found that 86 species (71.7%) are well supported (≥ 100 cells), 8 (6.7%) are modellable with caution (30–99), 7 (5.8%) are marginal (10–29), and 19 (15.8%) are insufficient (< 10). Roughly seven in ten species can be modelled with confidence. Still, nearly one in six carries too little data, with some having only the bare minimum to build a defensible model (or, in some cases, making it impossible to train the European-level habitat-only model). These tiers are conventional guide values and not thresholds derived from these data. Boundary cases in the 30–99 band deserve to be evaluated with caution given the somewhat broadness of this class in relation to actual SDM data requirements.

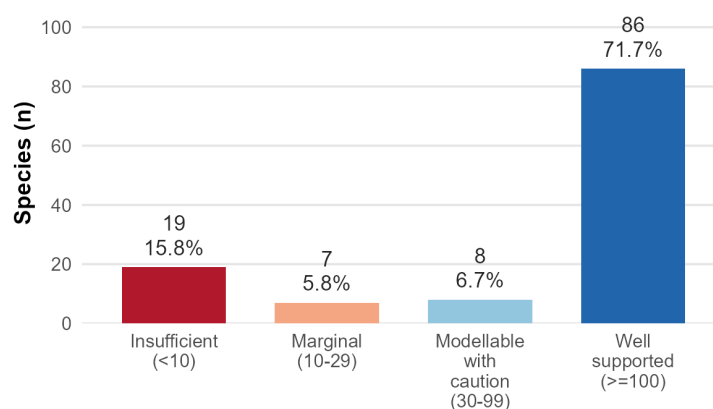


Figure 14 – The number of species per occurrence-data “sufficiency” tier. Tiers are set on unique 1×1 km cells with a cleaned GBIF record in Europe. 26 of 120 species fall below the 30-cell guide value for distribution modelling.





D5.1 Predicted maps of Invasive Alien Species

These counts describe general data availability, not species occupancy or abundance. Sufficiency is based on generally accepted criteria for SDM models.

Splitting the tier counts by taxonomic group enables biological identification of potential data gaps/insufficiencies (Figure 15). The insufficient tier is dominated by insects (7 of its 19 species) and grasses (3); the well-supported tier is dominated by herbaceous plants (27 of 86), trees and mammals. In other words, the data gap is not spread evenly across the OneSTOP target list but rather concentrates in invertebrates, exactly the group hardest to record at 1 km resolution. In terms of SDM model development, this signals that vertebrate and vascular-plant models will generally rest on firm data. In contrast, the invertebrate targets are where model support is thinnest, and thus where mobilisation and increased survey efforts should likely be directed.

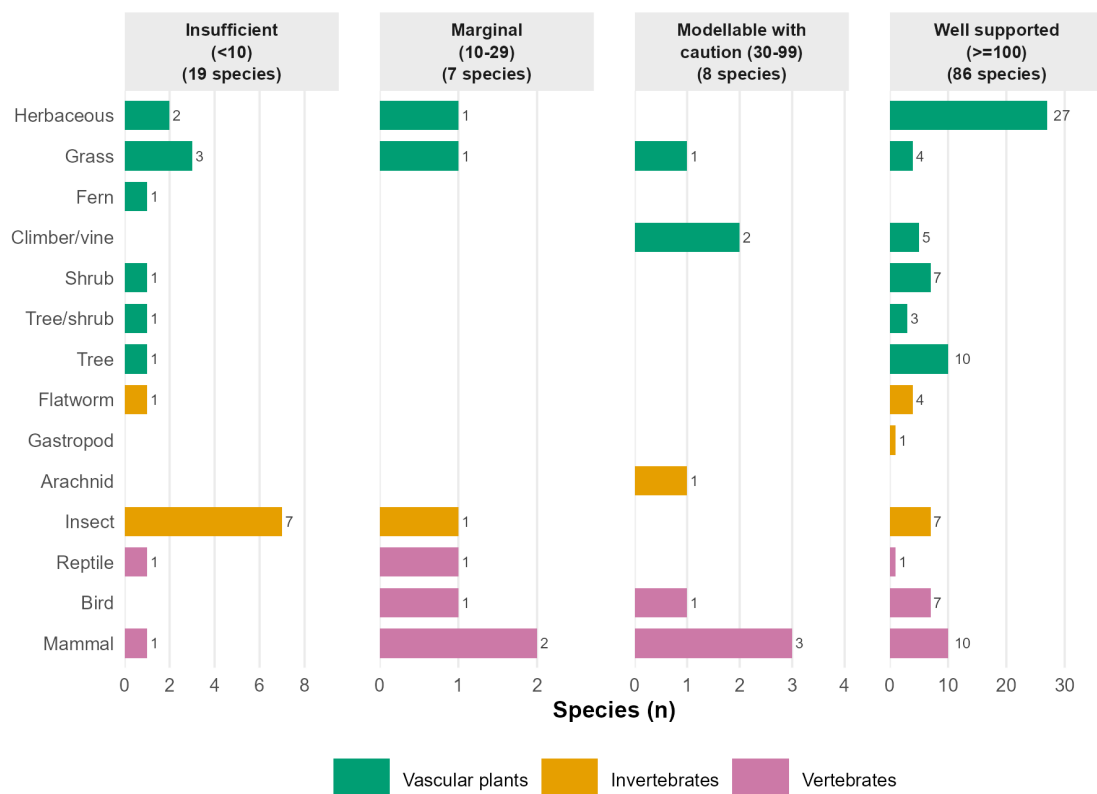


Figure 15 – Bar plot showing GBIF occurrence-data sufficiency by taxonomic group. Species counts within each tier are split by organism type. This plot is based on unique records for the European region (defined in subsection 2.2), which are distinct 1x1 km grid cells, i.e., SDM-ready records. Counts describe data availability for modelling, not species occupancy or abundance. A low European record count indicates that a species is likely poorly recorded in Europe, not that it is absent or rare there. Note the free horizontal scale per panel: the tiers differ greatly in size, so bar lengths are comparable only within a panel. All organism types are shown, including those with fewer than five species.

Based on the SDM data sufficiency analysis (see details in subsection 2.4–*Species occurrence data*), we aimed to define potential priority data gaps among the OneSTOP target species. In Table 9 (see also Supporting Table 7.1 for more information), we present the 25 species with the largest occurrence-data gaps in Europe, considering the full set of data-readiness criteria implemented in the wiSDM 2.0 filtering/cleaning workflow, and the requirement for spatially unique records within 1x1 km grid cells for SDM calibration,





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emphasising data requirements for the European model (given these are substantially more stringent and allow capturing the invaded niche).

Table 9 – The 25 species with the largest occurrence-data gap from a modelling requirement perspective in Europe (as defined in section 2.2–p.20). GBIF occurrence record counts were deduplicated by distinct coordinates, and then the number of unique records in 1×1 km grid cells is counted (i.e., “SDM-ready” count). Counts describe data availability, not species occupancy or abundance. A low European record count indicates that a species is poorly recorded in Europe, not necessarily that it is absent or rare there. Yellow highlight shows species with <30 1km unique 1km cells.

Rank	Species	Group	Unique Europe cells	Unique global cells	Europe conc. %	SDM sufficiency
1	<i>Lespedeza cuneata</i> (Dum.Cours.) G.Don	Herbaceous	0	11,432	0.00%	Insufficient (<10)
1	<i>Solenopsis geminata</i> (Fabricius, 1804)	Insect	0	2,258	0.00%	Insufficient (<10)
1	<i>Apis florea</i> Fabricius, 1787	Insect	0	2,022	0.00%	Insufficient (<10)
1	<i>Solenopsis richteri</i> Forel, 1909	Insect	0	93	0.00%	Insufficient (<10)
1	<i>Vespa mandarinia</i> Smith, 1852	Insect	0	1,538	0.00%	Insufficient (<10)
6	<i>Prosopis juliflora</i> (Sw.) DC.	Tree/shrub	3	3,231	0.09%	Insufficient (<10)
7	<i>Solenopsis invicta</i> Buren, 1972	Insect	4	7,791	0.05%	Insufficient (<10)
8	<i>Corvus splendens</i> Vieillot, 1817	Bird	16	107,756	0.01%	Marginal (10-29)
9	<i>Axis axis</i> (Erxleben, 1777)	Mammal	11	2,093	0.53%	Marginal (10-29)
10	<i>Parthenium hysterophorus</i> L.	Herbaceous	4	14,544	0.03%	Insufficient (<10)
11	<i>Baccharis spicata</i> (Lam.) Baill.	Shrub	6	427	1.41%	Insufficient (<10)
12	<i>Pycnonotus cafer</i> (Linnaeus, 1766)	Bird	72	117,161	0.06%	Modellable with caution (30-99)
13	<i>Pachycondyla chinensis</i> (Emery, 1895)	Insect	4	1,254	0.32%	Insufficient (<10)
14	<i>Elaphe taeniura</i> (Cope, 1861)	Reptile	17	778	2.19%	Marginal (10-29)
15	<i>Lygodium japonicum</i> (Thunb.) Sw.	Fern	1	9,748	0.01%	Insufficient (<10)
16	<i>Pueraria montana</i> (Lour.) Merr.	Climber/vine	98	10,290	0.95%	Modellable with caution (30-99)
17	<i>Triadica sebifera</i> (L.) Small	Tree	2	11,762	0.02%	Insufficient (<10)
18	<i>Tamias sibiricus</i> (Laxmann, 1769)	Mammal	152	8,522	1.78%	Well supported (>=100)
19	<i>Andropogon virginicus</i> L.	Grass	2	6,973	0.03%	Insufficient (<10)
19	<i>Cortaderia jubata</i> (Lemoine) Stapf	Grass	1	1,278	0.08%	Insufficient (<10)
21	<i>Pycnonotus jocosus</i> (Linnaeus, 1758)	Bird	163	57,547	0.28%	Well supported (>=100)
22	<i>Acridotheres tristis</i> (Linnaeus, 1766)	Bird	235	229,442	0.10%	Well supported (>=100)
23	<i>Platydemus manokwari</i> Beauchamp, 1962	Flatworm	1	737	0.14%	Insufficient (<10)
24	<i>Callosciurus erythraeus</i> (Pallas, 1779)	Mammal	48	2,700	1.78%	Modellable with caution (30-99)
25	<i>Wasmannia auropunctata</i> (Roger, 1863)	Insect	5	1,610	0.31%	Insufficient (<10)





D5.1 Predicted maps of Invasive Alien Species

As an example of these data gaps, we found that five species (four of which are insect species) have no unique 1km observation records for Europe: *Lespedeza cuneata*, *Solenopsis geminata*, *Apis florea*, *Solenopsis richteri*, and *Vespa mandarinia*. This assessment does not imply that these species are entirely unrecorded or have not been observed in Europe; rather, it indicates that the available records in GBIF meeting the required quality, spatial precision and deduplication criteria remain too scarce or unevenly distributed to provide robust support for SDM calibration in the study region. Such rationale extends to other species in Table 9 even if some species are in better data availability conditions.

Warning note

Species identified as having occurrence-data gaps (Table 9) do not necessarily correspond to those for which the combined climate–habitat model could not be produced. Failure to obtain a European habitat model may reflect the stringent data requirements of the continental land-cover component. Still, it may also result from other limitations, including poor model performance across modelling techniques, insufficient variation in land-cover predictors, or constraints on model evaluation arising from the spatial distribution of the available records.

In a subsequent analysis, we aimed to assess if species records tend to saturate in unique 1km cells. For this purpose, a survey-saturation assessment modelling the ratio of uniquely occupied 1×1 km grid cells (i.e., SDM-ready points) vs the total number of globally filtered/deduplicated records was performed. Results show that, as record volume increases, observations become progressively concentrated within already represented cells (Figure 16). Five species fall >2 studentised residuals below the line and are flagged low-resolution, namely: *Varroa destructor* (188,940 records in only 167 cells), *Wasmannia auropunctata* (13,698 vs 1,610), *Herpestes javanicus* (9,849 vs 1,130), *Elaphe taeniura* (1,304 vs 172), *Callosciurus erythraeus* (10,618 vs 2,700). Overall, it is relevant to note that these results reflect how the records were generated, not evidence of a restricted range.



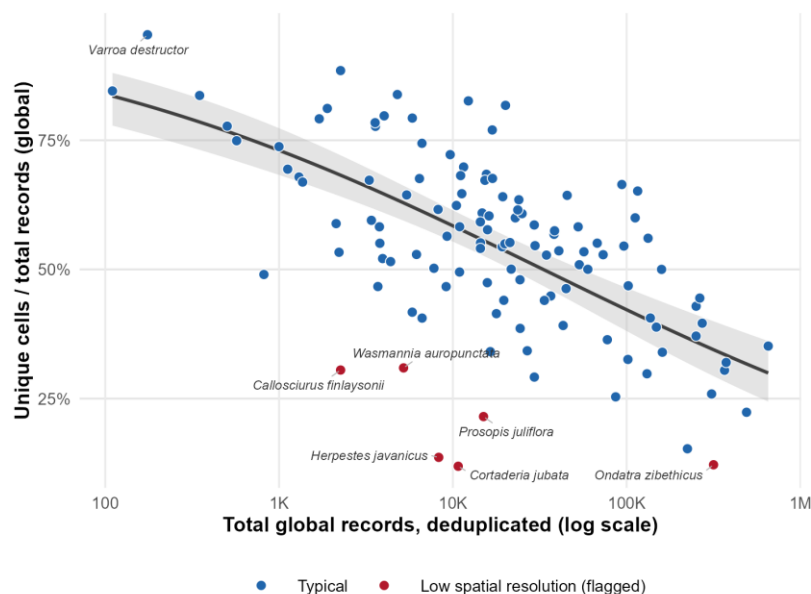


Figure 16 – Survey saturation plot showing how uniqueness generally decreases as record volume increases. Fitted logit-linear model: -0.95 logits per order of magnitude of records ($\text{adj. } R^2 = 0.36$, $n = 120$). Records are already deduplicated by coordinate, so a low ratio reflects genuine spatial clustering. The y-axis shows the ratio of unique 1×1 km grid cells (SDM-ready records count) to the total number of records, both for the global extent. The x-axis shows the log of the total number of records for the global extent. Counts describe data availability, not species occupancy or abundance. Flagged species fall more than 2 studentized residuals below the fitted relationship, which means that even after coordinate deduplication, their records occupy very few distinct 1 km cells relative to their volume (few localities). A caveat reflected in the available data and not evidence of a restricted range.

We also assessed the number of recorded species by country (i.e., unique cells summed within each state) in EU27+UK scope. Results show that the distribution is steeply uneven, with the United Kingdom (164,927 cells), Germany (140,230), and France (116,284) leading by a wide margin, together holding ~46% of all unique cells. In contrast, Bulgaria (1,123), Latvia (619), Malta (176) and Cyprus (174) hold low to very low counts (Figure 17). In general, and strictly from a modelling perspective, this means that these well-recorded states can support far more species-specific models, model-based assessments, and potentially a richer characterisation of species-environment relationships from global to country scale. This assessment also shows that some data-rich states have modest saturation and vice versa, a first indication that volume and quality are likely different axes (Figure 17). These results should, however, be interpreted with caution. At the country level, the accumulation of species records reflects the combined influence of the composition of the OneSTOP target list (largely comprising species of Union concern; 70 out of 120) and the broader landscape of data availability, sampling saturation and spatial coverage. These patterns are further shaped by differences among EU-27 member states plus the UK in monitoring intensity, reporting capacity and the scope and continuity of ongoing IAS data-collection initiatives (e.g., species- or group-specific official monitoring programs, citizen-science projects). This pattern may also reflect the strong focus on EU-listed IAS, many of which remain geographically restricted or are of limited relevance across parts of Europe.



D5.1 Predicted maps of Invasive Alien Species

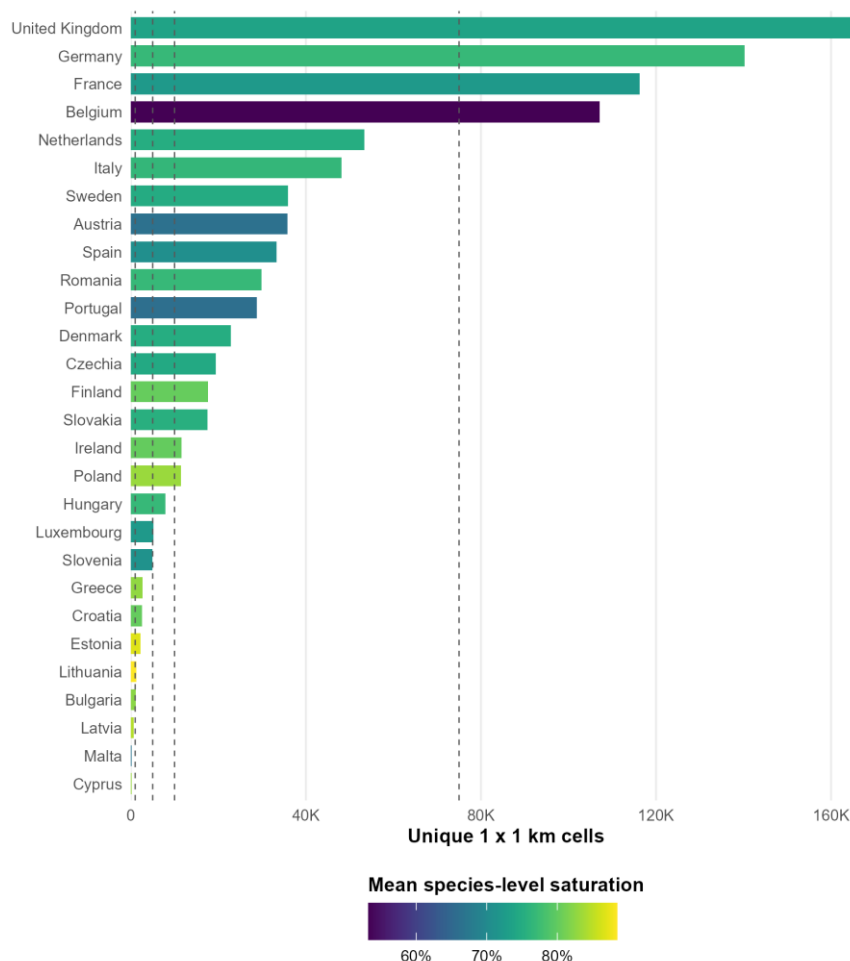


Figure 17 – Number of species recorded for EU-27 member states plus UK. This analysis assesses unique 1×1 km cells summed over the 120 target species. Labels give the number of species reaching the 30-cell modelling guide value in that country. GBIF occurrence records for the OneSTOP target species were deduplicated by distinct coordinate (latitude, longitude, and coordinate uncertainty). Unique records are distinct 1×1 km grid cells (SDM-ready data). Counts describe data availability, not species occupancy or abundance. Cell counts are summed within each country only. Counts are not additive across countries because a cell on a border is counted in each state it intersects, so these values must never be summed to a European figure. Dashed reference lines mark 1,000, 5,000, 10,000 and 75,000 unique cells. Saturation is the ratio of unique 1×1 km grid cells to the total number of records, then averaged across species within each country.

In a follow-up analysis, we assessed how many species present in each country according to EASIN data (see details in Annex 7.4–*EASIN species-country records, Supporting Table 7.4*) are supported by enough “cleaned” GBIF data to sustain a national distribution modelling-based assessment in the country concerned (i.e., ≥ 30 unique 1km occupied cells; Figure 18). This assessment aims to evaluate whether sufficient within-country occurrence data would be available to support hypothetical detailed, high-resolution modelling at 1-km or finer scales, capable of capturing relevant environmental gradients and incorporating country-specific datasets or predictors such as microclimate, soil properties or three-dimensional vegetation structure. Requiring at least 30 occupied 1-km cells per species and country, this assessment also provides a pragmatic indication of whether subsequent country-level analyses, including spread assessment or targeted detection using remote-sensing data, are likely to be sufficiently informed by occurrence records.





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Although some potential data shortfalls for species are obviously compensated by data availability at larger extents, we found that slightly less than half (~48%) of the 117 species currently present in EU27 plus the United Kingdom (as evidenced by EASIN) are currently backed by enough cleaned GBIF data to support distribution modelling at country level. In addition, we also found that this data shortfall is not confined to “data-poor states” since it grows in absolute terms precisely where recording is strongest. As such, even the best-covered members retain large “unmodellable” fractions. For instance, France, with 61 of 95 present species, leads in the modellable fraction, whereas, in contrast, the UK has 43 out of 80 or the Netherlands has only 35 of 82. In addition, in many smaller or less-intensively sampled states, much of the Mediterranean and the Baltic among them, the majority of present species also fall short in data sufficiency/fitness for country-level modelling purposes.

At its most severe, this shortfall entails the total absence of occurrence data. Across the 1,514 species–country presence combinations (out of 3,360 possible combinations = 120 species × 28 countries) documented by EASIN, 219 cases (14.5%) contained no cleaned GBIF occurrence record for the country concerned. Consequently, these officially reported presences lacked the quality-controlled, spatially explicit occurrence evidence required to support country-level SDM calibration, highlighting a potential and actionable gap in data mobilisation rather than an absence of the species themselves.

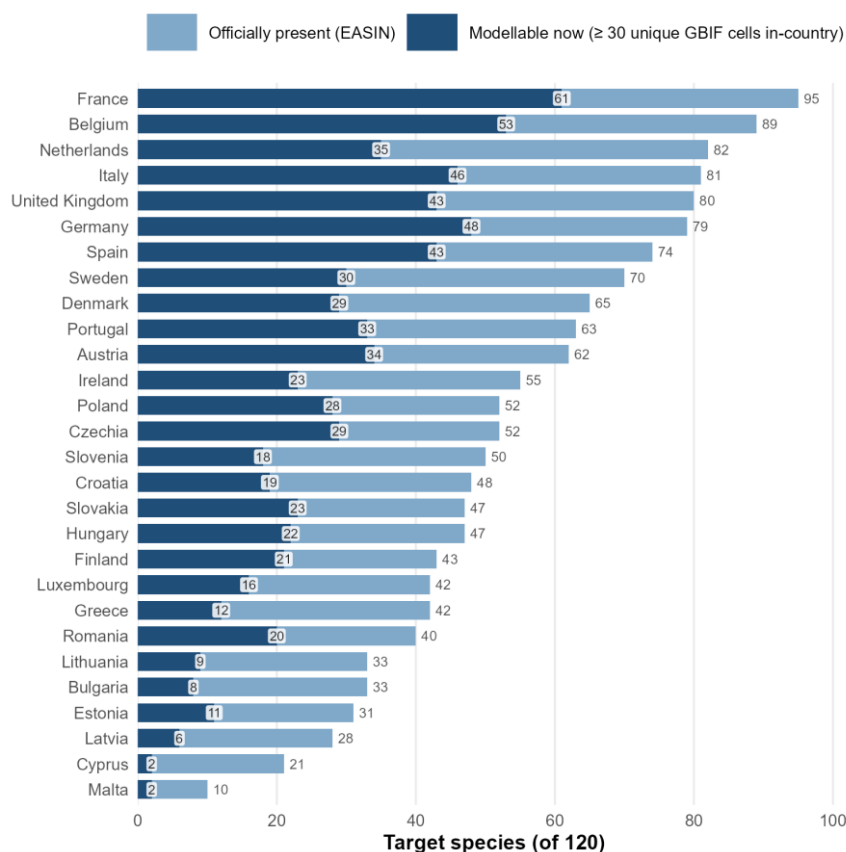


Figure 18 – Bar plot comparing species officially present (EASIN) versus modellable in-country, by EU-27 member states plus UK. Light bar: target species EASIN records as officially present. Dark bar: how many already carry enough cleaned GBIF data to model in that country. The overhang is the modelling gap. Plot data is based on distinct 1 x 1 km grid cells (the SDM-ready count). Counts describe data availability, not species occupancy or abundance. Official presence comes from EASIN (European Alien Species Information Network). Modellable equals at least 30 cells at 1km resolution. A species can be officially (EASIN) present and modellable globally or at the continental level, but it may have too few records in a given country.





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Crucially, these results reflect data availability and readiness primarily from an SDM development perspective. The assessment does not explicitly account for species-specific ecological, biogeographical or invasion history-related characteristics that may plausibly explain these patterns, as it is fundamentally a data-driven evaluation of occurrence-data sufficiency and distribution. Despite these assessment limitations, we found that the species are established, but they miss the mobilised, quality-controlled occurrence evidence needed to model them in great detail within Europe or within each country. The pattern thus points to a concrete and addressable priority that targeted and non-redundant surveying and mobilisation of occurrence data for officially present species, without which distribution models for a substantial share of the EU's list of IAS concern cannot yet be built on a country-relevant basis. These can, however, be compensated by data available at wider extents, as followed in the Task 5.1 modelling approach, but often at the expense of missing details and limited coverage of specific environmental gradients or conditions.

Overall, assessing occurrence-data gaps from an SDM-ready perspective provides a more realistic measure of whether available open-source data such as GBIF can support robust model calibration and evaluation than raw record counts alone. By accounting for data quality, spatial uniqueness, geographic representativeness and sampling imbalance, this approach helps identify species and regions requiring additional data mobilisation and targeted surveying, guides the interpretation of model uncertainty and supports more transparent and defensible IAS risk assessment across Europe.





3.2.2. Climate data

KEY HIGHLIGHTS

- Temperature change dominates the projected climatic signal: across the EU-27 plus the United Kingdom, temperature-related bioclimatic variables exhibited the largest and most consistent future shifts, led by maximum temperature of the warmest month (BIO05), annual mean temperature (BIO01) and minimum temperature of the coldest month (BIO06).
- Summer heat extremes are the principal driver of climatic displacement: by 2071–2100 SSP5-8.5, the standardised temperature-change distance was approximately five to six times greater than the corresponding precipitation-change distance. BIO05 was the dominant individual driver in 24 of 28 countries, highlighting the importance of summer thermal tolerance for future IAS establishment and suitability.
- A pronounced north–south precipitation contrast: although precipitation variables showed no uniform Europe-wide directional trend, the scenarios consistently indicated wetter conditions across northern and Baltic countries and progressive drying across Mediterranean countries. This “hotter-and-wetter north” vs “hotter-and-drier south” pattern became increasingly marked under stronger forcing scenarios.
- Scenario effects strengthen substantially towards the end of the century: at mid-century, differences among SSPs were comparable in magnitude to within-country climatic variability. By end-century, however, scenario choice more markedly influenced composite climatic change approximately three times more strongly than within-country spatial heterogeneity, demonstrating the increasing importance of the future forcing pathway.
- The broad geography of climatic change is robust, but country rankings are uncertain: south-eastern European countries, including Croatia, Romania, Bulgaria, Hungary and Slovenia, generally showed the largest composite climatic displacement, whereas several north-western and island countries showed lower values. Nevertheless, overlapping spatial variability and uncertainty indicate that results are more appropriately interpreted as broad severity bands than as a strict country ranking.
- Future IAS projections should retain the full scenario and time-period range: due to both the magnitude and spatial pattern of climatic change varying across SSPs and projection periods, IAS SDM outputs should be presented as scenario-dependent plausible futures for IAS environmental suitability rather than as a single central projection. This provides a stronger basis for identifying emerging invasion risks and supporting forward-looking surveillance, prevention and management.





D5.1 Predicted maps of Invasive Alien Species

This subsection examines the magnitude, direction and geographical distribution of projected change in the bioclimatic variables used as climatic predictors in the IAS distribution models. This assessment is highly valuable for understanding the environmental changes represented by the CHELSA future scenarios (as well as for land cover scenarios) and, in turn, for interpreting why projected IAS favourability and potential distributions change across periods and emissions pathways. This analysis is performed at the country level and considers EU27 states. Country-level summaries are compared between the 1981–2010 historical baseline and the future periods 2041–2070 and 2071–2100 under three contrasting CMIP6 pathways: SSP1-2.6, SSP3-7.0 and SSP5-8.5. Explicit consideration of the scenario and projection period is essential, as these define the degree to which future climatic conditions potentially diverge from those used to train the models (i.e., non-analogous conditions) and, consequently, the extent of potential extrapolation involved when estimating future habitat suitability. Nonetheless, models have been trained at a global extent for climate predictors to minimise potential effects of future non-analogous conditions.

This descriptive analysis aims to illustrate main trends in scenarios in a way that enables a richer interpretation of IAS models and their projections for future scenarios. It evaluates both individual temperature and precipitation variables and their combined bioclimatic displacement, enabling comparison among countries and identification of the climatic dimensions and regions expected to experience the greatest change. Particular attention is given to differences among scenarios, since the emissions pathway represents a major source of variation in projected climatic conditions and provides the context required to interpret future changes in IAS suitability, exposure and potential establishment risk.

This analysis first examined which bioclimatic indices exhibited the greatest projected changes across future periods and emission scenarios. Figure 19 summarises these patterns as rank-ordered distributions of standardised change across the EU-27 + UK, with indices ordered by median magnitude. The results reveal a clear and consistent hierarchy dominated by temperature-related variables. Maximum temperature of the warmest month (BIO5) shows the greatest median change, reaching approximately ~1.7 baseline standard deviations (SD), followed by annual mean temperature (BIO1; approximately ~1.3 SD), minimum temperature of the coldest month (BIO6), annual temperature range (BIO7) and temperature seasonality (BIO4). Their distributions remain consistently positive and shift progressively towards larger values from SSP1-2.6 to SSP5-8.5, indicating an increasingly pronounced and spatially coherent warming signal. By contrast, the four precipitation indices remain centred close to zero and frequently span the no-change threshold, suggesting the absence of a consistent European-wide directional trend and a much stronger influence of country-specific variation. This ordering provides an empirical basis for interpreting the relative potential contribution of the predictors; BIO5, BIO1 and BIO6 represent the climatic dimensions undergoing the strongest and most systematic displacement and are therefore likely to exert the greatest influence on projected changes in IAS climatic suitability.

In turn, precipitation variables contribute less to the overall directional signal, but remain important for distinguishing regional climatic trajectories, particularly the contrasting wetting and drying patterns identified in Figure 20. However, it is relevant to note that the figure does not represent within-country climatic variability because the analysis is based on country-level mean values. It also does not capture inter-model uncertainty, as the future projections are derived from GCM ensemble means.



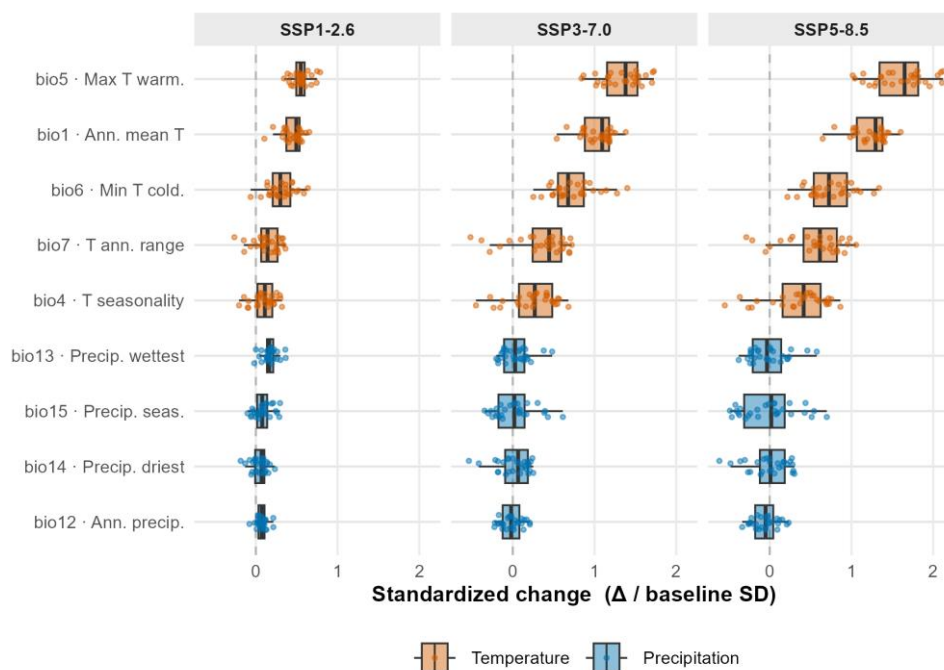


Figure 19 – Boxplots showing which bioclimatic indices are projected to shift most across EU-27 plus UK (end-century period: 2071-2100; each point is a country value). Distribution of standardised change across the 27 member states; indices ordered by median magnitude as standardised change = (future – current) / cross-country baseline SD of the variable. This plot shows projected future changes in bioclimatic indices across multiple CMIP6 SSP/RCP pathways using CHELSA v2.1 ensemble projections averaged across the contributing global climate models (GCMs).

Plotting annual warming (x-axis, °C) against relative precipitation change (y-axis, %) resolves the thermal pattern and allows a simple way to inspect the two-dimensional fingerprint of a changing climate in future scenarios (Figure 20). This exploration of the data (although lacking within-country variation, which slightly obscures macro differences) exposes a clear latitudinal “dipole” that strengthens across the scenario panels. As shown in Figure 20, the warming signal intensifies everywhere as the whole-country “cloud” slides right from ~1.0–2.5 °C, for the milder scenario SSP1-2.6, to ~4.0–6.0 °C, for the more severe SSP5-8.5 scenario.

In contrast, precipitation splits EU27+UK countries by latitude, with northern and Baltic states getting wetter (Finland, Sweden, Estonia, Latvia, Lithuania at +5 to +11%) while Mediterranean states get drier (Greece, Spain, Portugal, Malta, Cyprus, Italy at –7 to –11%). Under SSP5-8.5, the driest, hottest corner is occupied by the southern states.

This “hotter-and-drier south, hotter-and-wetter north” pattern is the canonical European climate-change signature and defines two widely distinct regimes that impact IAS distributions differently, challenging species suitability, adaptation, and ecological dynamics while redefining the geography of IAS impacts. In the Mediterranean, there is a progressive aridification favouring drought-tolerant invaders, and a warming, wetting north potentially opening to species previously excluded by cold.



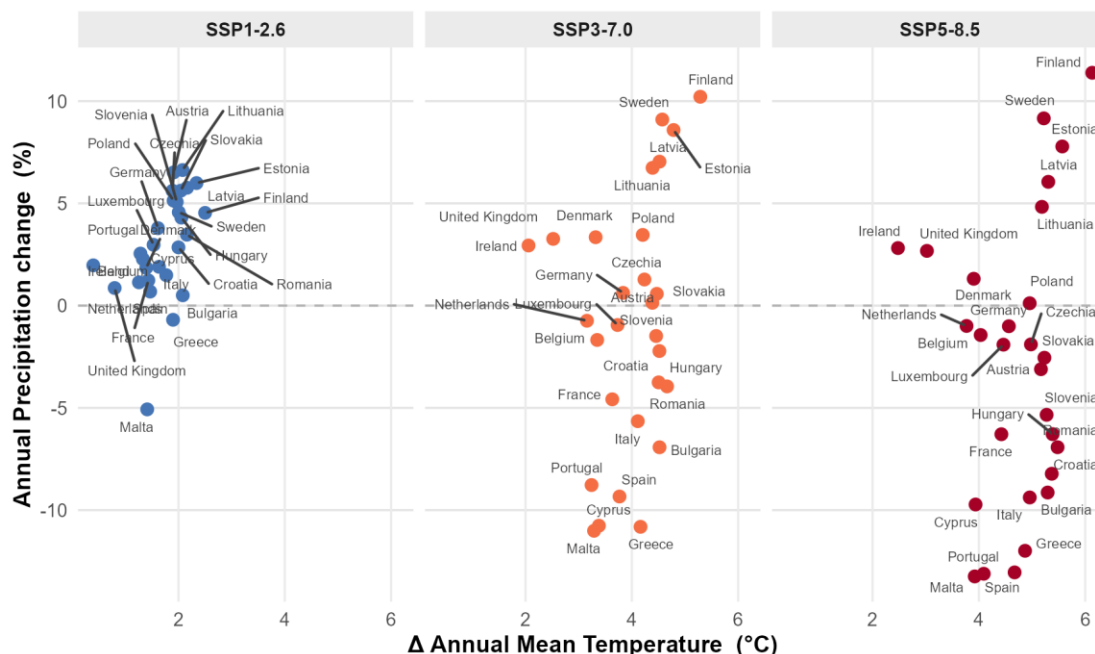


Figure 20 – Warming vs precipitation projected change, EU-27 plus UK (2071–2100; end-century). Each point is a country with annual warming against relative change in annual precipitation. Standardised change = (future – current) / cross-country baseline SD of the variable. This plot shows projected future changes in bioclimatic indices across multiple CMIP6 SSP/RCP pathways using CHELSA v2.1 ensemble projections averaged across the contributing global climate models (GCMs).

Although not shown, when checking the internal country-level spatial variation of average temperature vs precipitation, we found that the warming signal is spatially robust, whereas the precipitation change is “noisier” and much more variable sub-nationally. However, the macro-signal observed in the latitudinal gradient north-south dipole still holds. Overall, consequences for SDM-based projections for the future suggest that temperature predictors transfer cleanly to national scale, whereas precipitation-driven suitability needs finer spatial resolution given their spatial polarisation and higher sub-national variability. Although projected precipitation responses vary widely among countries under SSP1-2.6, this divergence becomes substantially more pronounced under SSP3-7.0 and SSP5-8.5, with national trajectories separating more clearly towards wetter or drier future conditions.

Performing a distance-based Euclidean analysis for country-level average values across future scenarios allows us to assess how much the country-level change ranking is signal and how much is potentially due to uncertainty (Figure 21). This analysis also allows us to assess how much, on average, countries will hypothetically diverge from current conditions and to rank them based on the magnitude of change, with whiskers indicating spatial variation (Figure 21). This is accomplished by plotting the two calculable spreads on the same axis and letting their sizes convey the difference. It can be best defined as a variance decomposition, not a significance test, in the sense that neither spread is an inferential confidence interval (the SSPs are prescribed pathways, and the whiskers reflect spatial heterogeneity, not sampling error).





Overall, the spread between scenarios widens toward the end-century period, while within-country spatial heterogeneity remains roughly constant. This is observable in the scenario spread defined by the three coloured SSP points and the grey band joining them moves a country's composite distance by a median of 1.52 standardised units (range 0.90–1.88 across the EU27 + UK). The spatial-SD whiskers, which mainly show the $\pm 1\sigma$ propagation of within-country heterogeneity through D (Euclidean distance), are about a third of that, with a median of 0.50 units, roughly a quarter of the distance they span. The two are comparable at mid-century (~ 0.5 each) but diverge sharply and by 2071–2100 the emissions pathway followed sets the magnitude of a country's bioclimatic change roughly three times more strongly than its internal climatic heterogeneity does.

The period considered is highly relevant for assessing scenario differences, and it is clear that scenarios diverge more as time progresses from mid to end of the century. At mid-century, the scenario span collapses to a median of 0.51 units, which is essentially equal to the spatial SD found (0.52). The SSPs have barely diverged by 2041–2070, so in the near term the two uncertainties are the same size, and neither dominates; the scenario axis is what opens up over the century, while the spatial term stays roughly constant.

Overall, the country-level rankings showcasing the magnitude of climate change across scenarios stay broadly similar; however, the exact ranks differ across time and scenario. The broad ordering is somewhat robust, with the five most-affected states (Croatia, Romania, Bulgaria, Hungary, Slovenia) sitting 1.1 units above the five least-affected ones (Cyprus, Denmark, Malta, Netherlands, Ireland), which represents about 2.2 times the spatial SD. As such, the south-east to north-west gradient is not merely an artefact of projective “noise”, but it holds validity. The fine ranking is not resolvable, however, as adjacent countries differ by a median of only 0.04 units in D (i.e., distance), deep inside the ± 0.50 whisker, and none of the 26 adjacent pairs has non-overlapping $\pm 1\sigma$ intervals. As a consequence of this interpretation, Figure 21 should be read as a set of severity bands rather than a strict EU27+UK ranking table.

Scenario choice also mildly reshuffles the geography, rather than uniformly shifting every country. Between the extremes, the orderings correlate strongly but imperfectly (Spearman $\rho = 0.79$, SSP1-2.6 vs SSP5-8.5), and a handful of states are genuinely scenario-sensitive, such as Estonia, which moves 12 places, the Baltics, Finland and Iberia 8 to 9, meaning that whether temperature or precipitation is their dominant driver responds differently and strongly to the forcing scenario under consideration.

For the development of IAS SDMs, these descriptive screening analyses support projecting climatic suitability across all three SSPs and both future periods, thereby capturing the breadth of plausible future conditions and enabling clearer communication of scenario-dependent outcomes. Because the emissions scenario strongly influences both the magnitude and geographical pattern of end-century change, results should be presented as a range of plausible suitability outcomes rather than as a single central projection. For the mid-century period, this range should also reflect that scenario-related and within-country spatial variability are of comparable importance.



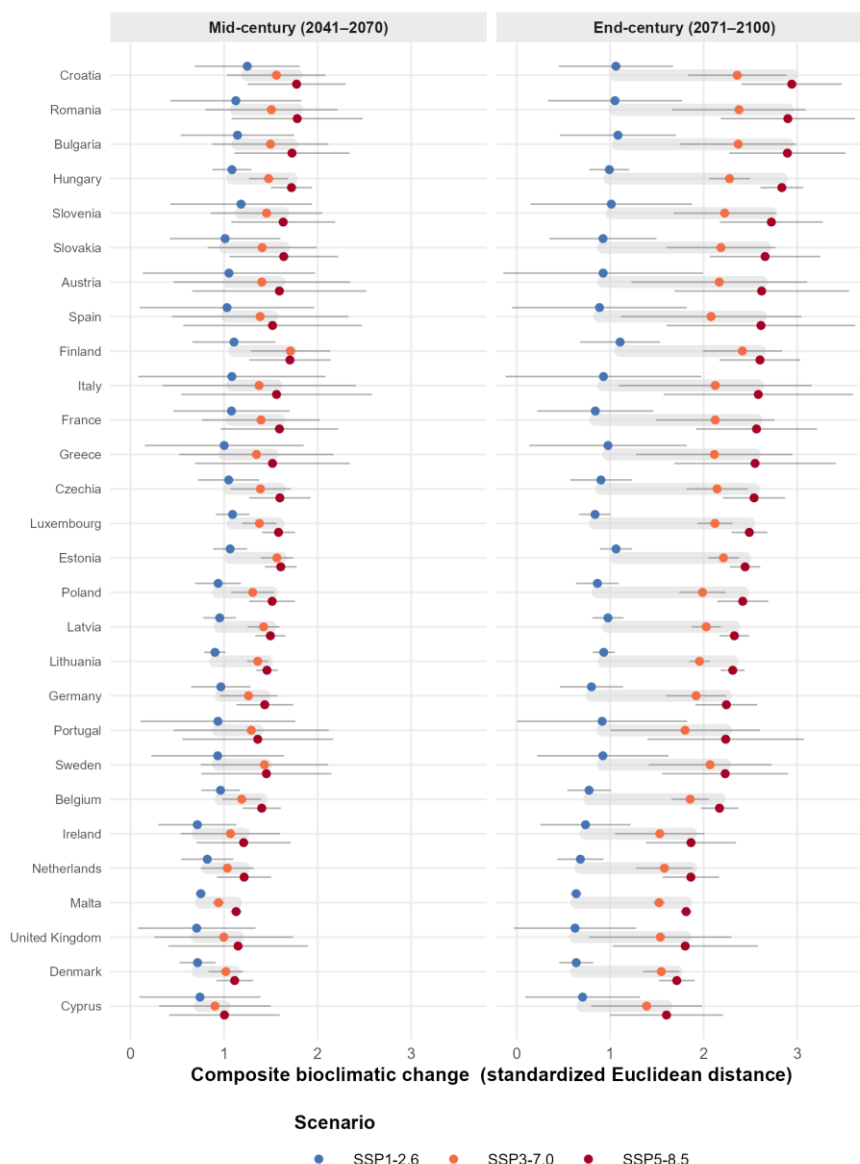


Figure 21 – Total bioclimatic change across EU-27 plus UK by scenario and depicting spatial variability. Composite change is based on Euclidean distance between historical and climate scenario means. Points represent the three SSPs (scenario spread is shown by the grey band); grey whiskers show the $\pm 1\sigma$ spatial propagation of within-country SD. The data are based on standardised change = (future – current) / cross-country baseline SD of the variable. Scenario band spans SSP1-2.6 to SSP5-8.5 (prescribed pathways, actual range). This plot shows projected future changes in bioclimatic indices across multiple CMIP6 SSP/RCP pathways using CHELSA v2.1 ensemble projections averaged across the contributing global climate models (GCMs).

Furthering this descriptive assessment, Figure 22 allows inspection of country-by-dimension change in greater detail, enabling a finer picture of how change impacts SDM and species distributional trajectories. Decomposing the composite country-level change in Figure 22 into its nine components reveals that the signal is almost entirely thermal. The five temperature indices (left block) are uniformly and strongly positive, with a progressive increase (more saturated red tones) from SSP1-2.6 to SSP5-8.5. In turn, the four precipitation indices (right block) stay close to zero (with paler tones and mixed signals across). Quantitatively, the temperature change distance (in standardised Euclidean space across scenarios) equals a median of 2.40 at end-century (SSP5-8.5), which is about 5 to 6 times the precipitation change





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distance (median ~0.44). Within temperature, BIO5 (maximum temperature of the warmest month) is the dominant driver in 24 of 28 states (BIO1, annual mean temperature, in the other 4), which means by far that summer heat extremes, not just average warming, lead the change. For IAS, this matters as warm-adapted invaders track summer-maximum temperature, so the leading axis of change is precisely the one governing establishment potential for thermophilic species capable of sustaining summer extremes.

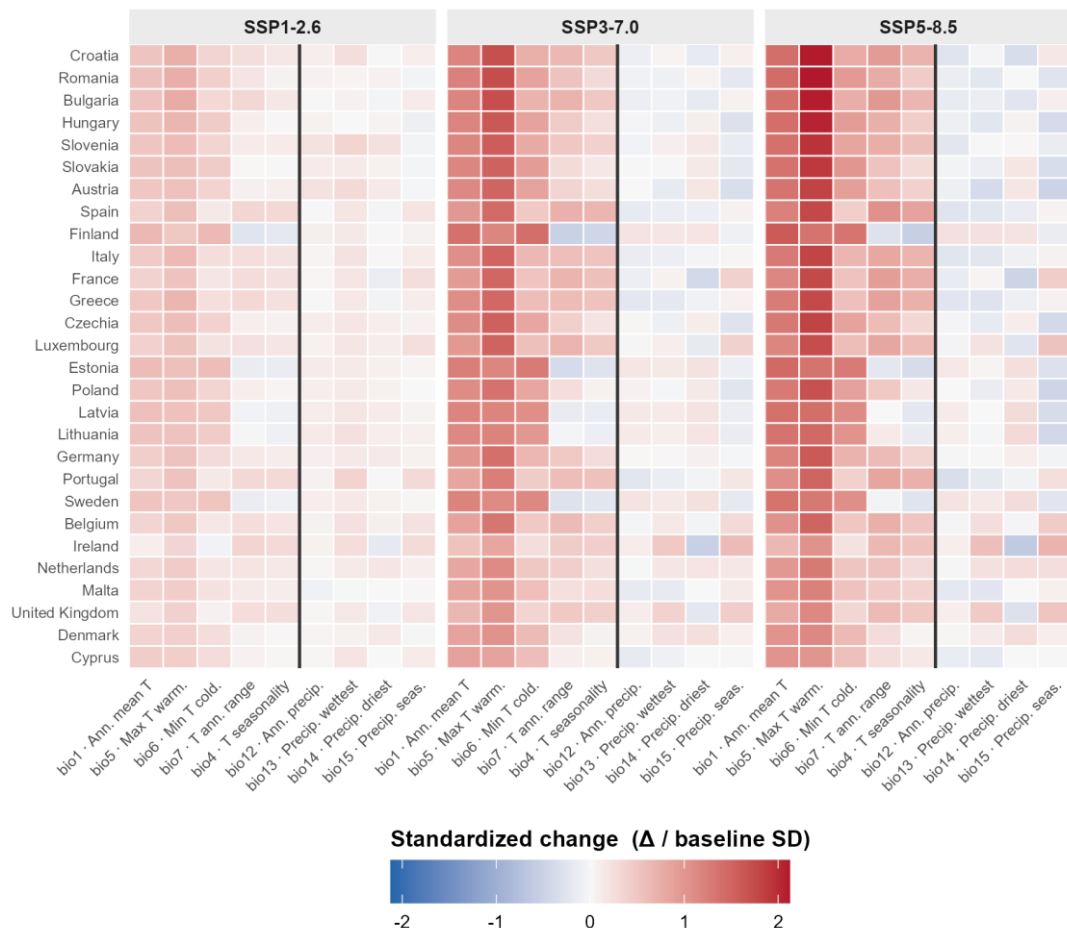


Figure 22 – Magnitude of projected change per bioclimatic index, EU-27 member states plus UK (end-century period: 2071-2100). Red = increase, blue = decrease. Temperature indices (left) | precipitation indices (right). Standardised change = (future – current) / cross-country baseline SD of the variable. This plot shows projected future changes in bioclimatic indices across multiple CMIP6 SSP/RCP pathways using CHELSA v2.1 ensemble projections averaged across the contributing global climate models (GCMs).

Overall, projected change in bioclimatic indices is strongly shaped by both the emissions scenario and the time horizon. Temperature-related variables provide the clearest and most consistent signal across Europe. These changes are likely to alter the climatic favourability of many invasive alien species, potentially enabling expansion into previously unfavourable regions while reducing it elsewhere. For the SDMs, the variability in the results across global models underline the importance of retaining the full range of SSP scenarios and future periods, rather than relying on a single central projection, and of interpreting model outputs as scenario-dependent envelopes of plausible future distributions. This approach provides a more robust basis for identifying areas of emerging invasion risk and for supporting forward-looking risk-based analysis, surveillance, prevention and management.





3.2.3. Land cover data

KEY HIGHLIGHTS

- Implications for IAS modelling are substantial: land-cover classes projected to change most are also among those most relevant to IAS establishment and spread. Incorporating land cover projections into SDMs therefore provides a more realistic basis for assessing future suitability, but pronounced national and scenario-specific heterogeneity requires results to be interpreted geographically.
- A predominantly agricultural baseline: land-cover composition is strongly shaped by agriculture, with cropland forming the largest class in 17 of the 26 countries. Marked regional contrasts nevertheless remain, including extensive needleleaf evergreen forest in Nordic and alpine countries, broadleaf deciduous forest across parts of central and Baltic Europe, grassland dominance in Ireland and the United Kingdom, and comparatively high shrubland and barren cover in Mediterranean states.
- Substantial variation in landscape composition: baseline land-cover composition differs markedly among countries, constraining future change because dominant classes have greater potential to contract, whereas initially scarce classes can primarily expand.
- Change is concentrated in a limited set of ecologically important classes: cropland, grassland, broadleaf deciduous forest and needleleaf evergreen forest exhibit the largest and most heterogeneous projected shifts. Urban cover generally increases, although from a smaller baseline, while barren land, shrubland, water and permanent snow and ice remain comparatively stable.
- Land-cover change shows a scenario inversion relative to climate change: for most countries, projected turnover is highest under SSP1-2.6 and lowest under SSP5-8.5. This pattern likely reflects stronger land-based mitigation and reallocation under lower-emission pathways, although Latvia, Lithuania and the United Kingdom show notable departures from this inversion trend.
- Shared and country-specific trajectories: across scenarios, the dominant pattern is a contraction of grassland and broadleaf deciduous forest alongside gains in cropland, urban land and needleleaf evergreen forest. However, the magnitude and composition of these shifts remain strongly country-specific.
- A small number of large countries drive much of the European change: France, Germany, Spain and Sweden account for substantial shares of projected grassland loss, while France, Germany and Spain lead cropland expansion; Finland and Sweden dominate gains in needleleaf evergreen forest, and Germany, France and Italy contribute strongly to urban growth.





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This subsection assesses the magnitude, direction and geographical distribution of projected land-cover change across the EU-27 Member States and the United Kingdom, with the aim of supporting interpretation of future invasive alien species (IAS) dynamics. The analysis uses the 1-km plant functional type projections developed by Chen et al. (2022), which were incorporated into Task 5.1 species distribution modelling framework. Country-level land-cover composition is compared between the 2015 baseline and two future periods: 2041–2070 and 2071–2100, under the SSP1-2.6, SSP3-7.0 and SSP5-8.5 scenarios. These future pathways represent contrasting socioeconomic, land-use, mitigation and climate trajectories and may therefore generate markedly different patterns of habitat reallocation. Importantly, the extent of land-cover change does not necessarily increase with emissions intensity, as lower-emission pathways may entail more extensive land-based mitigation and associated shifts in cropland, grassland, forest and other habitat classes. This analysis quantifies both overall land-cover turnover and changes in individual classes at the country level, providing the context needed to assess how future habitat availability may influence IAS distributions. Integrating these projections into the SDM framework extends the assessment beyond climate alone and enables future suitability to be evaluated under the combined effects of changing climatic conditions and a dynamic land-cover template, thereby providing a more ecologically realistic representation of potential IAS responses.

The 2015 baseline reveals the strong agricultural character of European land-cover composition. Cropland is the dominant class in 17 of the 27 countries assessed (Malta was excluded due to the lack of land cover data in the dataset; Figure 23) and accounts for at least half of the national territory across several eastern European countries, including Denmark (approximately 76%), Hungary (70%), Poland (60%), Lithuania (58%) and Romania (55%). This pronounced prevalence of agricultural land provides an important reference point for interpreting subsequent scenario-driven changes in habitat availability and their potential implications for IAS suitability. Latitude, relief and geomorphology set the rest, as needleleaf evergreen forest dominates the Nordic and alpine states (Finland $\approx 75\%$, Sweden 69%, Austria 48%), broadleaf deciduous forest the humid central and Baltic belt (Slovenia, Luxembourg, Latvia, Estonia), and grassland leads only two states, Ireland by a major fraction ($\approx 83\%$) and, the United Kingdom ($\approx 53\%$, ahead of its 29% cropland). Cyprus is the structural outlier, with almost no broadleaf deciduous forest (0.0%) or grassland (0.9%), but by far the EU's largest barren (17%) and shrubland ($\approx 15\%$), a Mediterranean composition rich in "open" land, which is exactly why its later reallocation is so extreme. The southern Mediterranean states (Spain, Italy, Greece, Portugal) are in general dominated by a cropland baseline ($\approx 35\text{--}51\%$) but are set apart from the northern EU countries by their substantial coverage of evergreen and deciduous shrubland and barren categories (Greece $\approx 16\%$ broadleaf-evergreen shrubland; Spain and Portugal $\approx 8\text{--}10\%$ shrubland). Alongside, these states hold comparatively little grassland, and their subsequent change is reallocated chiefly among cropland, forest, and scrub rather than through the grassland exchanges seen further north. Regarding artificial areas, the Netherlands have the highest coverage of urban area ($\approx 9.5\%$), followed by Belgium ($\approx 8.6\%$).

Overall, baseline between-country differences are important for interpreting projected turnover in land cover composition. This happens because the magnitude and direction of future change are partly constrained by the amount of each land-cover class initially present. In addition, dominant classes have greater potential for contraction, while classes that are scarce or absent can predominantly expand. This baseline therefore provides the essential context for comparing countries, interpreting the turnover rankings presented in the following figures



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and defining the present-day habitat conditions that in fact influence SDM development for the target IAS in OneSTOP.

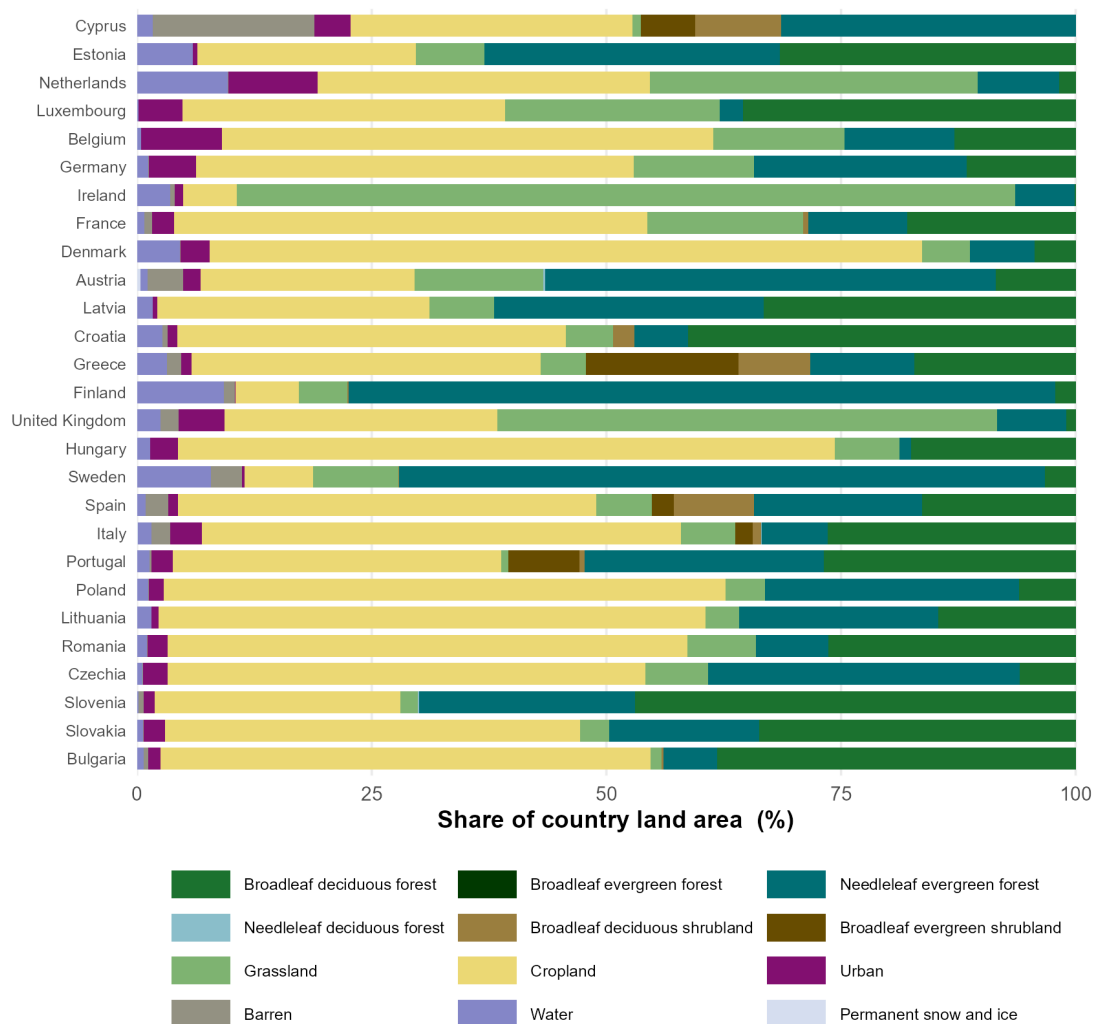


Figure 23 – Current land-cover composition, EU-27 plus UK from the 2015 baseline; all 12 classes sum to 100% by country. 1x1 km cells in an equal-area projection, so counts are km². EU-27 plus UK with data available for 27 states (Malta absent from source data). Countries ordered by end-century SSP1-2.6 turnover. These 12 classes were the classes used for species distribution modelling and projecting distributions in future scenarios.

Moving this preliminary analysis into future projections, we aimed to assess which classes were more dynamic and exhibited greater overall change. Cropland, broadleaf deciduous forest, grassland and needleleaf evergreen forest have the widest spreads (Figure 24). These categories are both the largest-changing and the most heterogeneous across countries, with national responses ranging over tens of percentage points (cropland from approximately –30% to +10%). Urban change is small in magnitude but almost always positive (a tight cluster just above zero, with outliers to +15% for the most urbanising states). Barren, shrubland, water and snow/ice cluster tightly near zero.

The main result here, impacting SDM and IAS future projections, is that the "active" habitat classes for IAS, including cropland, grassland, forest (specifically broadleaf deciduous and needleleaf evergreen subtypes), are precisely the ones that will influence the most. In addition,



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projections for the future are mostly country-dependent, so environmental favourability projections must account for this heterogeneity, with SDM results potentially better communicated not only at the European/continental level but also nationally, allowing for reporting of finer details.

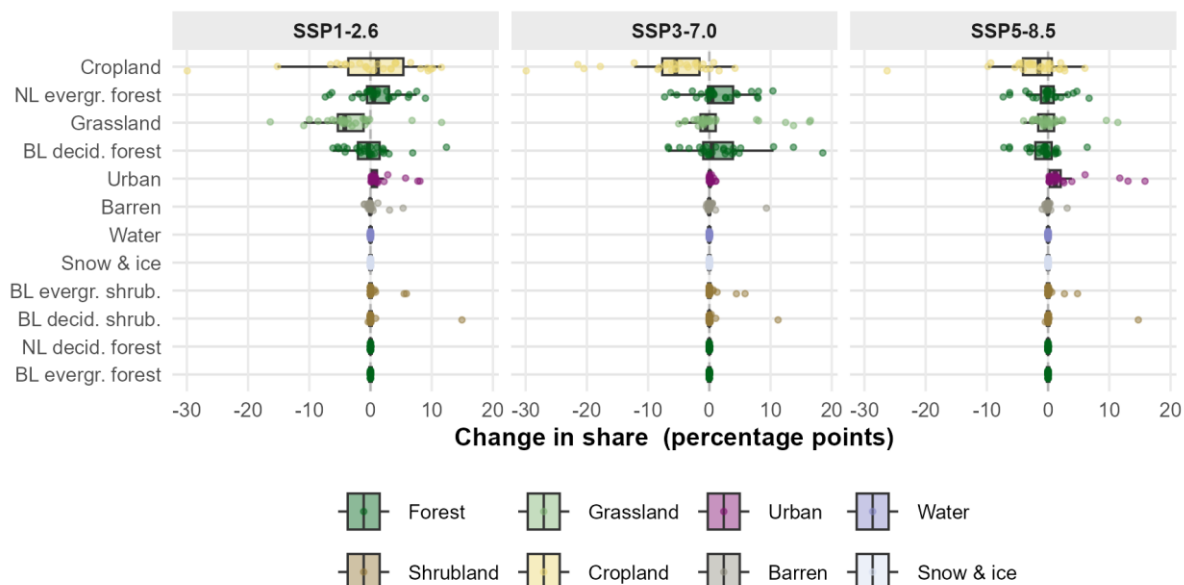


Figure 24 –Spread of national responses per class, EU-27 plus UK (2071–2100; end-century). Each point represents a country value; classes ordered by median absolute change. Data include 27 of the 28 EU-27+UK states (Malta is absent from the source data). Water and permanent snow & ice are identical in every projection (the source models present no change in them).

Results of the land cover turnover analysis, based on the SSP/RCP projections in Chen et al. (Figure 25), show a clear pattern that defines this projection dataset and one that deserves to be clearly stated due to its potential impact on SDM outcomes. Based on this analysis, we observe a “scenario inversion” in which land cover turnover is largest under SSP1-2.6 (low emissions scenario) and smallest under SSP5-8.5 for most countries in the analysis. This pattern contrasts with the climate projections, for which the magnitude of change generally increases with emissions. Land-cover dynamics, although partly influenced by climate trajectories, are shaped by a broader and more complex set of anthropogenic and socio-ecological processes, including socioeconomic development, land-use policy and mitigation measures. This inversion also likely reflects that the strongest land reallocation in these projections comes from land-based mitigation (afforestation, cropland change), which is most aggressive in the low-emissions pathway. For habitat modelling, this means the most sustainable emissions future is also the one that most rearranges the landscape compositional template IAS respond to in SDM projections. Also, when addressing the overall magnitude of change per country (EU27 plus UK; Figure 25) we can see that for most states, the SSP1-2.6 point (blue) sits at the high-turnover end and SSP5-8.5 (dark red) at the low end, with the grey band spanning the range, with the EU-27 end-century medians are respectively, for SSP1-2.6, SSP3-7.0 and SSP5-8.5: 9.47%, 6.62% and 4.10%. A few states break the pattern strikingly, such as Latvia, Lithuania, as well as the United Kingdom, showing far more turnover under the higher-emissions SSP3-7.0 (UK 16.9%) and SSP5-8.5 (UK 13.4%) than under SSP1-2.6 (UK 9.0%). Such results point to the fact that although this land cover vs climate “scenario inversion” is a general tendency, it is not a rigid outcome, and that national land-use



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trajectories can diverge sharply from the EU aggregate. It is also key to note that the variability in this assessment (Figure 25) is the actual range across three future scenarios/emission pathways, not an inferential interval, so it should be read as how much the answer depends on which future materialises.

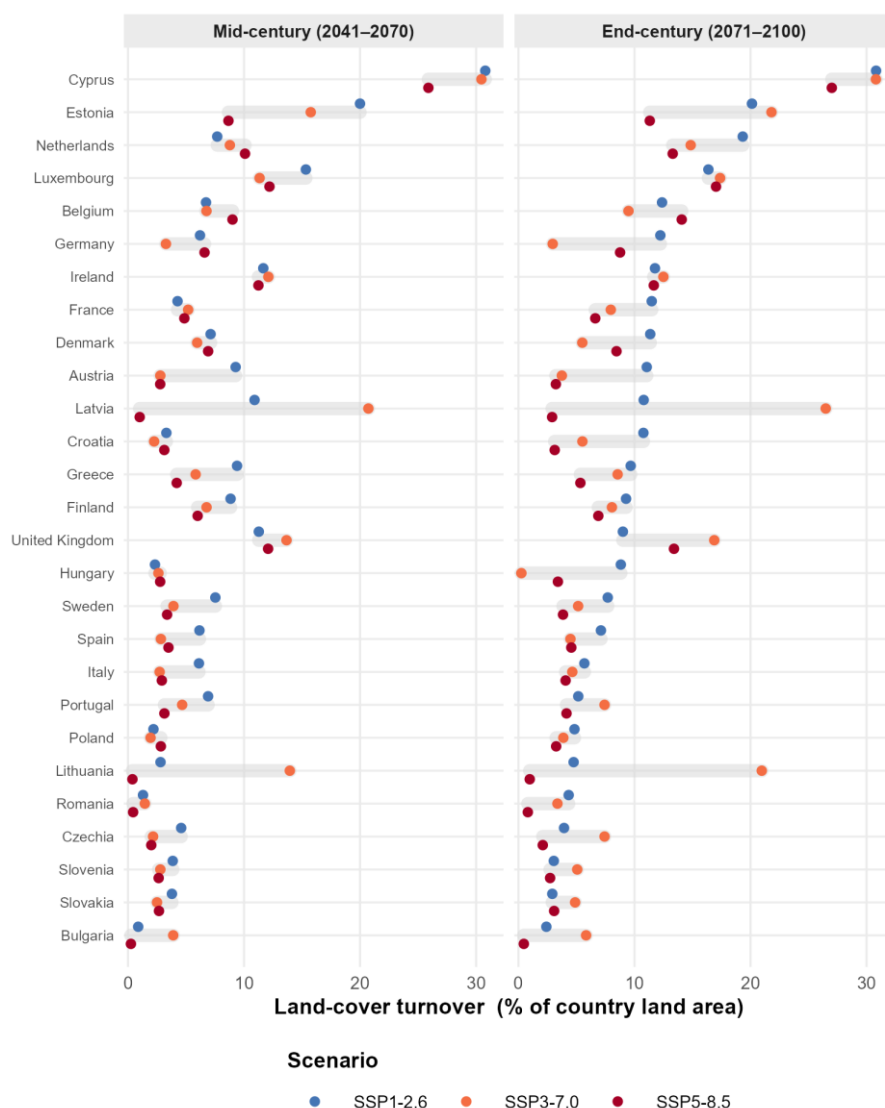


Figure 25 – Land-cover turnover across EU-27 showing the spread in land cover trajectories across emission scenarios. The grey band spans SSP1-2.6 to SSP5-8.5, with higher median turnover under SSP1-2.6. Data include 27 of 28 EU27+UK states (Malta is absent from the source data). Turnover generally accounts for the share of national land area reallocated between classes. The plot shows variability as the actual range across response change for the three SSP/RCP scenarios (not a confidence interval). No within-country dispersion is shown.

When decomposing the observed turnover (Figure 24 and Figure 25) into its 12 classes available in the dataset (Figure 26) and by country, we see that the change is concentrated in a few classes. The recurring signature is grassland and broadleaf deciduous forest losing (blue) while cropland, urban and needleleaf evergreen forest gain (red), strongest in the high-turnover northern states at the top. Water and the snow/ice columns are uniformly blank. Despite generalizable outcomes across these scenarios, the country-by-country results vary; for instance, some diverging states, such as Cyprus, are characterised by large gains in





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broadleaf-deciduous-shrubland and grassland loss, while the Baltic states are characterised by forest reallocation. However, the EU-wide trend toward cropland and urban expansion at the expense of grassland and deciduous forests is evident across the panel. These land-cover classes are also potentially associated with major IAS introduction pathways (see section 3.1–*Introduction pathways*), meaning that the habitats most likely to receive new introductions may simultaneously undergo substantial environmental change, with important implications for the spatial patterns projected by SDMs.

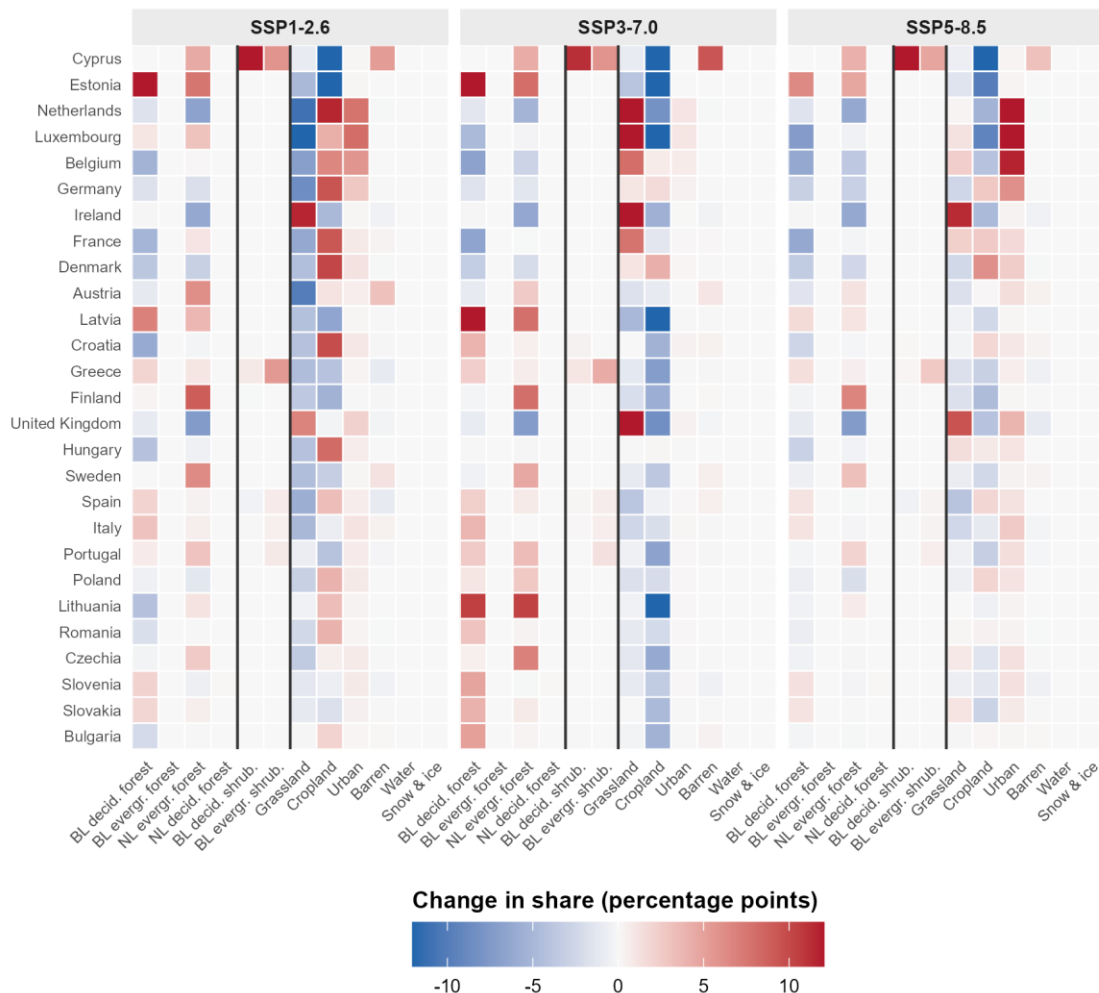


Figure 26 – Land-cover change by class, EU-27 plus UK (2071–2100; End-century). Red = gain, blue = loss. Blocks are: forest categories | shrubland | grass, crop, urban, barren, water, ice. Countries are ordered by end-century SSP1-2.6 turnover. Colour scale capped at the 98th percentile of |change|; extremes shown at the limit. Water and permanent snow & ice are identical in every projection (the source models no change in them). Data include 27 of 28 EU27+UK states (Malta is absent from the source data).

In a follow-up analysis, we examined which countries primarily drive EU27 change (Figure 27; gains in red, losses in blue for the 2071–2100 end-century SSP1-2.6 scenario). As expected, the largest countries drive the large aggregates; grassland loss is led by France, Germany, Spain, and Sweden (and gains by the UK and Ireland), whereas cropland gain is led by France, Germany, and Spain. The needleleaf evergreen forest gains are overwhelmingly led by Finland and Sweden (a sort of “Nordic-countries afforestation” trajectory). On the other hand, urban gains are led by Germany, France and Italy. A few classes show opposing national contributions within the same EU total (e.g. France gains cropland but loses broadleaf





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deciduous forest), which the net EU figure conceals. It is worth noting that these results are net marginal changes indicating whether each class grows or shrinks, not what it converts to (i.e., the analysis is not based on a transition-matrix approach). As such, these descriptive results allow us to localise the EU trends to specific states but not specific change transitions.

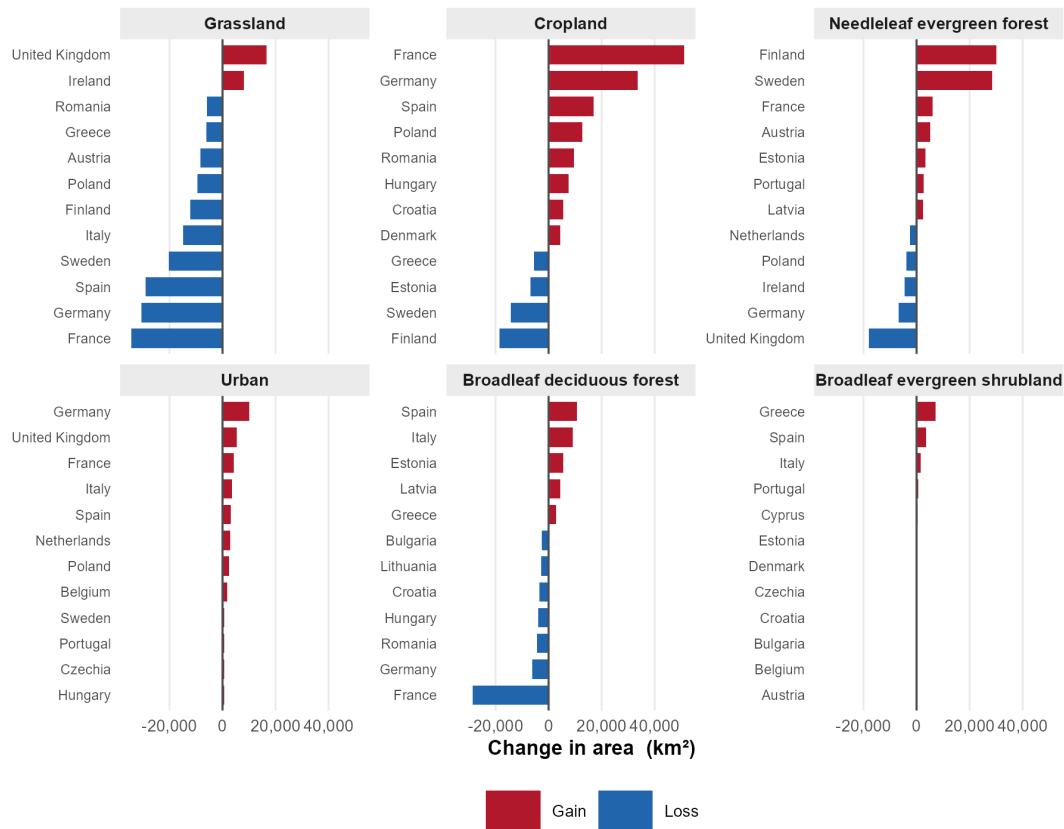


Figure 27 – Bar plots showing which countries drive each class's EU-wide change (considering 2071-2100 end-century and the greatest change SSP1-2.6 scenario). Six classes with the largest EU-27 plus UK area change; up to 12 largest-contributing member states each. Plots show only net per-class change, since this is not based on transition information. Data include 27 of 28 EU27+UK states (Malta is absent from the source data).

Overall, both the current composition and projected trajectories of land cover vary markedly across EU Member States, reflecting the complex interactions between environmental conditions, socioeconomic development, land-use policy and mitigation measures. This heterogeneity strongly shapes the magnitude, direction and ecological character of projected change in each country, with important implications for future environmental favourability and the potential redistribution of invasive alien species.

Combining high-resolution climate and land-cover predictors at a common 1-km spatial resolution offers important advantages for developing more realistic, scenario-based SDMs. By representing both climatic conditions and landscape composition, this approach provides a more comprehensive basis for assessing future IAS suitability than climate-only modelling. However, the contrasting trajectories identified across scenario components may generate complex and potentially non-linear responses. For example, the largest projected land-cover changes occur under SSP1-2.6, whereas the strongest climatic changes are generally associated with the higher-emission SSP3-7.0 and SSP5-8.5 emission pathways. These divergent patterns may produce interactions in which climate- and land-cover-driven effects reinforce, offset or modify one another, resulting in projected distributional dynamics that may





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not be readily anticipated from either dataset in isolation. This finding also highlights the importance of systematically examining the structure, magnitude and internal consistency of scenario datasets before modelling. Such preliminary assessment is essential for interpreting SDM outputs, identifying the environmental drivers underlying projected changes and developing more robust conclusions regarding future IAS trajectories.





3.3. Species Distribution models

KEY HIGHLIGHTS

- Complete species coverage: baseline and future projections were produced for all 120 target IAS with good performance, using ensemble climate–habitat models for 96 species and climate-only models for the remaining 24.
- Widespread baseline favourability: at least one target species encountered favourable conditions across 97.5% of the modelled area, with mean potential richness of 24.96 species per 1-km cell.
- Western and central baseline hotspots: the highest potential IAS richness occurred across the British Isles, France, Belgium, Netherlands, Luxembourg, Germany and northern Italy, including pronounced concentrations around urbanised/artificialized areas.
- Northward and upward redistribution: future projections for IAS consistently indicate increasing environmental favourability at higher latitudes and elevations, alongside more heterogeneous or declining conditions across southern and eastern Europe.
- Spatially polarised change: by end-century, mean potential richness increased to 25.91 species per cell under SSP1-2.6 but declined to 22.00 under SSP5-8.5, reflecting northern gains and southern losses rather than a uniform reduction in IAS risk for our set of 120 focal species.
- Strongly differentiated species responses: across all six future combinations, 50 species consistently expanded their favourable area and 43 consistently contracted.
- Increasing polarisation under stronger forcing: from SSP1-2.6 to SSP5-8.5 at end-century, the number of species showing little change fell from 33 to 13, while strong contractions increased from 11 to 34, indicating progressively more gains and losses.
- Taxonomic affiliation alone explains little of the projected trajectory: differences in central tendency between organism groups are modest whereas within-group variability is considerably larger. These outcomes support species-specific rather than taxon-wide prioritisation for surveillance, risk assessment and management.
- Substantial scenario dependence: for 28 species (23%), the projected direction of change differed between SSP1-2.6 and the higher-forcing pathways (SSP3-7.0 and SSP5-8.5), demonstrating that future outcomes are highly species-specific and cannot be reliably communicated without explicit reference to scenario and time horizon.





- Clear national redistribution: sixteen of 27 countries showed increasing mean favourable area, led by Denmark, Finland and Sweden, whereas the strongest declines were projected for Hungary, Bulgaria, Croatia and Italy. Country-level exposure also differed regionally between the intensity of change and the number of species affected.
- Operational early-warning value: the analysis identified 225 emerging species-country combinations, compared with 122 receding combinations, and 552 combinations that were environmentally favourable across at least 5% of national territory but absent from both EASIN and GBIF. These mismatches can support surveillance and horizon scanning, but should not be interpreted as evidence of current or inevitable future presence.

3.3.1. Model completeness and performance

Model completeness was found to vary systematically across the stages of the two-stage (climate/global plus habitat/continental) hierarchical workflow (see Figure 28 and

Table 10). A global climate-only model was successfully calibrated and cross-validated for every one of the 120 target species (100 %), establishing a complete baseline against which the European-extent models could be assessed.

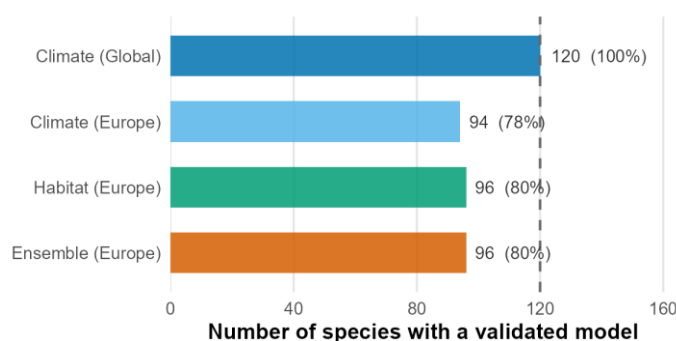


Figure 28 – Successful models across species. Dashed line represents all 120 species; every species has a global climate model. Europe-extent models are absent where a species has too few European records to train or validate. “Climate (Global)”: climate-only model component trained and evaluated for the global extent with climate predictors; “Climate (Europe)”: the previous climate-only model but evaluated only for the European subset of occurrence data; “Habitat (Europe)”: the habitat-only model component that is trained and evaluated for the European extent and uses only land cover predictors; “Ensemble (Europe)”: the combined/ensemble climate and habitat model assessed for the European extent.

Although models could be developed for all species at the global level, the stricter data requirements of the European habitat component limited the continental habitat and ensemble models to 96 species (80%). The full list of 24 species for which it was not possible to reliably train the habitat and ensemble sub-models is shown in Table 10. From these, *Lespedeza cuneata*, *Solenopsis geminata*, *Apis florea*, *Solenopsis richteri* and *Vespa mandarinia* hold zero unique observations with fitness requirements required by the wiSDM-2.0 modelling





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framework. This outcome reflects the occurrence-data limitations identified in the preceding assessment (see subsection 3.2. 1–*Species occurrence data*), particularly insufficient numbers of quality-controlled, spatially unique and geographically representative records for European model calibration and evaluation.

Table 10 – List of the 24 species for which the European habitat and combined models were not performed due to few records in the European region set for OneSTOP Task 5.1 (n<20 unique records). # *raw global records GBIF* – number of raw global records retrieved from the GBIF query; # *unique 1km cells Europe* – number of unique 1x1 km cells available for modelling considering the European bounds set for the project (i.e., SDM- or modelling-ready records). (*) Species with an asterisk were not identified as data deficient by the gap assessment in subsection 3.2.1–*Species occurrence data*; all the remaining 19 species in the table were.

Organism type	Species scientific name	# raw global records GBIF	# unique 1km cells Europe
Invertebrate – flatworm	<i>Platydemus manokwari</i> de Beauchamp, 1963	1089	1
Invertebrate – insect	<i>Apis florea</i> Fabricius, 1787	4798	0
Invertebrate – insect	<i>Pachycondyla chinensis</i> (Emery, 1895)	3288	4
Invertebrate – insect	<i>Solenopsis geminata</i> (Fabricius, 1804)	14404	0
Invertebrate – insect	<i>Solenopsis invicta</i> Buren, 1972	21589	4
Invertebrate – insect	<i>Solenopsis richteri</i> Forel, 1909	682	0
Invertebrate – insect	<i>Vespa mandarinia</i> Smith, 1852	3693	0
Invertebrate – insect	<i>Wasmannia auropunctata</i> (Roger, 1863)	13698	5
Vascular plant – fern	<i>Lygodium japonicum</i> (Thunb.) Sw.	18165	1
Vascular plant – grass	<i>Andropogon virginicus</i> L.	10845	2
Vascular plant – grass	<i>Cortaderia jubata</i> (Lemoine ex Carrière) Stapf	11127	1
Vascular plant – grass	(*) <i>Ehrharta calycina</i> Sm.	9906	14
Vascular plant – grass	(*) <i>Microstegium vimineum</i> (Trin.) A. Camus	21742	8
Vascular plant – herbaceous	<i>Lespedeza cuneata</i> (Dum.Cours.) G.Don	19327	0
Vascular plant – herbaceous	<i>Parthenium hysterophorus</i> L.	28141	4
Vascular plant – shrub	<i>Baccharis spicata</i> (Lam.) Baill.	740	6
Vascular plant – tree	<i>Triadica sebifera</i> (L.) Small	23976	2
Vascular plant – tree/shrub	<i>Prosopis juliflora</i> (Sw.) DC.	20699	3
Vertebrate – bird	<i>Corvus splendens</i> Viellot, 1817	1498637	16
Vertebrate – mammal	<i>Axis axis</i> (Erxleben, 1777)	5502	11
Vertebrate – mammal	(*) <i>Nasua nasua</i> Linnaeus, 1766	7028	7
Vertebrate – mammal	(*) <i>Sciurus niger</i> Linnaeus, 1758	95672	13
Vertebrate – reptile	<i>Elaphe taeniura</i> (Cope, 1861)	1304	17
Vertebrate – reptile	(*) <i>Lampropeltis getula</i> (Linnaeus, 1766)	2753	4





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The reliability of the modelled projections was evaluated through a spatially cross-validated assessment of predictive performance across the 120 target invasive alien species, quantifying both the discriminatory capacity and the calibration of each model configuration. Regarding performance indices, the area under the ROC curve (AUC) ranges from 0 to 1 and quantifies discrimination as the probability that a randomly chosen presence is ranked above a randomly chosen absence. The value 0.5 denotes no better than random, and values commonly interpreted as acceptable are above 0.7, good above 0.8, and excellent above 0.9. The True Skill Statistic (TSS) ranges from -1 to $+1$ (0 indicating random performance), with values above roughly 0.4 generally regarded as useful and above 0.75 as strong. The continuous Boyce index ranges from -1 to $+1$, positive values indicating predictions consistent with the observed distribution of presences, values near zero no better than random, and negative values indicating a model whose predictions are inverted relative to occurrence. Sensitivity and specificity each range from 0 to 1 and express, respectively, the proportion of presences and of absences correctly classified.

The results indicate a generally high level of predictive accuracy (Figure 29) and demonstrate that the multi-algorithm ensemble affords a statistically significant improvement over its climate- and habitat-only counterparts, with the largest and most consistent gains observed in the threshold-independent measures of ranking and calibration (Table 11). On AUC, the median values are 0.953 for Climate (Global), 0.882 for Ensemble (Europe), 0.857 for Climate (Europe) and 0.806 for Habitat (Europe). All four configurations therefore fall within the "good" to "excellent" range, and, overall, the ensemble is the strongest discriminator of presence from absence, exceeding both of its constituent models. The metric-by-metric dispersion reinforces the pattern seen in Figure 29. The Boyce index distribution for Climate (Europe; not a model simply a cross-validation substage) is by far the widest, with its calibration mainly being pulled down by habitat-poor species, whereas the ensemble's distributions are consistently high and comparatively narrow across all five indices. Taken together, the two performance figures demonstrate that the harmonic combination of the climate and habitat signals raises the weaker of the two on each metric without eroding the stronger, which is the defining property of an effective ensemble (Table 11 and Table 12).

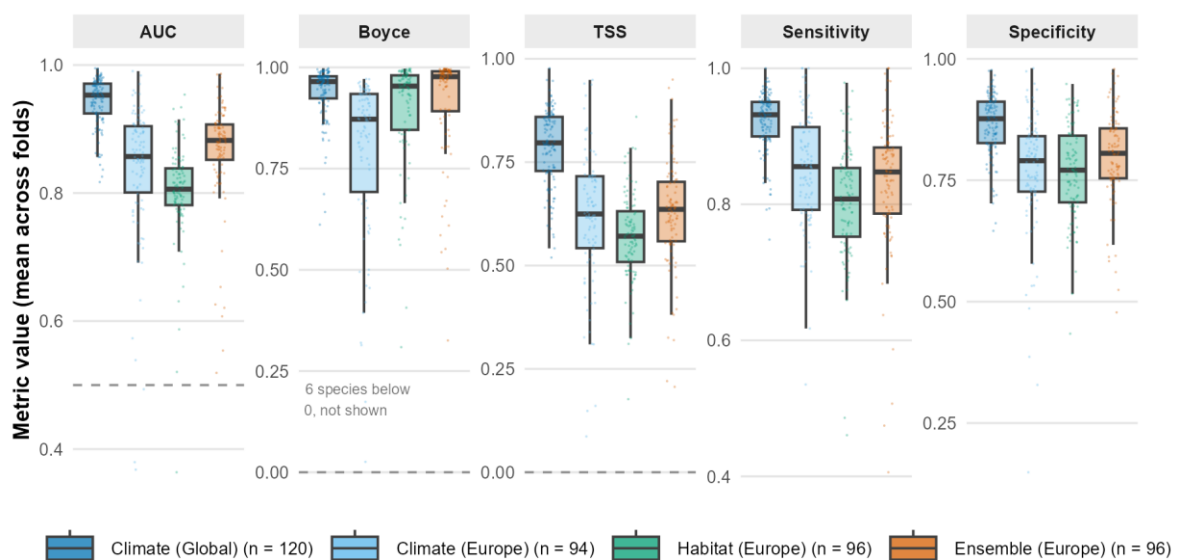


Figure 29 – Validation metrics across the model stages/levels. Each point represents a species value. Panels use independent y-axes; dashed line marks the no-skill reference. Model fits are indicated by AUC values greater than





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0.5, Boyce values greater than zero; sensitivity and specificity being closer to one. “Climate (Global)”: climate-only model component trained and evaluated for the global extent with climate predictors; “Climate (Europe)”: the previous climate-only model but evaluated only for the European subset of occurrence data; “Habitat (Europe)”: the habitat-only model component that is trained and evaluated for the European extent and uses only land cover predictors; “Ensemble (Europe)”: the combined/ensemble climate and habitat model assessed for the European extent.

Table 11 – Model performance by stage. Climate (Europe) is not a model but a validation sub-stage presented here just for comparison purposes.

Model	n	AUC	Boyce	TSS	Sensitivity	Specificity
Climate (Global)	120	0.943 ± 0.003	0.938 ± 0.006	0.787 ± 0.009	0.922 ± 0.004	0.865 ± 0.006
Climate (Europe)	94	0.835 ± 0.012	0.765 ± 0.028	0.615 ± 0.017	0.850 ± 0.009	0.765 ± 0.014
Habitat (Europe)	96	0.801 ± 0.008	0.878 ± 0.020	0.569 ± 0.011	0.802 ± 0.009	0.767 ± 0.010
Ensemble (Europe)	96	0.865 ± 0.009	0.899 ± 0.021	0.627 ± 0.014	0.830 ± 0.010	0.797 ± 0.010

Table 12 – Comparison between the Climate-only (Global), the Habitat-only (Europe) and the Ensemble climate-habitat models focusing on improvements of the latter over the former two.

Comparison	Metric	n	Partial	Ensemble	Median difference (95% CI)	Effect size r	p-value (Holm)	Favours
Ensemble vs Climate (Europe)	AUC	94	0.857	0.884	0.028 (0.017, 0.040)	0.55	< 0.001	ensemble
	Boyce index	94	0.872	0.978	0.106 (0.086, 0.142)	0.9	< 0.001	ensemble
	True skill statistic (TSS)	94	0.625	0.636	0.013 (-0.007, 0.032)	0.15	0.35	no difference
	Sensitivity	94	0.855	0.848	-0.009 (-0.022, 0.005)	-0.16	0.35	no difference
	Specificity	94	0.79	0.803	0.025 (0.003, 0.047)	0.27	0.066	no difference
Ensemble vs Habitat (Europe)	AUC	96	0.806	0.882	0.072 (0.062, 0.080)	0.8	< 0.001	ensemble
	Boyce index	96	0.954	0.977	0.018 (0.009, 0.027)	0.47	< 0.001	ensemble
	True skill statistic (TSS)	96	0.571	0.636	0.070 (0.052, 0.086)	0.67	< 0.001	ensemble
	Sensitivity	96	0.808	0.848	0.030 (0.015, 0.046)	0.44	< 0.001	ensemble
	Specificity	96	0.771	0.805	0.037 (0.019, 0.055)	0.43	0.001	ensemble





3.3.2. Historical/baseline and future patterns of IAS distribution

This subsection presents the main results of the species distribution modelling undertaken for the 120 invasive alien species included in OneSTOP Task 5.1. The analysis examines recent historical patterns (i.e., baseline) of environmental favourability and their projected trajectory under alternative future climate and land-use SSP/RCP scenarios, providing an integrated assessment of how the potential distribution of the target species may change across Europe. Results are evaluated across complementary spatial and taxonomic levels, including individual species and taxonomic groups, as well as geographically aggregated results by country for the EU-27 plus United Kingdom. This multi-level approach enables both species-specific responses and broader assemblage-level patterns to be identified, while distinguishing changes in the overall extent of favourable environmental conditions from changes in the number of species potentially distributed within each country.

Particular attention is given to the magnitude, direction and consistency of projected changes across future periods and SSP/RCP scenarios. The analysis therefore considers not only whether environmental favourability is projected to increase or decrease, but also the geographical redistribution of favourable conditions, the emergence or contraction of species–country combinations, and the extent to which responses remain consistent across alternative future scenarios. Multi-level summaries are used to assess whether common response patterns occur among related groups, whereas country-level analyses examine differences in both the intensity of projected change and the breadth of the IAS assemblage potentially affected.

Model-based patterns are subsequently compared with available occurrence information from GBIF and, most significantly, with officially reported national records compiled through EASIN (from 2.3 and 2.4). This comparison provides an additional perspective on the correspondence between modelled environmental favourability as projected by SDMs and documented IAS distributions, highlighting countries where observed or reported richness broadly aligns with model expectations, as well as those where fewer or more species are recorded than predicted. Such differences may reflect genuine ecological or biogeographical conditions, but also indicate a complex interplay and variation in recent socio-ecological regional dynamics, introduction history, pathway intensity, propagule pressure, monitoring or control effort, as well as reporting practices or data availability. Accordingly, the results should always be interpreted cautiously and pragmatically, accounting for SDM limitations and their inherent uncertainty (see also subsection 3.4–*Limitations and uncertainty in introduction-pathway analyses and SDM-based assessments of current and future IAS risk*). The results here must also be interpreted as potential distributions under projections of environmental favourability rather than predictions of occupancy, establishment or future invasion, and are intended to support comparative risk assessment, horizon scanning and the prioritisation of surveillance and prevention activities or recommendations in OneSTOP.

All analyses and indicators presented in this subsection were derived from the best-performing model available for each species: this was the ensemble climate–habitat model for 96 species (80% of the total) and the climate-only model for the remaining 24 species (20%) for which insufficient data inhibited training the European habitat-only submodel. Malta was excluded from country-level statistics because the required land-cover data were unavailable from the



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source dataset. The SDM outputs were represented as binary maps of projected environmental favourability for the 120 target IAS, using the 10% minimum training presence threshold for favourable/unfavourable dichotomous classification.

The wiSDM 2.0 modelling pipeline generated spatial projections of environmental favourability under baseline/historical climate and land-use conditions, together with corresponding projections for future scenarios. These outputs – illustrated here for *Vespa velutina* (Figure 30) – support the description and assessment of broad spatial patterns and temporal trends in potential IAS distributions, rather than predictions of realised presence, establishment or abundance. Their primary value lies in identifying emerging risks, including species and locations projected to experience increasing environmental favourability, and they may therefore provide an important early-warning basis for surveillance, horizon scanning and anticipatory management. By contrast, projected decreases in favourability should be interpreted more cautiously, as they do not necessarily imply a proportional reduction in invasion risk or the disappearance of established populations. Local persistence and adaptation, dispersal, propagule pressure, biotic interactions and management responses may allow species to remain present even where future environmental conditions become less favourable.

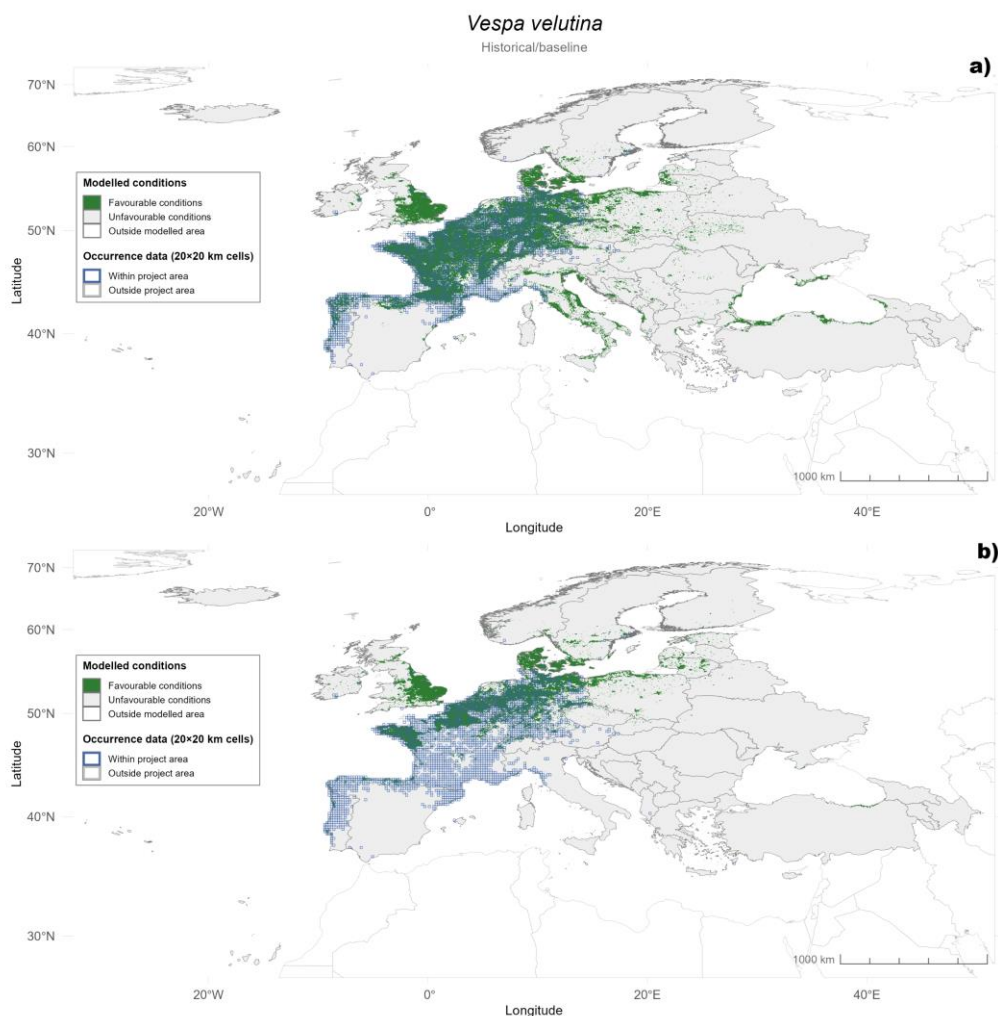


Figure 30 – Potential distribution (favourable/unfavourable environmental conditions) of *Vespa velutina* across European bounds, considering the ensemble climate-habitat model for (a) historical/baseline conditions (CHELSA-2.1: 1981–2010) and (b) end-century projection (2071–2100) for the SSP3-7.0 scenario. Favourable areas in green,





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unfavourable in grey; blank/white areas are outside the modelling region. Blue squares are current occurrences (1981- 2010 from GBIF) at a 20x20 km grid. Maps here use the same cartographic layout as the one in OneSTOP IAS SDM Gallery.

Beyond modelled projections, the adopted semi-automated wiSDM 2.0 modelling framework also generates spatial layers of model agreement alongside species distribution projections. These outputs quantify inter-model or inter-algorithm variability using the standard deviation of predictions produced by the different modelling techniques, thereby providing a spatially explicit indication of ensemble coherence (illustrated here for *Vespa velutina*; Figure 31). Areas with low standard deviation reflect comparatively consistent predictions across algorithms, whereas high values identify locations where model outputs are more likely to diverge, and projections should be interpreted with greater caution. Such maps provide an important diagnostic complement to favourability projections, as they help identify spatial patterns potentially associated with limited data support, model extrapolation, sensitivity to algorithmic assumptions or inconsistent responses to environmental predictors. Their systematic inspection therefore strengthens model evaluation and transparent communication of uncertainty, while supporting the identification of regions where additional data, methodological refinement or more cautious interpretation may be required.

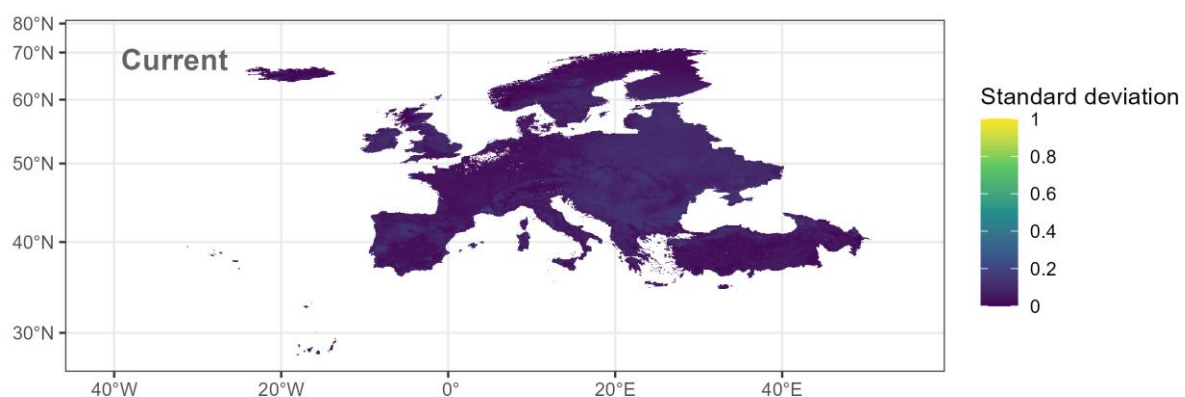


Figure 31 – Between-model coherence assessed by calculating the standard deviation of predictions given by the five modelling algorithms selected by the wiSDM 2.0 modelling pipeline for the ensemble model of *Vespa velutina* historical/baseline conditions. Lighter-shaded areas show stronger disagreement. This output map resembles the default/automated reporting produced by the modelling pipeline.

The modelling pipeline also automatically generates species-specific response curves and estimates of predictor importance (as illustrated in Figure 32 for *Vespa velutina*). These diagnostic outputs provide insight into how individual environmental variables influence projected favourability and indicate which predictors contribute most strongly to each model. Although a detailed interpretation of these relationships for all 120 target species exceeds the scope of the present report, their systematic production substantially improves the transparency, traceability and ecological interpretability of the modelling process. By exposing the relationships between species responses, environmental gradients and model predictions, these outputs help move the analysis beyond a purely “black-box” representation (which machine-learning SDMs are often linked to) towards a more interpretable, “glass-box” framework. These outputs may thus support the identification of potentially implausible responses, excessive dependence on individual predictors, model extrapolation and other





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sources of uncertainty, while providing a stronger basis for understanding and critically evaluating species-environment relationships.

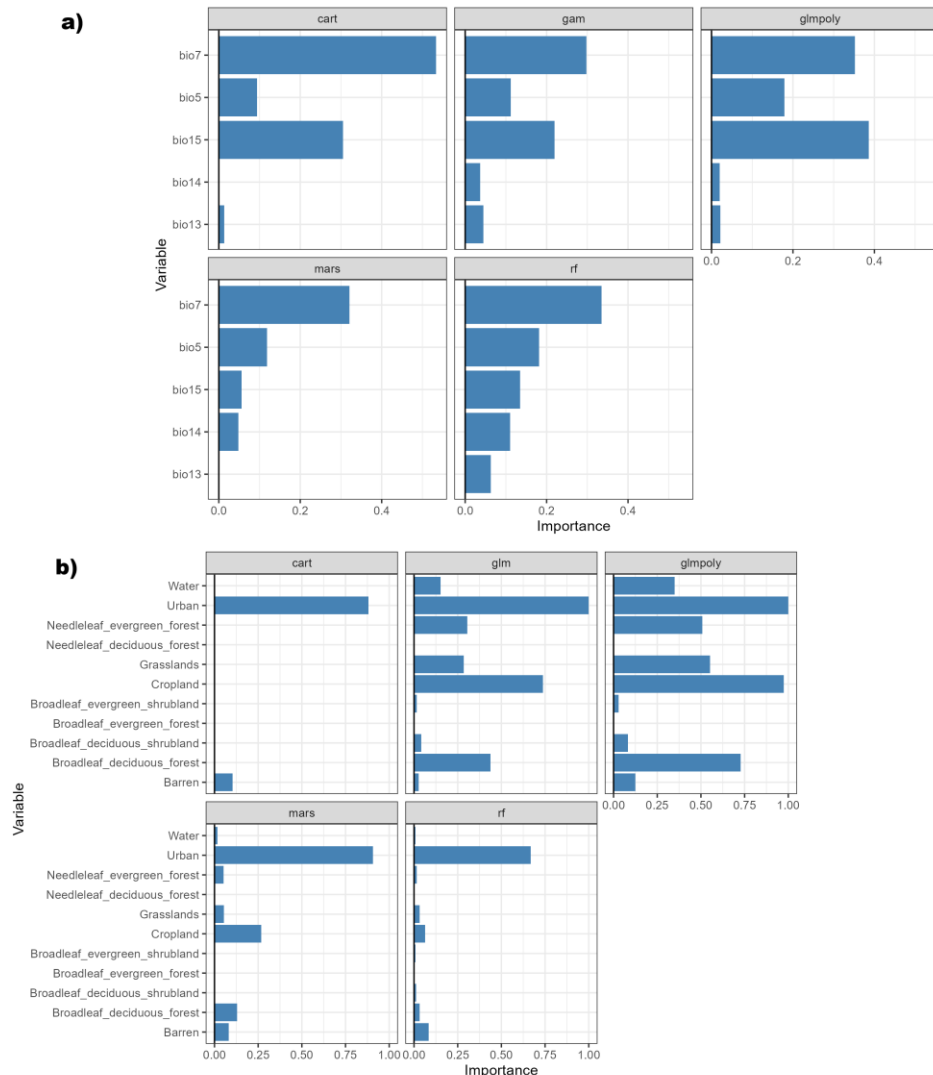


Figure 32 – Variable importance plots showing each of the variables used for the (a) global climate-only model and (b) the European habitat/ land cover-only model. The x-axis range varies between (a) and (b), and different values often arise from distinct levels of model fitness between a and b. The titles name each one of the five selected modelling methods: (a) cart – classification and regression trees; glm – generalised linear models (linear terms-only); glm poly – generalised linear model (with polynomial/non-linear terms); mars – multivariate adaptive regression splines; and rf – random forest classification; selected predictors in (a) after correlation removal are: bio5 – Max Temperature of Warmest Month; bio7 – Temperature Annual Range; bio13 – Precipitation of Wettest Month; and, bio14 – Precipitation of Driest Month; bio15 – Precipitation Seasonality.

Potential IAS richness was estimated by summing the binary projections of environmental favourability for all target species within each 1-km grid cell. The resulting richness surfaces represent the number of modelled IAS for which local environmental conditions are projected to be favourable (Figure 33 and Figure 34). These spatially explicit results identify areas of comparatively high environmental favourability for multiple IAS and provide a consistent basis for examining how potential richness may be redistributed under future scenarios. Baseline maps such as the ones illustrated indicate where favourable conditions are currently concentrated, whereas comparisons with future projections (i.e., delta maps; Figure 35) reveal



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the direction and magnitude of change, including emerging hotspots, areas of potential richness accumulation and locations where favourable conditions may decline.

Results from this geographically and taxonomically broad analysis show projected gains at higher latitudes and more heterogeneous or declining richness in parts of southern Europe (Figure 35). A comparable pattern is projected along elevational gradients. In addition to the northward redistribution of environmental favourability, several European mountain systems are expected to become increasingly favourable for some IAS, suggesting a potential upward shift into higher-elevation areas. These changes may expose mountain ecosystems, already pressured by climate and land use changes, to a broader range of IAS and thereby emerging management and conservation challenges. However, such projections indicate increasing environmental opportunity rather than inevitable colonisation, as realised expansion will also depend on dispersal, propagule pressure, habitat connectivity, local land use and the capacity of species to establish under harsh mountain conditions.

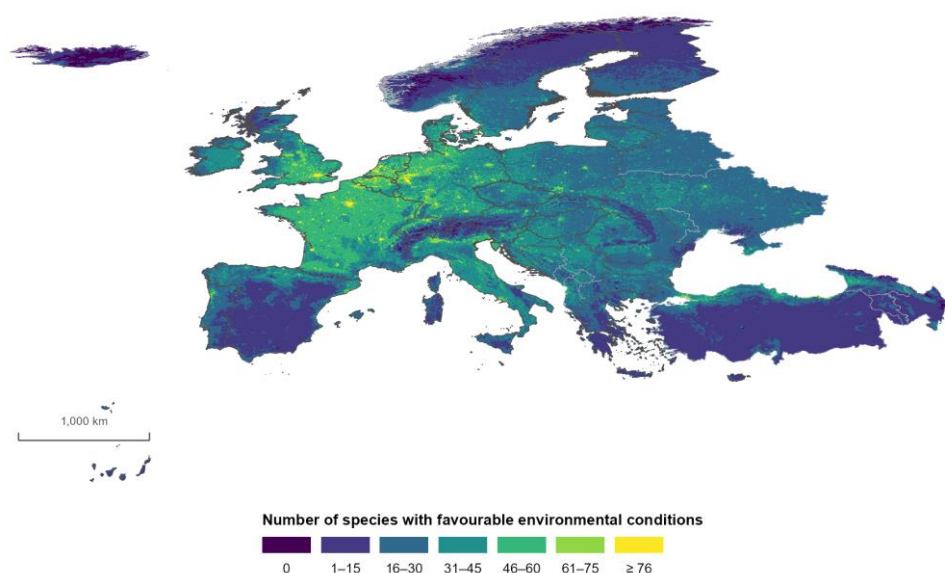


Figure 33 – Potential IAS richness for historical/baseline conditions based on summing the binary projections of environmental favourability for all 120 target species. The Azores archipelago is not shown since it is unreadable at this scale.

Regarding general broad geographical patterns, Figure 33 presents the projected potential richness of the complete assemblage of 120 target IAS. Under baseline conditions, the mean potential richness is 24.96 species per cell, with a median of 23 and a maximum of 87 species. At least one species is projected to encounter favourable conditions across 97.5% of the modelled area, indicating that environmental suitability for IAS is geographically widespread. Spatial variation is therefore primarily characterised by compositional and numerical richness differences, rather than by the presence or absence of favourable conditions. The highest potential IAS richness values are concentrated across western and central Europe, particularly in the British Isles, France, Belgium, the Netherlands, Luxembourg, Germany and northern Italy, with pronounced local maxima around several urbanised areas (reflecting both a concentration of sampling effort and recording density but also more likely a combination and high level of intensity of distinct introduction pathways). Comparatively lower values occur across much of the Iberian Peninsula, the Balkans and Anatolia. Future projections indicate a





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marked geographical redistribution of potential IAS richness. By the end of the century, mean richness increases moderately to 25.91 species per cell under SSP1-2.6 but declines to 22.00 under SSP5-8.5. This lower aggregate value under stronger climatic forcing should not be interpreted as a uniform reduction in IAS risk or environmental favourability. Rather, it reflects a spatially polarised pattern with projected losses across the Mediterranean arc and southern continental regions and generalised gains or persistence at higher latitudes (and altitudes), particularly in northern Europe and the Baltic region.

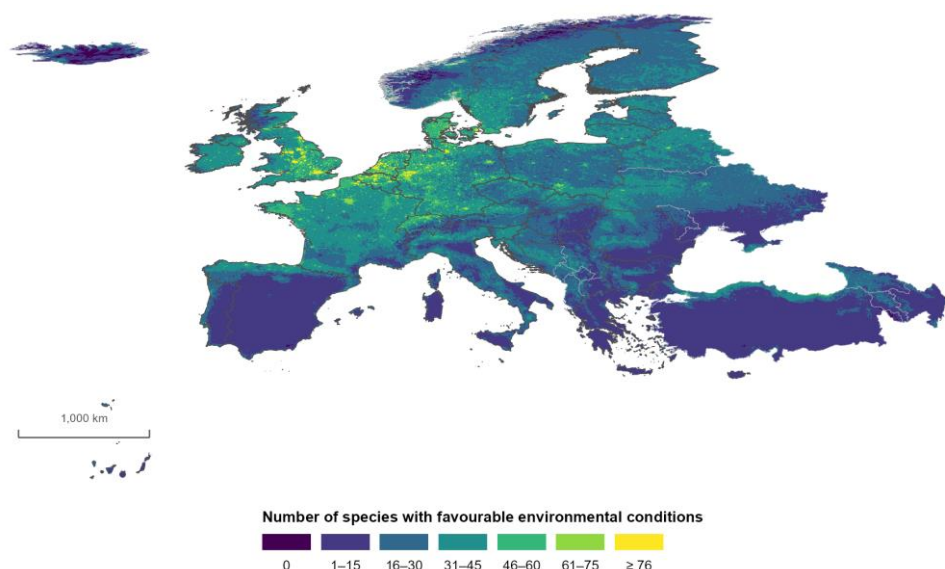


Figure 34 – Potential IAS richness projection for end-century (2071–2100) future scenario SSP3-7.0 based on summing the binary projections of environmental favourability for all 120 target species. The Azores archipelago is not shown since it is unreadable at this scale.

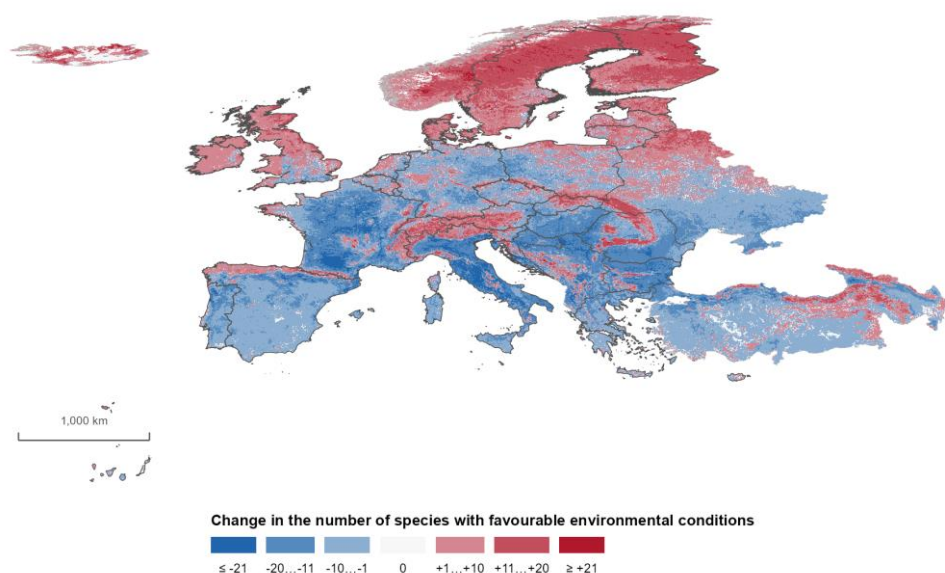


Figure 35 – Projected change (delta) in IAS potential species richness for all target species at end-century (2071–2100), SSP3-7.0. The colour classes are symmetric about zero and fixed across the six projection horizons. The Azores archipelago is not shown since it is unreadable at this scale. This SDM-based delta accounts only for environmental favourability and carries no information on dispersal, propagule pressure, biotic interactions, or management drivers.





D5.1 Predicted maps of Invasive Alien Species

Together, these broad macro-ecological patterns that emerge from IAS SDMs must be interpreted as projections of potential rather than realised IAS richness. A high value indicates that environmental conditions are favourable for a comparatively large number of modelled species, but does not imply that those species are currently present or will necessarily arrive. As such, comparisons should therefore focus primarily on changes across time horizons and future scenarios. In this context, these results are also more informative for risk assessment and precautionary prioritisation in areas projected to gain environmental favourability than for anticipating local or regional extirpation of established IAS as a consequence of combined climate and land-use or land-cover change drivers.

At the species level, projected changes in favourable area reveal a highly differentiated but broadly balanced response across the 120 target IAS. Detailed per-species results are presented in Annex 7.5—*Changes in environmental favourability by species*, containing the percentage change in average environmental favourability (Supporting Table 7.5) and the percentual change in favourable area (Supporting Table 7.6).

For most species, the direction of change is generally consistent across the target species pool: 50 species are projected to expand and 43 contract under all six future horizons, with widely varying magnitudes, indicating that the strongest responses are not driven by individual scenarios. The largest and most robust expansions are projected for *Sciurus niger* (average across periods/scenarios: +28%), *Ambrosia trifida* (+25%), *Solenopsis invicta* (+24%), *Callosciurus erythraeus* (+22%) and *Andropogon virginicus* (+21.8%) [Figure 36]. These species may constitute particularly relevant horizon-scanning and surveillance priorities, especially where they are not yet widespread or are associated with substantial ecological and socioeconomic impacts. By contrast, some already widespread IAS, including *Heracleum mantegazzianum*, *Nyctereutes procyonoides* and *Impatiens glandulifera*, are among those projected to experience the largest overall contractions (Figure 36).

Overall, modelling outcomes indicate that scenario dependence increases markedly over time. Differences among emissions pathways remain comparatively limited at mid-century but become substantially more pronounced by the end of the century. Species at the upper and lower extremes of the ranking generally retain a consistent direction of change across pathways, whereas outcomes for many intermediate-ranked species remain contingent on the scenario considered (not shown due to the large number of species in the ranking). This distinction is also evident among some of the species showing the largest changes, such as leading expanders such as *S. niger*, *A. trifida*, *S. invicta* and *C. erythraeus*, which exhibit consistently large gains across futures, while species such as *Axis axis* and *Triadica sebifera* show greater variation in the magnitude and ranking of their responses. Similarly, contractions projected for *Lysichiton americanus*, *Cotula coronopifolia*, *Robinia pseudoacacia* and *H. mantegazzianum* become considerably stronger under SSP5-8.5.

The classification of species responses further indicates that stronger forcing leads to increasing polarisation rather than a uniform shift in favourable area (Figure 37). By the end of the century, the number of species classified as undergoing little change decreases from 33 under scenario SSP1-2.6 to 13 under SSP5-8.5, while both expansion and contraction classes increase; the number of strong contractions, for example, rises from 11 to 34 species. Thus, future conditions progressively reduce the proportion of species with relatively stable projections and increase the frequency of more pronounced gains and losses (Figure 38). Extreme species-level responses are comparatively robust (less scenario-dependent),



D5.1 Predicted maps of Invasive Alien Species



whereas outcomes for species near the centre of the distribution remain much more sensitive to the future emissions pathway.

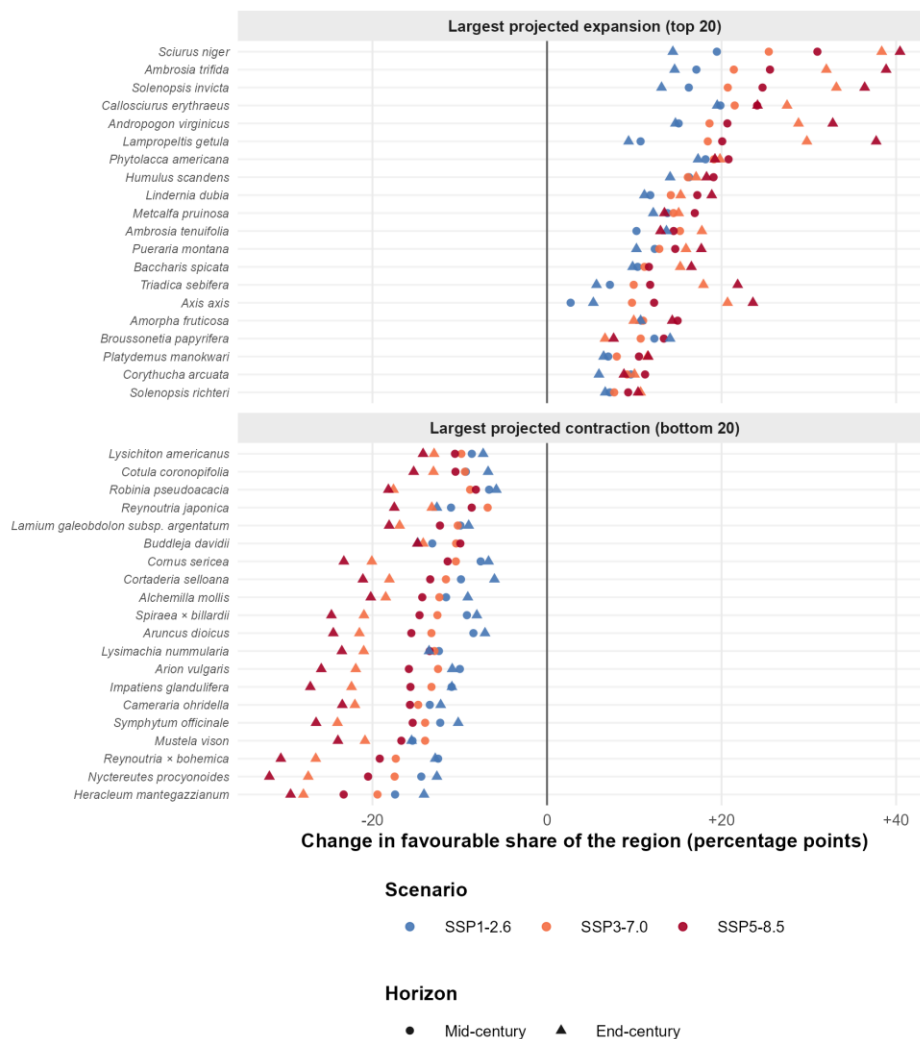


Figure 36 – The 40 species with the largest projected change. Each species is represented under all six future projection horizons. Where the six points are tightly grouped, the ranking is scenario-independent; where they diverge, it is not. SDM projections comprise EU27 + UK, 27 countries (Malta is absent from these projections). This figure summarises species' potential distributions; gaining a favourable area means increasing environmental opportunity for a species, not directly expanding or spreading.

Generally, the results here indicate an increasingly polarised response of the target IAS assemblage to interacting climate and land-cover change. Stronger forcing widens the distribution of projected outcomes, with some species gaining substantial favourable area while others undergo pronounced contractions (Figure 38). The results also indicate that the median for this region tends to decline, i.e. by the end of the century there tends to be a decline in the area of favourability. This is particularly evident in stronger forcing scenarios, which widen the distribution in both directions rather than shifting; however, the downward shift in median favourability (Figure 38) results from a heavier contraction tail, not from a general retreat of IAS risk. Interpretation is further complicated by the scenario structure of the environmental predictors, and it only applies to the set of 120 species considered in this report – this should not be interpreted as reducing concern about IAS in the light of climate change and potential land use change. Scenario SSP1-2.6 represents a comparatively moderate





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climatic trajectory but, in the land-cover projections used (i.e., Chen et al. (2022) dataset), entails more pronounced land-use change for many countries. These land-cover transitions may reinforce, counteract or buffer climatic effects depending on the species, location and environmental context. Consequently, apparently sharper responses under SSP1-2.6 in particular cases should not be regarded as contradictory, but as evidence of the interacting and potentially opposing influence of climate and land-use change on future environmental favourability. In fact, for a substantial minority of the 120 target species, the emission pathway determines the direction of projected change, not merely its magnitude. Defining a reversal as an SSP1-2.6 projection opposite in sign to both SSP3-7.0 and SSP5-8.5, the two high-forcing pathways agreeing with one another, 28 species (23 %) qualify at one or both horizons and eight retain the reversal at both horizons in a consistent direction, with no reversal is confined to mid-century. Seven of those eight expand only under mitigation, and by 2071–2100 *Heracleum persicum* gains 12.5% of its favourable area under SSP1-2.6 but loses 18.3% under SSP5-8.5, *Paulownia tomentosa* +7.7% against –30.3%, *Tradescantia fluminensis* +6.5% against –30.1%, *Ailanthus altissima* +5.1% against –17.1%, and *Heracleum sosnowskyi*, *Tamias sibiricus* and *Spiraea alba* likewise switch from modest gains to losses of 44.7%, 13.7% and 5.1%. *Sciurus carolinensis* alone inverts these results by losing 12.8% under mitigation and gaining 16.9% under high forcing. Twelve further species reverse at end-century only, among them the largest divergences in the assemblage happen for *Acacia saligna* (+47.9% / –31.7%), *Cardiospermum grandiflorum* (+23.6% / –28.3%), *Linepithema humile* (+19.9% / –28.2%) and *Alnus cordata* (+10.5% / –36.3%). Considering these outcomes, we argue that for these species, a result reported without its scenario risks carrying the wrong sign. It also shows that future projections for IAS can be strongly pathway-dependent and species-specific.

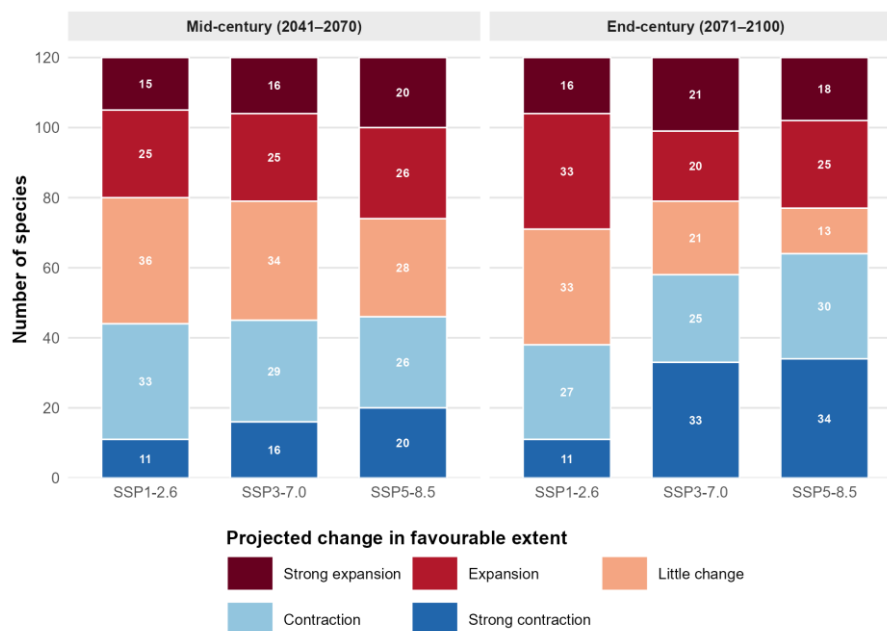


Figure 37 – Barplot showing how the 120 species divide between change classes, by future period/scenario. Each bar totals the full species list, so the stack is a composition. Classes are cut on the change in a species' favourable coverage/share of the modelled European region: strong expansion $\geq +10\%$, expansion $+2$ to $+10\%$, little change -2 to $+2\%$, contraction -10 to -2% , strong contraction $\leq -10\%$. SDM projections comprise EU27 + UK, 27 countries (Malta is not intersected by the projections due to the lack of data). This figure summarises species' potential





D5.1 Predicted maps of Invasive Alien Species

distributions; gaining a favourable area means increasing environmental opportunity for a species, not directly expanding or spreading.

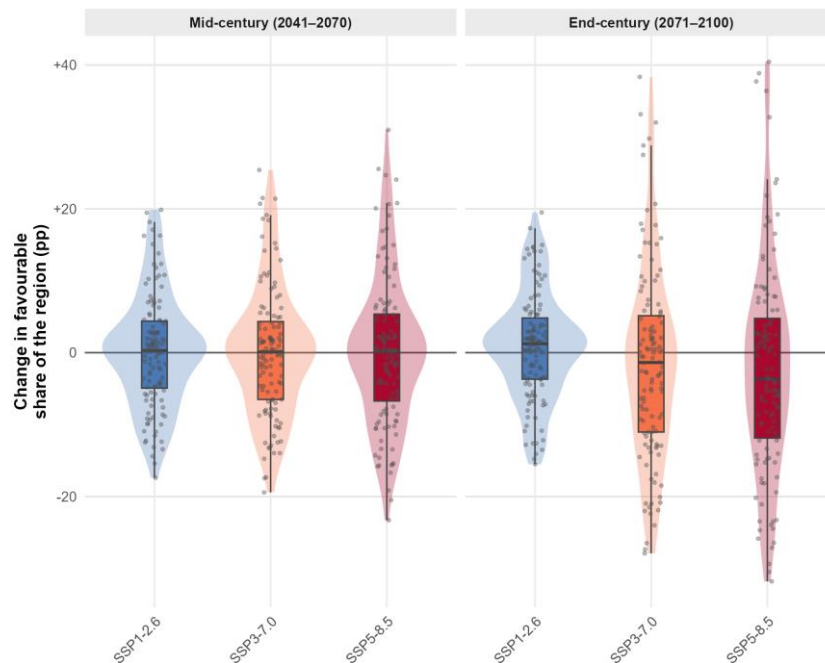


Figure 38 – Overlapped violin/box plots showing how stronger forcing (i.e., SSP3-7.0 and SSP5-8.5) polarises the assemblage rather than shifting it. SDM projections comprise EU27 + UK. This figure summarises species’ potential distributions; gaining a favourable area means increasing environmental opportunity for a species, not directly expanding or spreading.

Beyond species-level assessment, projected changes in favourable area varied widely within all organism groups, with both expansions and contractions occurring across the taxonomic spectrum. Although some differences in central tendency were observed, these were modest relative to the substantial within-group variability. Herbaceous plants, the largest group represented, showed the most negative median response (approximately -7.7%), while trees also tended towards contraction (approximately -3.4%). By contrast, mammals ($+1.9\%$), climbers and vines ($+1.7\%$), and reptiles and insects showed slightly positive median responses. However, these group-level tendencies provide limited predictive value because the range of species responses within each group was considerably larger; among mammals, for example, projected changes extended from -20.7 to $+28.2$ percentage points. Interpretation must also account for the strongly unequal number of species represented in each group, with larger groups supporting more stable summaries and being more likely to capture the full range of responses. In contrast, results for sparsely represented groups are more sensitive to individual species and should be treated cautiously. Overall, taxonomic affiliation alone explains little of the projected trajectory, supporting species-specific rather than taxon-wide prioritisation for IAS surveillance, risk assessment or management.



D5.1 Predicted maps of Invasive Alien Species

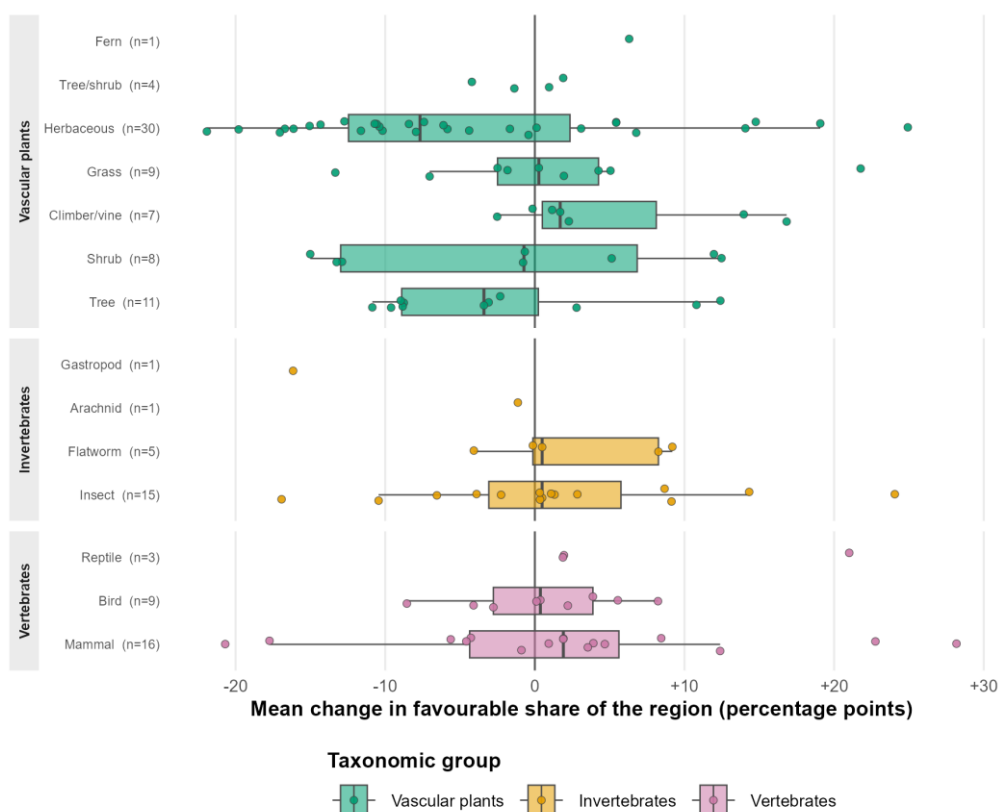


Figure 39 – Distribution of projected change in species' favourable share of the region averaged by period/scenario and displayed by taxonomic grouping. Boxplots are drawn only for groups with at least five species; the remaining groups are shown as individual species. Points show species points. Boxes show the 25th, 50th, and 75th percentiles, and whiskers show the minimum and maximum without outliers.

Country-level projections reveal that 16 of the 27 countries show an increase in the mean share of national area projected to be favourable per species for this set of 120 species (Figure 40). Averaged across the six future combinations, all eight Northern European countries occupy the highest positions in the ranking, led by Denmark (+7.91%), Finland (+7.68%) and Sweden (+7.61%). In contrast, the strongest declines occur mainly in Eastern and Southern Europe, including Hungary (−7.86%), Bulgaria (−7.08%), Croatia (−6.89%) and Italy (−6.33%). This geographical structure is also reflected in the sub-regional medians, which decline progressively from Northern Europe (+5.51%) through Western (+0.85%) and Eastern Europe (−1.79%) to Southern Europe (−3.88%). Overall, the results indicate that the environmental opportunity available to the modelled IAS assemblage is projected to increase towards northern Europe while declining across substantial parts of the south and east.

Country-level results sustain (as expected) the general spatial patterns observed before, with the magnitude of this gradient increasing with both time and forcing levels expressed in the future scenarios for climate and land cover. Differences among scenarios remain comparatively limited at mid-century but become markedly larger by the end of the century, when northern gains and southern losses intensify under the SSP5-8.5 scenario. The direction of change is therefore relatively robust for countries at the geographical extremes, whereas several central European countries, including Germany and Luxembourg, show scenario ranges that cross zero and consequently remain pathway-dependent. This pattern confirms





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that the decline in aggregate European favourability under stronger forcing does not represent a uniform contraction. Rather, it results from increasingly pronounced losses in southern and eastern countries occurring alongside continued or strengthened gains in northern Europe.

National exposure was further evaluated through two complementary dimensions: intensity, defined as the change in mean favourable national area per species, and breadth, defined as the change in the number of species exceeding the national favourability threshold (Figure 41). These dimensions generally covary, with northern countries gaining on both and southern countries tending to lose on both, but important exceptions demonstrate that they should not be reduced to a single indicator. Germany, for example, shows a slight decline in favourability intensity but an increase of approximately 11 species in breadth, indicating that a country may become favourable for more IAS even while the average favourable area per species decreases. Conversely, large changes in favourable area may occur with little corresponding change in the number of species affected. Northern gains and southern losses are broadly robust across both dimensions, while the joint position of several central countries remains sensitive to the scenario considered (Figure 41).

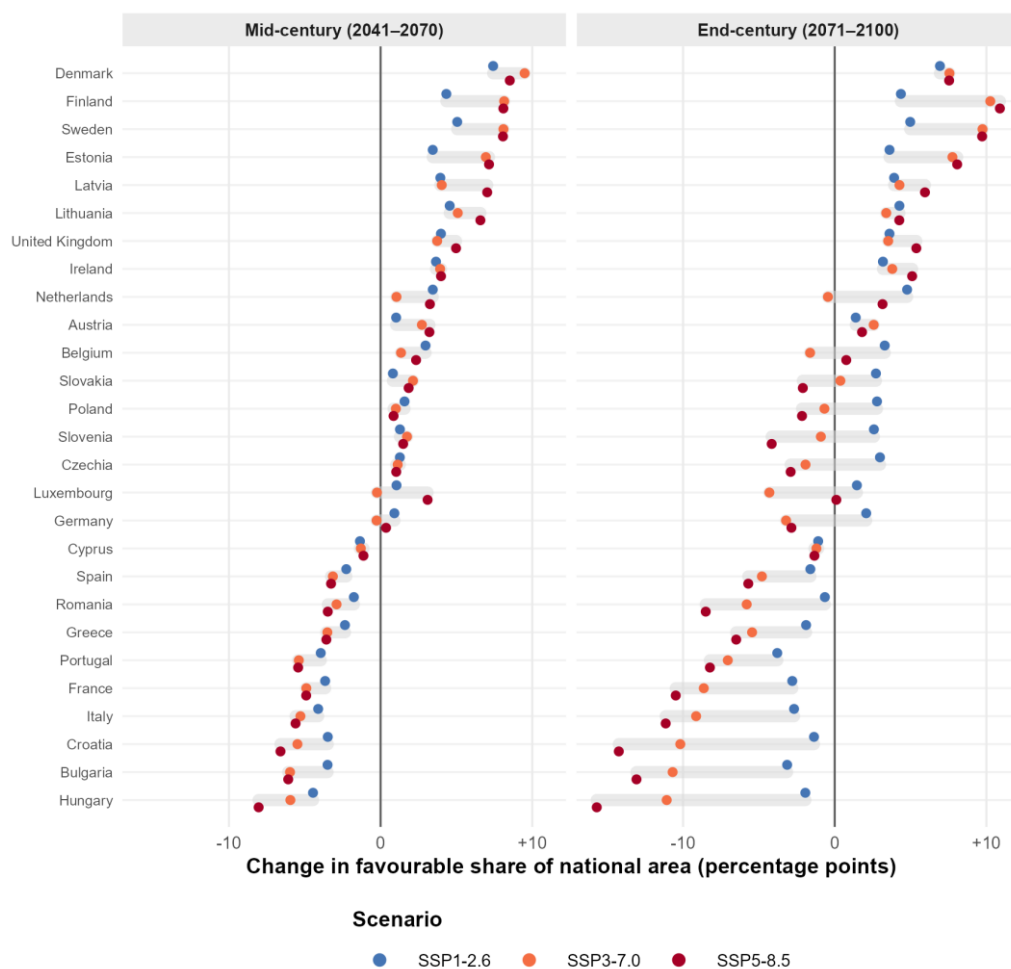


Figure 40 – Projected change across emission scenarios and horizons, showing the variation/spread across scenarios. The grey band spans the three SSPs within each period; points are the individual scenarios averaged for all 120 focal species. Data shown for EU27 + UK, 27 countries (Malta is not included in the projections due to absent land cover data in future scenarios).



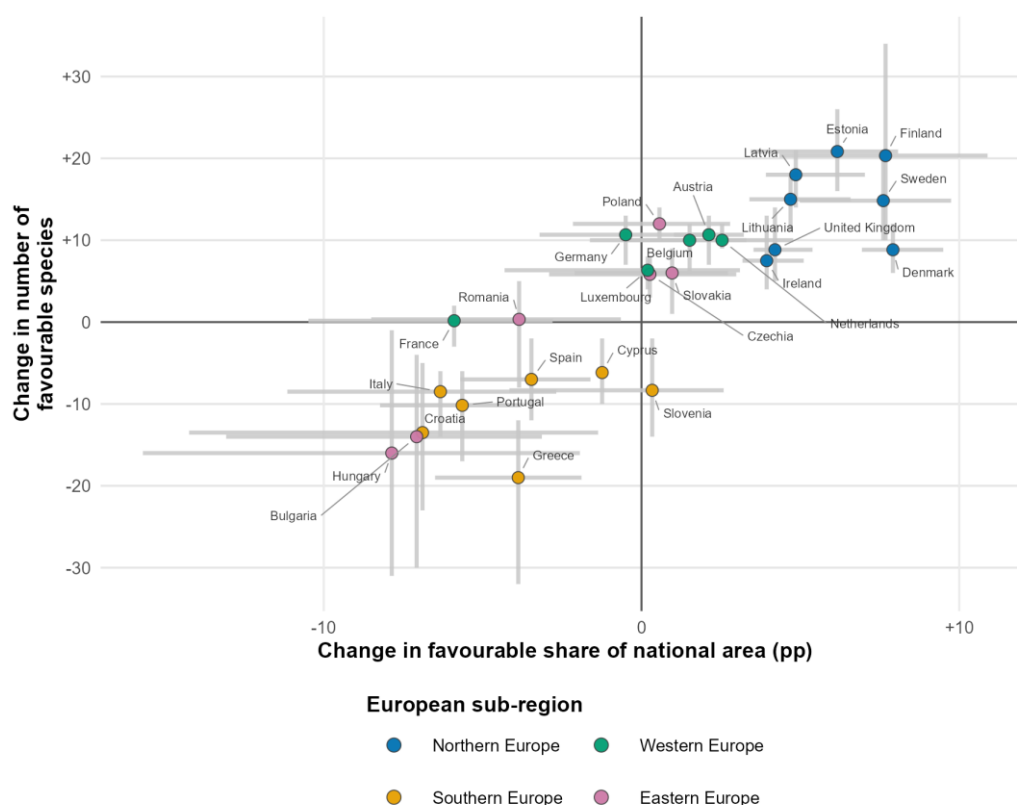


Figure 41 – Biplot showing two dimensions of national exposure to future changes in potential distribution and environmental favourability of IAS. A species counts as favourable in a country at ≥ 1 % of national area, and as effectively absent below 0.1 %. Mean values average the six future combinations (two periods times three SSPs) equally. Favourable area is counted in 1 x 1 km equal-area cells. Data for EU27 + UK, 27 countries (Malta excluded from model projections). Bars represent the range across the six future combinations.

Building on the broader northward redistribution identified in the country-level analysis, transitions in national favourability provide a more operational indication of where new IAS risks may emerge. Species vs country combinations were classified as “emerging” (i.e., species newly given as favourable) when projected favourability increased from less than 0.1% to at least 5% of national area, and as “receding” when the reverse transition occurred (i.e., generalised loss of favourability), thereby avoiding classifications driven by minor fluctuations.

Based on this assessment, 225 “emerging” species-country combinations were identified, compared with 122 “receding” combinations (Figure 42). “Emerging” transitions were also more robust across futures, with 99 occurring in at least four of the six scenario-horizon combinations, compared with only 19 robust “receding” transitions. These emerging combinations involved 49 species across 25 countries and were concentrated particularly in northern and Baltic Europe, with Estonia showing the highest number, whereas Spain showed no emerging transitions and Hungary recorded the largest number of receding combinations. These results therefore reinforce the earlier country-level pattern: future change is characterised not only by an average favourability *for the current IAS of concern* (as defined by inclusion in our focal list) at higher latitudes, but also by the appearance of new species-specific opportunities at distinct geographies.



D5.1 Predicted maps of Invasive Alien Species

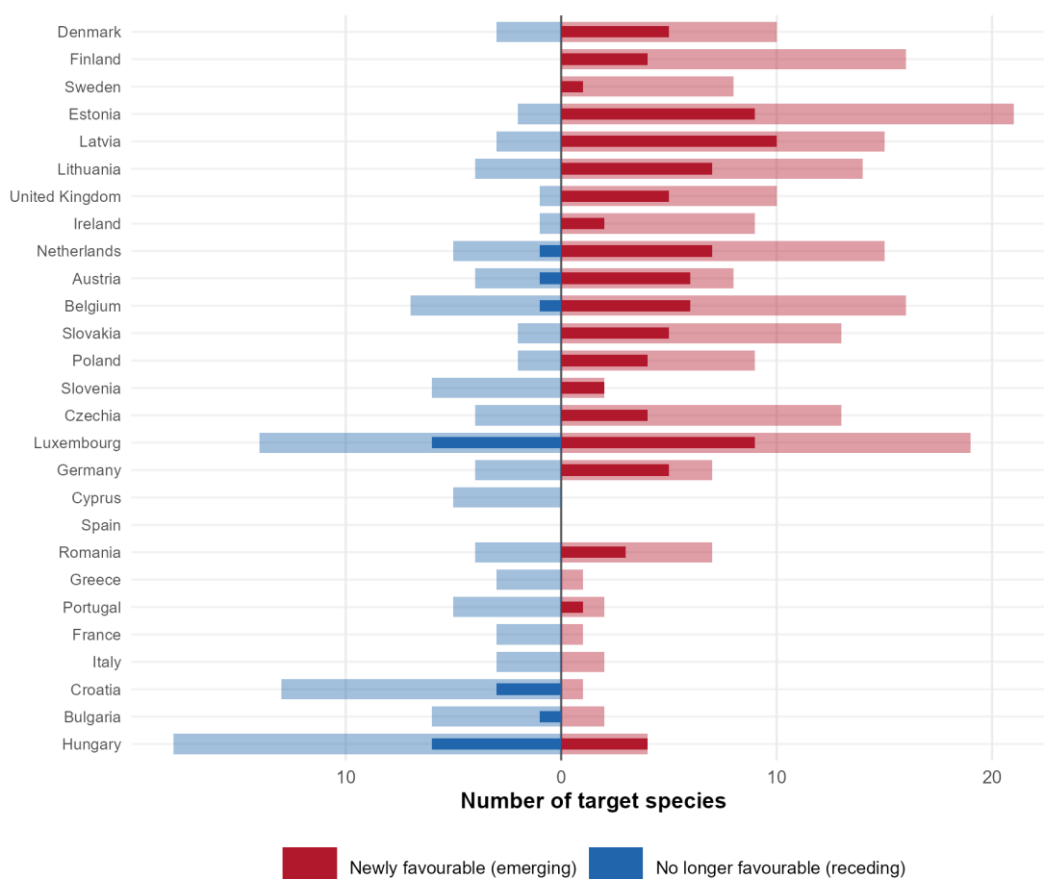


Figure 42 – Bar plot showing projections indicative of newly favourable or no longer favourable species, by country. Pale bars are for any of the six futures, whereas solid inner bars consider species if at least four out of six projection horizons (more robust). Bars left of zero indicate “receding” species, while right are “emerging” ones; both axes count species. Data for EU27 + UK, 27 countries (Malta not intersected by the projections). A species is considered “emergent” (newly favourable) in a country when it moves from below 0.1 % of national area to at least 5 %, and “receding” if the reverse happens. The band between the two thresholds is deliberately wide, so a species drifting either side of a single cut-point cannot be considered as “transitional”.

To assess the correspondence between modelled environmental favourability and documented IAS presence, we compared, for each country, the number of target species projected to have favourable conditions with the number officially reported by EASIN (see details in *Annex 7.4–Supporting Table 7.4*) complemented by GBIF records. The assessment covered 3,240 species–country combinations across 120 species and 27 countries within the EU-27 plus United Kingdom study area, excluding Malta because comparable projections were unavailable for the complete assemblage. Species were classified according to whether they were environmentally favourable and documented by either evidence source, with particular attention given to “unnoticed” combinations, defined here as species favourable across a defined proportion of national territory but absent from both EASIN and GBIF records.

At a 5% national-area threshold (i.e., a species has to cover at least or more than 5% of a country's area to be counted as environmentally favourable, a sufficiency criterion to avoid spuriousness), 552 such combinations were identified for these species, while 23 of the 27 countries contained more environmentally favourable target species than officially registered species. The largest deficits in species recording based on SDM distribution maps vs GBIF/EASIN available record data occurred in Croatia, Luxembourg, Bulgaria and Latvia.





D5.1 Predicted maps of Invasive Alien Species

Overall, 82.2% of EASIN-recorded presences were also supported/corroborated by modelled favourability, although agreement varied substantially among countries (Figure 43 and Figure 44). Future projections further indicated that the gap between the number of EASIN's documented species and favourable species may widen in northern Europe while narrowing in southern and eastern regions.

At country level, the number of species projected to have favourable conditions but are absent from both the EASIN register and GBIF occurrence records is widely variable among countries (Figure 43). Averaged across the four favourability thresholds, the five countries with the largest number of “emerging”/“unrecorded” species are Croatia (45.5±3.9 species, mean ± SE across thresholds), Greece (39.5±6.4), Slovenia (36.5±2.8), Bulgaria (34.8±5.8) and Luxembourg (33.5±0.6). These countries have between three and five times as many environmentally favourable but unrecorded species as the five with the fewest: Germany (11.8±2.0), the United Kingdom (11.0±1.6), Sweden (10.0±1.6), Belgium (9.3±0.3) and Finland (8.8±1.1). At group level, the contrast is 38.0±3.9 against 10.2±1.3 species, a 3.7-fold difference that persists at every threshold tested and is therefore not an artefact of the cut-point. In addition, although the absolute number of flagged species varies with the national-area threshold applied, the relative ranking of countries remains broadly stable across thresholds (Figure 43).

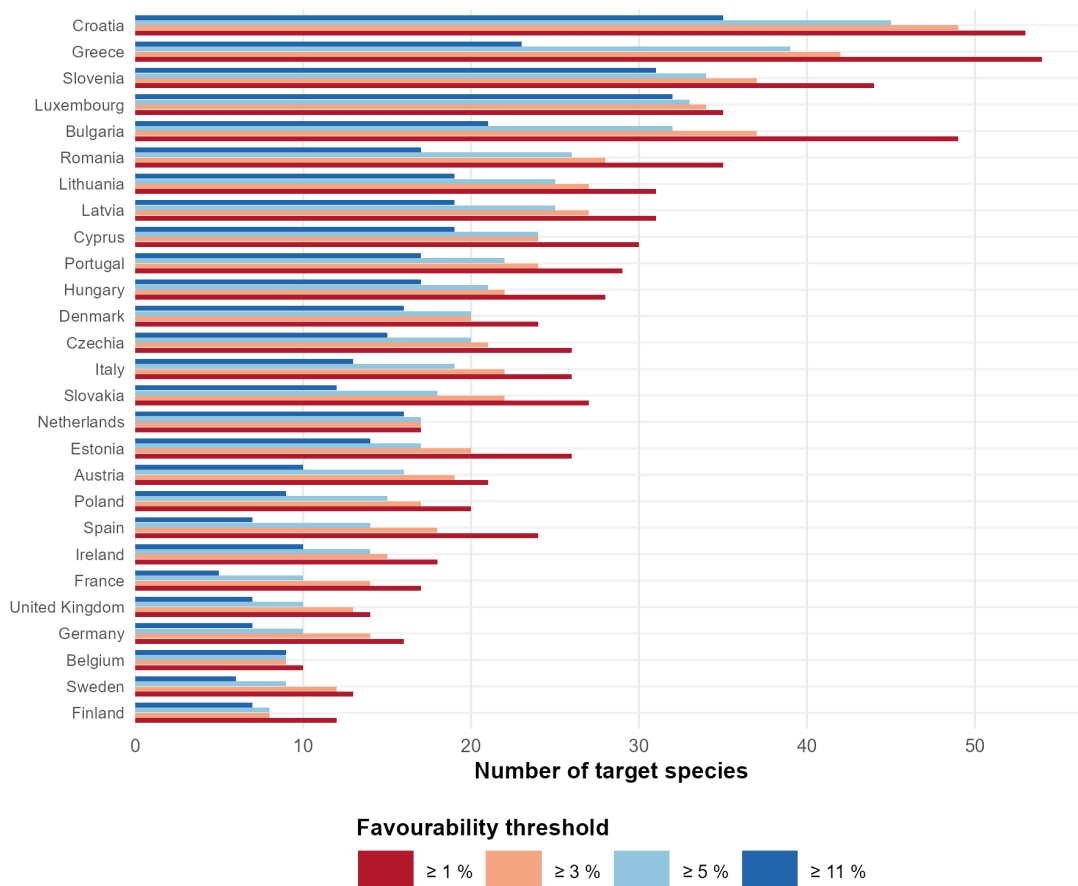


Figure 43 – Bar plot showing the number of species predicted as having favourable conditions at ≥1%, ≥3%, ≥5% and ≥11% of that country's surface area but held by neither EASIN nor GBIF records, by country. The ranking is stable across area thresholds, so which countries carry the largest screen does not depend on the cut-point even though the counts do. Model favourability projections used the 10 % minimum-training-presence binarisation





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criterion; EASIN official presence (EU/EEA/JRC). The geographical scope is EU27 + UK, 27 countries × 120 species = 3,240 pairs (Malta was excluded due to the lack of model projection data). Counts depend on the favourability threshold, so all four (i.e., 1%, 3%, 5%, 11%) are reported throughout. Thresholds 1%, 3% and 5% are arbitrary and 11 % is the one the data themselves select since it maximises the country-mean True Skill Statistic against the EASIN register (TSS = 0.443; sensitivity 0.74, specificity 0.70), and is corroborated independently by Cohen's κ (optimum 10.95 %) and by redefining register presence to include GBIF records (11.02 %).

Consistent with the broader country-level redistribution described above, the comparison between EASIN-recorded presence and modelled environmental favourability reveals substantial geographical variation in the relationship between realised and potential IAS distributions (Figure 44). For each country, the analysis contrasts two independently derived quantities: on the x-axis, the number of target species officially recorded as present in EASIN, and on the y-axis, the number of species projected to encounter favourable conditions across at least 5% of the national territory.

Under baseline conditions, 23 of the 27 countries contain more environmentally favourable target species than EASIN-recorded species. This pattern indicates that further reinforces that many countries may provide suitable environmental conditions for a broader set of IAS than is currently known to occur there. Differences between the two counts may reflect a wide array of socio-ecological dynamics, including species that have not yet arrived, insufficient propagule pressure, dispersal or establishment constraints, effective management, biotic interactions, or overprediction and other inherent limitations of the data and the models. Conversely, countries with more recorded than favourable species also require cautious interpretation of such patterns. Possible explanations may include established or transient populations persisting outside the modelled environmental envelope estimated by SDMs, locally favourable conditions not captured by the predictors, lack of specific predictors, data limitations, model omissions, and threshold-related effects.

The percentage reported for each country provides an additional measure of baseline corroboration (i.e., percentages enclosed in parentheses in Figure 44), calculated as the proportion of EASIN-recorded species that are also projected to experience favourable conditions. This indicator expresses the degree of agreement between the two sources but should not be interpreted as model accuracy, because verified absence data are unavailable and EASIN presence may include populations with different establishment status. The projections reinforce the previously identified geographical pattern. By end-century, in 2071–2100 projections and particularly under stronger forcing, the number of environmentally favourable species generally increases in northern and Baltic countries, including Estonia, Latvia, Lithuania and Finland, while decreasing across several southern countries, including Croatia, Italy, Spain and Greece.



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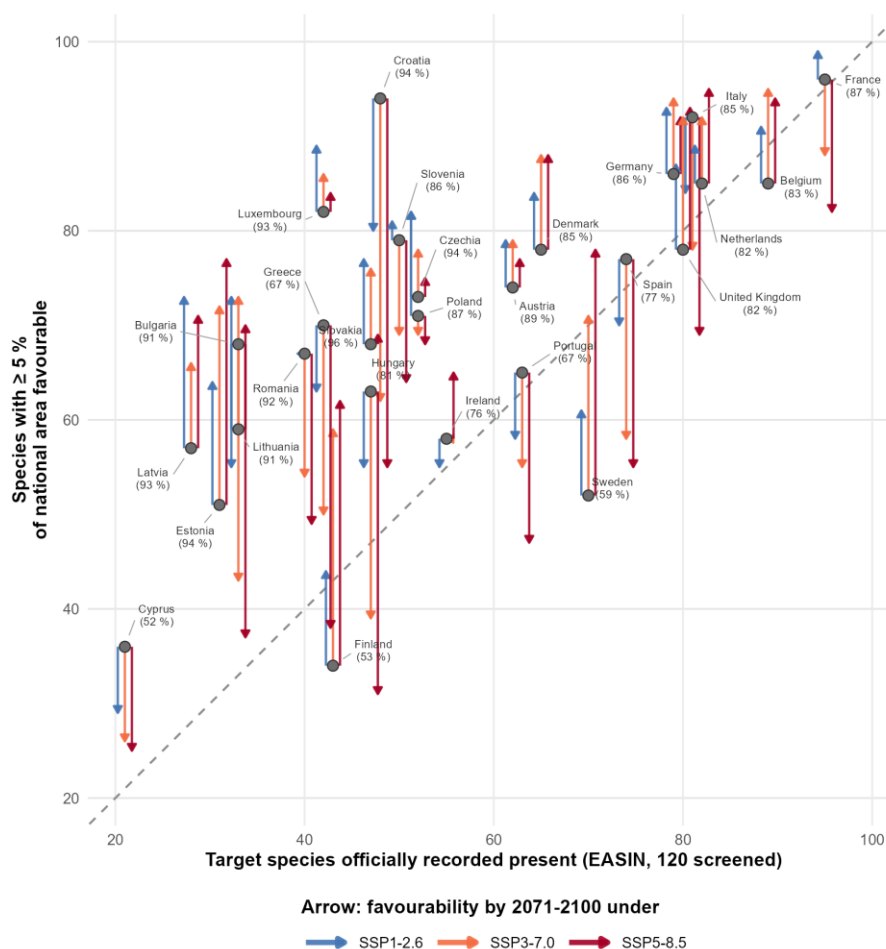


Figure 44 – Number of species officially recorded (in EASIN) against environmentally favourable, by country. Above the dashed 1:1 line, more target species are environmentally favourable than the records hold. The figure in parentheses is the share of each country's registered species the model also finds favourable (i.e., number of corroborated species if the area of distribution is $\geq 5\%$ of national area; corroboration = $100 \times (\text{favourable and registered}) / (\text{registered})$). The three arrows per country show the projection in number of species with $\geq 5\%$ of favourable national area (for 2071-2100 under each future scenario). The horizontal axis is static since EASIN records have no time dimension, so a country's documentation is the same under every future scenario and in every panel. The geographic scope is EU27 + UK, 27 countries $\times$ 120 target species = 3,240 pairs. Malta is excluded due to lack of data/SDM projections.

Taken together, the comparison between SDM-derived environmental favourability and EASIN country-level records provides a consistent basis for identifying regions where targeted surveillance/monitoring, horizon scanning and data mobilisation may warrant greater priority under both current and future scenarios. The projected patterns suggest a potential redistribution of favourable conditions, including a broader northward shift for the 120 target IAS, but should not be interpreted as direct forecasts of future occurrence. In particular, species-country combinations for which favourable conditions are projected in the absence of a corresponding EASIN presence record may serve as “operational early-warning signals”, indicating where establishment could become environmentally plausible and where additional monitoring or record validation may be additionally justifiable. However, such mismatches do not constitute evidence of undetected invasions, reporting failures or confirmed absence, because both SDMs and occurrence databases are affected by important limitations. SDMs estimate potential environmental favourability without fully representing important ecological





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mechanisms, propagule pressure, dispersal constraints, biotic interactions, management responses and other socio-ecological determinants of realised distributions. In turn, absent database records may reflect incomplete detection, uneven reporting or delayed data mobilisation. These outputs should therefore be interpreted cautiously as a prioritisation and a potential governance-support tool rather than as definitive evidence of current or future IAS presence.





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3.3.3. Species Distribution Models Map Gallery

The SDM IAS Map Gallery (GitHub repository URL: https://github.com/OneSTOP-CIBIO/OneSTOP_SDM_Map_Gallery; v0.1.0 DOI: 10.5281/zenodo.21852671; Gallery URL: https://onestop-cibio.github.io/OneSTOP_SDM_Map_Gallery/) developed for the OneSTOP Task 5.1 project is conceived as a lightweight, transparent and reproducible dissemination interface for visualising potential distribution maps of invasive alien species. Its primary intent is to provide project partners and external users with a structured, early visual access point to static map outputs, enabling comparative inspection across species, time periods, and socio-climatic scenarios without requiring GIS software or access to the underlying modelling environment.

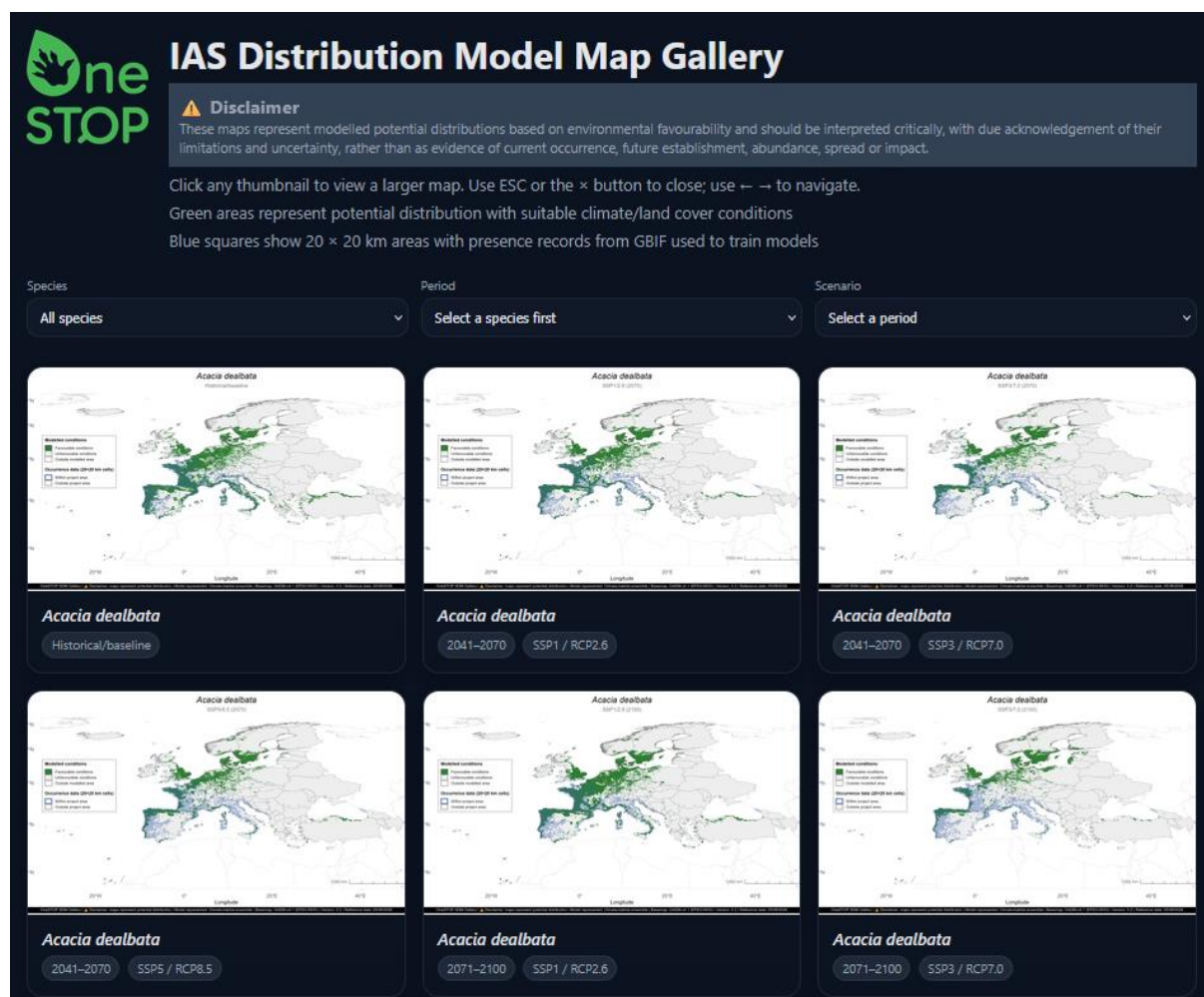


Figure 45 – Print screen of OneSTOP's SDM gallery in GitHub Pages.

The gallery is deliberately designed as a static web product (Figure 45 and Figure 46). It is served through GitHub Pages and consists of a generated index.html file, a curated image directory containing final PNG maps, and the relevant OneSTOP and EU branding assets. This architecture avoids dependence on an application server, a database, a webGIS backend, or server-side map rendering. As a result, the system is technically simple, portable and robust, with all the metadata, styling and browser-side behaviour embedded in the



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generated HTML, while the map images are accessed as ordinary static files. This design choice also clearly separates the gallery from the upstream analytical workflow since the gallery does not generate, transform or interpret species distribution models, but publishes already prepared cartographic outputs for visual exploration. The gallery follows general principles of content accessibility, consistency and controlled interpretation (see more details in Annex 7.6–*SDM Map Gallery full description*).

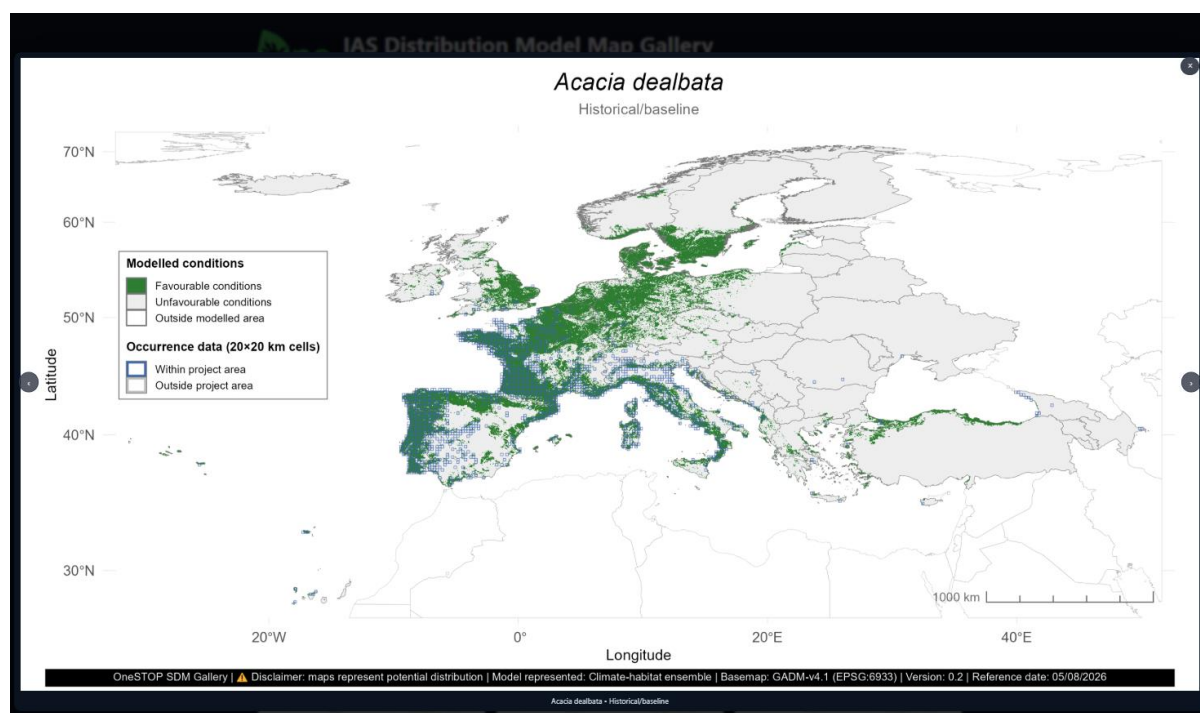


Figure 46 – Web page modal showing *Acacia dealbata* potential distribution for historical/baseline conditions.

The main user-facing functionalities comprise an initially visible grid of map cards with ‘lazy-loaded’ thumbnails, species-based filtering, period filtering, scenario filtering for future periods, chronological and scenario-aware sorting, and a full-size lightbox view with mouse and keyboard navigation. Additional interface elements include a scroll-to-top control, italicised species links to GBIF searches, and OneSTOP/EU visual identity in the page header and footer. The system is intentionally not an interactive webGIS. Due to this design decision, users cannot pan, zoom, query raster cells or toggle spatial layers. This constraint is a core design principle, ensuring that the gallery remains a controlled visualisation tool rather than an analytical platform. The maps should therefore be interpreted as preliminary visual research outputs showcasing IAS potential distributions based on environmental favourability and not as validated evidence for quantitative risk assessment, management decisions or local-scale intervention planning.





3.4. Limitations and uncertainty in introduction-pathway analyses and SDM-based assessments of current and future IAS risk

Species Distribution Models (SDMs) provide a spatially explicit means of relating species occurrence records to environmental conditions and are therefore central to the OneSTOP assessment of the current and potential future distributions of invasive alien species (IAS). Within Work Package (WP) 5, these outputs are intended to inform several interconnected activities, including horizon scanning, species and pathway prioritisation, assessment of risks to European Red List species, and the communication of spatial priorities to practitioners and decision-makers. OneSTOP project design recognises that model outputs must be combined with detection data, pathway information, impact evidence, expert assessment and stakeholder knowledge rather than treated as self-contained predictions of invasion risk. The limitations discussed below should therefore be understood as conditions governing the interpretation and appropriate use of the model results, rather than as reasons to disregard them. Uncertainty arises at multiple stages and stems from multiple sources, including the collection and processing of occurrence records, selection and spatial resolution of environmental predictors, model specification and evaluation, construction of climate and land-cover scenarios, and transfer of fitted relationships to future or otherwise novel environmental conditions. These sources of uncertainty may interact and propagate through the modelling chain. Consequently, the outputs are most appropriately interpreted as conditional, scenario-based estimates of environmental favourability and potential distribution, rather than deterministic forecasts of future occurrence, abundance, spread or impact.

Limitations in the spatial assessment of introduction pathways

The introduction-pathway assessment conducted in this deliverable identified important patterns in pathway frequency, co-occurrence, multiplicity and temporal development. However, the available information was generally sufficient to characterise which pathways are associated with species introductions, but not consistently where, when or at what intensity those pathways operate. This prevented the production of a coherent, spatially explicit assessment of introduction mechanisms and pressures across Europe.

This distinction is important because introduction pathways are not only categorical mechanisms. Their contribution to invasion risk largely depends on details such as the number of introduction events, the number and condition of propagules transported, the geographical connectivity of origins and destinations, and the temporal frequency and intensity of movement. Propagule pressure is consistently associated with establishment success, but direct observations of propagule arrivals are uncommon; pathway studies must therefore frequently rely on indirect indicators, some of which may be weakly validated or may represent only selected aspects of the underlying process.

Certain pathway components can be represented relatively readily based on pre-existing spatial datasets. The location of roads, railways, waterways, airports and maritime ports, for example, can be mapped from existing geospatial data (e.g., Open Street Map). Nevertheless, the presence of infrastructure alone does not quantify the intensity or biological relevance of the corresponding pathway. Road length cannot substitute directly for vehicle flow; proximity to a port does not describe vessel origin, cargo type, ballast-water discharge, container movements or commodity volume; and the location of a railway does not reveal the frequency,





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direction or composition of transported materials. Similarly, the pathways associated with horticulture, the pet trade, contaminated commodities and intentional or accidental release would require information on nurseries, garden centres, pet retailers, e-commerce transactions, distribution warehouses, private gardens, waste-disposal sites and release events. Such information is currently fragmented across countries, administrative levels and sectors, unevenly accessible, temporally inconsistent and, in some cases, commercially sensitive.

The gap is particularly relevant to OneSTOP because Task 5.1 originally envisaged complementing environmental models with pathway-related variables to derive spatial estimates of potential propagule pressure. In practice, the absence of integrated and comparable data at European scale constrained the implementation of these analyses. The resulting SDMs address the environmental component of establishment risk primarily by indicating where conditions could support a species if it arrives; however, they do not estimate the probability that it will be transported to or released at a particular location.

Land cover can provide a partial proxy for some pathway processes. Urban and peri-urban areas may be associated with horticultural trade, pet ownership and transport activity; croplands may indicate exposure to contaminated seed or agricultural commodities; and transport corridors may be associated with disturbed habitats that facilitate establishment and secondary spread. However, these relationships are neither universal nor sufficiently specific to reconstruct individual introduction mechanisms.

Automated modelling across large sets of IAS

The modelling of large numbers of species at continental extent and at 1×1km resolution is computationally and analytically demanding. Semi-automated workflows are therefore necessary to achieve a consistent, transparent and reproducible assessment across the OneSTOP target species list. The wiSDM framework (and later adaptations under OneSTOP Task 5.1) was developed to facilitate open and reproducible IAS risk mapping by harmonising climate and land-cover data, mitigating aspects of spatial sampling bias, screening correlated predictors and producing ensemble hierarchical projections at a 1-km resolution.

Nevertheless, automation necessarily standardises decisions that may ideally differ among species. Species vary in their environmental requirements and niches, dispersal capacity, life history, detectability, habitat specialisation, and invasion stage, all of which limit their distributions. A common workflow cannot fully accommodate this ecological diversity without becoming prohibitively complex.

Automated SDMs inevitably involve methodological and ecological simplifications that can affect model performance and transferability. Standardised predictor screening, pseudo-absence selection, model complexity, regularisation, weighting and classification thresholds may not be optimal for every species, while differences among algorithms and parameter settings can substantially influence projected distributions and may lead to overfitting, oversmoothing or unstable extrapolation.

Several complementary approaches can be used to augment ecological realism, including dynamic occupancy models, joint SDMs, dispersal simulations, demographic models and process-based or mechanistic models. However, these methods require substantially more detailed and taxonomically consistent data for species. Their implementation for hundreds of





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taxa across Europe at 1-km resolution would also involve a substantial increase in computational demand, parameter uncertainty and model-specific development.

A proportionate response is therefore preferable to attempting full biological complexity for every species. The automated workflow can serve as a standardised first-tier assessment, while species associated with poor data coverage, weak evaluation, strong extrapolation, substantial policy relevance or contradictory model behaviour can be selected for targeted/detailed modelling and assessment. Such review may include ecologically informed predictor selection, improved model specification, additional hyperparameter tuning, alternative pseudo-absence generation strategies, comparison of dispersal assumptions and consultation with taxonomic or invasion experts.

This tiered structure is well-aligned with OneSTOP's wider approach. Automated outputs provide the breadth required for continental prioritisation, whereas expert evaluation, Living Lab testing and targeted surveillance supply depth for species and locations requiring more detailed consideration. Automation should therefore be understood as a means of achieving consistency and scalability, not as a substitute for ecological judgement.

Limitations, gaps and biases in input occurrence data from GBIF

GBIF provides an indispensable infrastructure for mobilising and integrating biodiversity observations from museums, herbaria, research projects, monitoring schemes and citizen-science platforms. Its global extent was essential for constructing models for all OneSTOP target species, particularly because records from native ranges can provide information on the environmental niche that may not yet be expressed in the invaded European part of the range. OneSTOP also identifies GBIF as a central infrastructure for the publication and mobilisation of new detection data and for connecting data products with EASIN and other European systems. Moreover, GBIF also provides substantial benefits for reproducibility and the implementation of FAIR data principles, as its occurrence data are fully citable, traceable and linked to persistent provenance information.

However, GBIF-mediated data are not generated through a single, statistically designed survey. Occurrence records' quantity and properties differ markedly across countries, taxa, time periods and environments. Well-surveyed and easily accessible localities, urban areas, protected areas and regions with active recording communities may be strongly overrepresented. Charismatic, conspicuous and readily identifiable taxa generally receive more attention than small, cryptic or taxonomically difficult groups.

This assessment (see details in section 3.2.1–*Species occurrence data*) quantifies these constraints directly. Although all target species had sufficient global data for climate-model calibration, only 86 species were classed as well supported by European SDM-ready records. Eight were modellable with caution, seven were marginal and 19 had insufficient data; 26 species fell below the guide value of 30 unique occupied 1-km cells. Five species had no European occurrence satisfying the full quality, spatial-precision and deduplication criteria. Data limitations were disproportionately concentrated among invertebrates, particularly insects. Overall, these gaps propagated into model availability. The stricter requirements of the European land-cover component limited the combined models to 96 species, leaving 24 represented by global climate-only models. The absence of a habitat component does not necessarily imply a complete absence of European records since it can also reflect inadequate





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spatial variation, clustered observations, weak model performance or insufficient data for robust evaluation.

Raw record volume was also an unreliable measure of effective model information. Several species had large numbers of records concentrated in comparatively few unique 1-km cells, demonstrating that repeated observations from the same localities do not necessarily broaden environmental or geographical representation. These differences partly reflect real variation in IAS distributions, but also monitoring intensity, reporting capacity, citizen-science activity and data mobilisation. No single correction can remove all these limitations in occurrence data from heterogeneous sources such as GBIF. The preferred response is a combination of complementary measures, many of which are already implemented in the wiSDM 2.0 modelling pipeline.

Data integration is equally important. GBIF records should ideally be complemented, where available, by national surveillance or other targeted or species-specific datasets, EASIN and GRIIS information, systematic surveys, museum and herbarium datasets/collections not yet mobilised, verified citizen-science observations and expert-derived distribution information.

Uncertainty and error propagation in future projections

Model projections considering future scenarios combine uncertainty originating from several distinct systems, data, processes and algorithms. These sources do not combine through a simple additive process, nor is the magnitude of each component easily addressable or quantifiable. Their interactions can amplify, compensate for or redirect projected change. A model fitted to a geographically or environmentally truncated invaded range may underestimate the species' climatic tolerance. A small difference among GCMs may have little effect in the central portion of a response curve but produce a large difference near a threshold or close to niche boundary conditions. Land-cover change may reduce habitat in a region becoming climatically more favourable or create habitat in an area that remains inaccessible. As a result, similar aggregate estimates of potential range area may conceal markedly different spatial and temporal trajectories.

Transferability represents one of the most consequential uncertainties. SDMs assume that the fitted species–environment relationship remains sufficiently stable when transferred to another region or period (i.e., niche conservatism). This assumption may be weakened by niche unfilling in invaded ranges, adaptation, altered biotic interactions, changes in the availability and correlation structure of predictors, and non-analogue environmental conditions. Extrapolation is especially problematic where future predictor values fall outside the range used for calibration or where familiar values occur in novel combinations. Under such conditions, models are required to infer responses without direct observational support, and different algorithms may extrapolate in contrasting ways.

Future climate and land-cover scenarios should also be interpreted correctly. SSP–RCP scenario combinations describe internally coherent trajectories of socioeconomic development and radiative forcing; however, they are not assigned probabilities within the present assessment. Differences among scenarios indicate how IAS favourability could respond under alternative futures rather than which future is expected to occur, given the progression of present-day conditions and trajectory. Likewise, the differences between baseline and future model outputs represent conditional changes in environmental favourability, not direct forecasts of distributional change.





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For policy and management, the most defensible use of the projections is thus to guide prioritisation in a robust way rather than deterministic prediction. Locations that remain favourable across algorithms, periods and scenarios may justify sustained surveillance or preventive planning or reinforced measures. Areas with high favourability but no official occurrence record may indicate priorities for verification, targeted monitoring or data mobilisation, but do not demonstrate an unreported invasion. Conversely, regions characterised by strong model disagreement may be priorities for additional data collection rather than immediate intervention.

Overall value and appropriate use of the OneSTOP SDM outputs

The limitations described above define boundaries on the inferences that can be derived from SDMs; however, these do not negate their value for IAS management, policy, risk assessment or prioritisation. In Task 5.1, a total of 120 IAS were analysed across global and European extents at 1-km resolution for which fully mechanistic and individually customised models would not be feasible for the complete species set. As such, semi-automatic, standardised SDMs remain one of the few methods capable of synthesising the available occurrence, climate and land-cover information consistently across this breadth of taxa, geography and environmental scenarios.

Their principal strength lies in comparative and strategic assessment. They can identify broad geographical gradients, identify hotspots of environmental favourability and potential species richness, regions where future conditions may become more or less suitable, species that show contrasting trajectories, and locations where modelled favourability and recorded distributions diverge. These outputs provide a quantitative basis for horizon scanning, surveillance design, prioritisation of data mobilisation, selection of species for more detailed assessment, and evaluation of potential pressures on Red List species. As such, SDM outputs like the ones generated in Task 5.1 can be regarded as hypotheses to be tested and updated through additional observations rather than as final representations of species distributions.

This interpretation fits into the OneSTOP project design and overarching aims. Model outputs are embedded within a wider system that combines improved detection with novel systems and tools, FAIR data mobilisation, EASIN and GBIF integration, impact assessment, pathway analysis, expert validation, Living Lab experimentation and co-designed decision tools. New detections can expose model omissions, model outputs can direct surveillance towards poorly sampled or environmentally favourable regions, and the resulting observations can be incorporated into subsequent model updates. Uncertainty therefore becomes part of an iterative evidence and model improvement or refinement cycle rather than a static deficiency. This limitation should be explicitly recognised, transparently communicated, and incorporated into subsequent prioritisation, data reuse, and decision-making processes, so that model outputs are interpreted in proportion to their underlying evidence, assumptions, and uncertainty rather than treated as definitive estimates of IAS occurrence or risk.

Used in this way, the OneSTOP SDMs provide a transparent, reproducible and updatable approximation of current and potential future IAS dynamics. They cannot determine with certainty where an invasion will occur or what its consequences will be, but they substantially improve the capacity to organise incomplete evidence, compare plausible trajectories, identify emerging spatial priorities and direct limited monitoring and management resources. Their greatest value lies not in eliminating uncertainty, but in making environmental risks, evidence gaps and alternative futures more explicit and therefore more actionable.





4. Conclusions, evidence-based recommendations and future work

For a target list of 120 terrestrial invasive alien species (IAS) of European relevance, this deliverable reports three linked assessments: (i) the characterisation of introduction pathways from EASIN–CBD records; (ii) the sufficiency and adequacy of available occurrence data for distribution modelling; and (iii) the projection of species potential distribution and environmental favourability under baseline conditions and alternative climate and land-cover futures. Together these define the analytical sequence implemented in Task 5.1, from evidence base and pre-existing data to scenario-based projection.

The pathway assessment shows that introduction is rarely a single-route phenomenon. Across 426 deduplicated EASIN/CBD records, target species carried a median of three pathways each and only 14% a single one, with escape from confinement recorded for 72% of species and resolving into a connected complex of ornamental, horticultural, botanic-garden and pet-trade activities. Co-occurrence patterns, derived empirically rather than assumed a priori, separate these pathways into a “cultivation-and-release” cluster and an “accidental-transport” cluster with clear taxonomic signatures. The “escape and release” dominates among plants and vertebrates, while the “contaminant and stowaway transport” dominates among invertebrates. These results indicate that prevention measures designed around a single pathway will address most species only partially.

The initial descriptive assessment of model inputs identifies where GBIF occurrence data, despite its volume, especially at a global extent, exhibits deficiencies and limitations. Although all 120 species carry sufficient global occurrence data for climate-model calibration, only 94 meet the stricter quality, precision and deduplication criteria required for European habitat/land cover modelling. In addition, 219 of 1,514 EASIN-documented species–country presences (14.5%) hold no fit-for-purpose GBIF record at all. These recording deficits are structured rather than random, concentrating in invertebrates, in the Mediterranean and Baltic Member States, and in species officially reported as present that nonetheless lack the records needed to calibrate European-extent models and thus to characterise the invaded portion of their range. Data sufficiency deteriorates further at national level, and not only in data-poor states: while roughly half of EASIN documented species–country presences meet the ≥ 30 -cell guide value (often used for SDM development), the absolute shortfall is largest where recording effort is greatest, with France, the United Kingdom and the Netherlands each retaining substantial “unmodellable” fractions. Record volume (i.e., number of “raw” records) is therefore a poor proxy for modelling support since, as counts rise, additional observations accumulate disproportionately in already-sampled 1-km cells, the units on which model calibration depends.

Despite this assessment and highly variable levels of data support for describing the native and invaded ranges, predicted distribution maps were nonetheless delivered for the complete 120 OneSTOP species list defined for Task 5.1. Ensemble climate–habitat models were calibrated for 96 species and climate-only models for the remaining 24, with spatially cross-validated performance in the good-to-excellent range (median ensemble AUC ≈ 0.88) and consistent, statistically significant gains of the ensemble over its constituent climate- and habitat-only sub-models. Baseline projections and six future combinations (2041–2070 and





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2071–2100 under SSP1-2.6, SSP3-7.0 and SSP5-8.5) are accompanied by inter-algorithm agreement layers, response curves and variable-importance diagnostics, and are disseminated openly through the OneSTOP SDM Map Gallery.

The model projections describe a generalised IAS redistribution across Europe rather than a uniform change in pressure and overlap. At least one target species finds favourable conditions across 97.5% of the modelled area, with baseline hotspots concentrated in western and central Europe. Under future scenarios, favourability moves consistently northwards and upslope, with 16 out of 27 countries gaining species or environmental favourability, led by Denmark, Finland and Sweden, while, in contrast, Hungary, Bulgaria, Croatia and Italy record the steepest declines. Overall, 50 species expand, and 43 contract across all six futures, and stronger forcing polarises rather than shifts the assemblage, with species showing little change falling from 33 to 13 by end-century. Critically, 23% of species reverse the direction of change between mitigation and high-forcing pathways, so any result reported without its projection scenario and horizon risks carrying the wrong sign. Taxonomic affiliation explains little of this variation, supporting species-specific rather than taxon-wide prioritisation and detailed assessment.

Finally, the confrontation of modelled favourability with documented presence yields an operational screen highlighting 225 emerging species–country combinations, and 552 combinations favourable across at least 5% of national territory yet absent from both EASIN and GBIF, concentrated in countries such as Croatia, Greece, Slovenia, Bulgaria and Luxembourg.

It is key to note that these outputs describe environmental favourability or opportunity, not occupancy, establishment or inevitable arrival, and gains in favourability are more robust guides to action than losses, which do not imply that established populations will disappear. Read with these interpretative constraints in mind, the outputs provide a defensible and reproducible basis for surveillance targeting, horizon scanning and precautionary prioritisation across Europe.

Recommendations for policy, prioritisation and future project developments

Building on the results presented in this deliverable report, the following high-level recommendations are proposed to support prioritisation, risk assessment, surveillance and prevention of terrestrial IAS at European level, and to guide the uptake of Task 5.1 outputs in subsequent OneSTOP tasks:

- i. **Develop a multi-level, tiered risk-assessment workflow.** Semi-automated continental species distribution models are well suited to serve as a reproducible first-tier screen, with low data requirements and cost, and updatable as new data become available. Their function at this tier is not directly to determine risk, but to rank or identify species and species–country combinations that can be targeted or prioritised for closer examination or data mobilisation. Detailed assessment should then follow transparent criteria, several of which are already available from the assessment and modelling outputs: (i) insufficient occurrence data to support European calibration; (ii) projection into environmental conditions poorly represented in the training data; (iii) a reversal in the direction of projected change between emissions pathways; (iv) substantial





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projected expansion of favourable area; and (v) the emergence of new species–country combinations. To these should be added criteria external to the models, notably documented impact, management feasibility and relevance to obligations under Regulation (EU) 1143/2014. Expert assessment and Living Lab review also retain an essential role here, but should be directed by this screening rather than duplicate it, concentrating expert effort on the cases the first tier flags as relevant or uncertain.

- ii. **Develop and implement preventive measures through integrated pathway management.** Because most species use several pathways, isolated interventions will likely underperform at containing them or reducing their pressure or intensity. Measures should pair controls on intentional-use pathways (such as horticulture, ornamentals, or the pet trade) with biosecurity measures for contaminants and stowaways on commodities and in transport. These measures should also progressively incorporate spatial and temporal indicators of trade, transport and propagule pressure, and aim to link environmental favourability to likelihood of introduction. Coordinated mobilisation and harmonisation of spatial data on pathway-associated activities and infrastructure (e.g., horticultural and ornamental production, the pet and aquarium trade, ports, transport corridors, and logistics hubs) are required and should be prioritised to derive continental indicators and spatially explicit estimates of introduction likelihood and potential propagule pressure associated with these routes.
- iii. **Treat data gaps on species occurrence as explicit surveillance and investment priorities.** The evidence assembled in this deliverable report shows that these gaps are structured rather than incidental. Gaps concentrate in under-recorded invertebrates, in species lacking “modelling-ready” records for Europe, and in countries where documented EASIN presence is unsupported or poorly supported by fit-for-purpose GBIF evidence (namely 14.5% of species–country presences for which no such record exists). Addressing this requires more than the further mobilisation of existing records. IAS should be explicitly included within European biodiversity and species monitoring programmes rather than treated as a by-product of general biodiversity recording or left to opportunistic reporting. Existing frameworks, including monitoring under the Habitats and Birds Directives, the forthcoming Biodiversity Monitoring Coordination Centre conceived by EuropaBON, and national schemes established under Regulation (EU) 1143/2014, should aim to explicitly provide for IAS data/evidence, with harmonised protocols, sustained funding and defined reporting obligations. Alongside this, dedicated surveys should be designed for priority species and regions, using spatially structured sampling rather than relying solely on opportunistic recording. Such designs should aim to deliver not only presence but also the abundance, density and site-level attributes needed to characterise establishment status, population trends and impact. In addition, sampling effort should be allocated to maximise spatial and environmental novelty and complementarity rather than to increase record volume in already well-covered cells or regions, giving priority to under-sampled Member States, environmental gradients poorly represented in existing data, and the less known invaded portion of species' ranges that models can inform.





- iv. **Plan for IAS ranges and assembly redistribution, not uniform change.** Rising environmental favourability in northern Europe, the Baltic region and higher elevations warrants strengthened, cross-border horizon scanning, targeted monitoring and overall preparedness. These potential early-warning signals emerging from model-assisted assessments can therefore inform prioritisation at two levels. First, geographically, by directing surveillance and preparedness towards countries and regions where new species–country combinations are projected to emerge. Second, taxonomically, by identifying species that warrant detailed assessment or strengthened management and monitoring. Their value lies in anticipating where attention may be required, not in confirming that arrival or establishment will occur. Mechanistic and advanced dispersal-based spread models and simulations would complement the correlative approach applied here by incorporating demographic processes, dispersal constraints, and propagule pressure that determine whether favourable conditions are actually realised. On the other hand, projected declines in southern and eastern Europe must not trigger automatic relaxation of management or control for established populations. Current surveillance and management efforts should be maintained, with resources reallocated progressively as monitoring evidence confirms or contradicts the projected changes. Moreover, EU-wide and national strategies on IAS should weigh both the intensity of change and the identity of species affected. At European level, prioritisation and surveillance efforts should likewise maintain taxonomic and biogeographical coverage in balance with projected redistribution, rather than concentrating on regions of current potential richness alone.
- v. **Foster and embed SDM outputs in an adaptive biosecurity evidence-based system.** Task 5.1 outputs already provide screening and prioritisation triggers rather than stand-alone risk estimates. The added value of this task lies in identifying where further attention is most justified, where targets can be set, as well as defining supported criteria for prioritisation. These include species projected to undergo large or scenario-sensitive changes in environmental favourability, species–country combinations emerging as newly suitable, areas of increasing potential richness, and cases where model reliability is constrained by sparse, incomplete, or biased data, as well as potential model extrapolation. Within OneSTOP, these outputs should define transparent triggers for follow-up, including targeted surveillance, species-specific assessment, expert review, and stakeholder validation through the living labs. Knowing the boundaries of this assessment is also critically important as models projected favourability demonstrate neither arrival, establishment, nor impact, and projected contractions do not license relaxed management of established populations. Used in this way, the assessment supports the selection of species and places for deeper examination, exposes data and knowledge gaps, and directs the project's detection and validation capacity to where it most efficiently reduces uncertainty. Used in this way, this integration would convert the present static assessment into an adaptive cycle of data mobilisation, modelling, taxonomic/geographical prioritisation, targeted detection, verification, model updating, and management responses that continuously (re-) align. This closely matches both OneSTOP's design and IPBES recommendations for integrated, evidence-based, information-rich, participatory and anticipatory governance of biological invasions.





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D5.1 Predicted maps of Invasive Alien Species

7. Annexes / supplementary information

7.1. Complete list of selected species and calculated indicators

Supporting Table 7.1 – Full list of selected species, taxonomic framing and calculated indicators based on GBIF downloaded data (with reference DOIs). The ‘Living Lab country’ column identifies if a species was flagged by a specific LL. The remaining unfilled/blank rows are for species that pertain to the EU list of concern (plus candidate species) subset. The number of records reported here is after harmonisation, deduplication, and cleaning processes implemented in the wiSDM 2.0 chain, which are always less than the original number of retrieved records. # raw total – Number of “raw” records retrieved by the GBIF global search using wiSDM-2.0 query formulation; # total global (n_total_global) – Total number of records globally available after applying the wiSDM chain for cleaning and deduplication; # total Europe (n_total_eur) – Total number of records available in countries selected for the modelling after applying the wiSDM chain for cleaning and deduplication; # total Europe (bbox) (n_total_eur_bbox) – Total number of records available in the bounding box plus the 100km buffer applied to selected countries, resulting in a much less strict check after applying the wiSDM chain for cleaning and deduplication; # unique global (n_unique_global) – Number of unique records at 1x1 km cells globally available (i.e., “modelling-ready” or “SDM-ready” records); # unique Europe (n_unique_eur) – Number of unique records at 1x1 km cells available for Europe; Rat. Uniq. Glob. (r_uni_global) – Ratio between unique and total record counts globally available; Rat. Uniq. Europe (r_uni_eur) – Ratio between unique and total record counts globally available; Rat. Conc. Eur. (r_conc_eur) – Concentration ratio of unique records in Europe as the proportion between unique records for Europe divided by unique records at the global extent

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Acacia dealbata</i> Link	Portugal	Tree	10.15468/dl.s6up22	61308	52607	20090	20008	30643	10476	0.58	0.52	0.34
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Acacia longifolia</i> (Andrews) Willd.	Portugal	Shrub/tree	10.15468/dl.zad258	41452	36571	3766	3679	16407	1696	0.45	0.46	0.10
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Acacia mearnsii</i> De Wild.		Tree	10.15468/dl.kfqb4m	33247	29402	1275	1267	17231	605	0.59	0.48	0.04
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Acacia melanoxylon</i> R.Br.	Portugal	Tree	10.15468/dl.m7zduq	62904	56756	6460	6326	30320	3090	0.53	0.49	0.10
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Acacia saligna</i> (Labill.) H.L.Wendl.		Tree	10.15468/dl.94z6nf	21547	19639	9979	2673	8646	1663	0.44	0.62	0.19
Chordata	Aves	Passeriformes	Sturnidae	<i>Acridotheres cristatellus</i> (Linnaeus, 1758)		Bird	10.15468/dl.2evzpf	202459	33617	2349	2203	14794	425	0.44	0.19	0.03





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Chordata	Aves	Passeriformes	Sturnidae	<i>Acridotheres tristis</i> Linnaeus, 1766		Bird	10.15468/dl.zekmz4	3511470	652402	28615	742	229442	235	0.35	0.32	0.00
Arthropoda	Insecta	Coleoptera	Buprestidae	<i>Agrilus planipennis</i> Fairmaire, 1888	Finland	Insect (beetle)	10.15468/dl.9kejcg	4255	3570	95	40	2799	25	0.78	0.63	0.01
Tracheophyta	Magnoliopsida	Sapindales	Simaroubaceae	<i>Ailanthus altissima</i> (Mill.) Swingle		Tree	10.15468/dl.v8sze7	178754	136919	89383	87469	55592	33481	0.41	0.38	0.60
Tracheophyta	Magnoliopsida	Rosales	Rosaceae	<i>Alchemilla mollis</i> (Buser) Rothm.	Finland	Herbaceous plant	10.15468/dl.fea5fh	25366	12279	11639	11389	10145	9439	0.83	0.83	0.93
Tracheophyta	Magnoliopsida	Fagales	Betulaceae	<i>Alnus cordata</i> (Loisel.) Duby	Belgium	Tree	10.15468/dl.jpuntc	10640	5421	5364	5343	3492	3424	0.64	0.64	0.98
Chordata	Aves	Anseriformes	Anatidae	<i>Alopochen aegyptiacus</i> Linnaeus, 1766		Bird	10.15468/dl.629gzz	2165397	489647	384338	380785	109471	59869	0.22	0.16	0.55
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Ambrosia artemisiifolia</i> L.	Finland	Herbaceous plant	10.15468/dl.8r72g4	162308	93869	53552	50282	62365	30256	0.66	0.60	0.49
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Ambrosia tenuifolia</i> Spreng.	Romania	Herbaceous plant	10.15468/dl.5sph9f	688	503	77	26	391	21	0.78	0.81	0.05
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Ambrosia trifida</i> L.	Romania	Herbaceous plant	10.15468/dl.qzhk2r	41575	38469	1156	219	22113	181	0.57	0.83	0.01
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Amorpha fruticosa</i> L.	Romania	Shrub	10.15468/dl.a3wmmm	31174	25017	12087	11200	15211	7006	0.61	0.63	0.46
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Andropogon virginicus</i> L.		Grass	10.15468/dl.7c9cy3	10845	9655	21	2	6973	2	0.72	1.00	0.00
Arthropoda	Insecta	Hymenoptera	Apidae	<i>Apis florea</i> Fabricius, 1787	Belgium	Insect (bee)	10.15468/dl.a2zswz	4798	3398	275	0	2022	0	0.60	NA	0.00
Mollusca	Gastropoda	Stylommatophora	Arionidae	<i>Arion vulgaris</i> Moquin-Tandon, 1855	Romania	Gastropod (slug)	10.15468/dl.2jrjs8	32241	19220	19202	18530	10451	9998	0.54	0.54	0.96
Platyhelminthes		Tricladida	Geoplanidae	<i>Arthurdendyus triangulatus</i> (Dendy, 1894) Jones & Gerard (1999)		Flatworm	10.15468/dl.9xgtun	4949	3586	3495	3388	2786	2629	0.78	0.78	0.94
Tracheophyta	Magnoliopsida	Rosales	Rosaceae	<i>Aruncus dioicus</i> (Walter) Fernald	Finland	Herbaceous plant	10.15468/dl.yehakg	77306	45467	37520	36674	29253	23784	0.64	0.65	0.81





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Arundo donax</i> L.	Portugal	Grass	10.15468/dl.m6rzzf	73570	38218	24169	22442	21708	12709	0.57	0.57	0.59
Tracheophyta	Magnoliopsida	Gentianales	Apocynaceae	<i>Asclepias syriaca</i> L.		Herbaceous Plant	10.15468/dl.8avzjj	112235	102129	7957	7668	47834	4550	0.47	0.59	0.10
Platyhelminthes		Tricladida	Geoplanidae	<i>Australoplana sanguinea</i> (Moseley, 1877)	United Kingdom	Flatworm (land planarian)	10.15468/dl.wjg2vs	404	349	233	230	292	195	0.84	0.85	0.67
Chordata	Mammalia	Artiodactyla	Cervidae	<i>Axis axis</i> (Erxleben, 1777)		Mammal	10.15468/dl.e32grn	5502	3801	65	65	2093	11	0.55	0.17	0.01
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Baccharis halimifolia</i> L.		Shrub	10.15468/dl.wnmqzn	37526	24335	5962	5775	11682	1933	0.48	0.33	0.17
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Baccharis spicata</i> (Lam.) Baill.	Portugal	Shrub	10.15468/dl.m3jp4z	740	570	28	28	427	6	0.75	0.21	0.01
Platyhelminthes		Tricladida	Geoplanidae	<i>Bipalium kewense</i> Moseley, 1868		Flatworm	10.15468/dl.mewu9t	4534	4025	242	241	3209	169	0.80	0.70	0.05
Tracheophyta	Magnoliopsida	Rosales	Moraceae	<i>Broussonetia papyrifera</i> (L.) L'Hér ex Vent.		Tree	10.15468/dl.w6p2ym	47687	40731	17867	17841	21832	9903	0.54	0.56	0.45
Tracheophyta	Magnoliopsida	Lamiales	Scrophulariaceae	<i>Buddleja davidii</i> Franch.	Finland	Shrub	10.15468/dl.d3qnyp	289225	160475	151220	150568	54523	48085	0.34	0.32	0.88
Chordata	Mammalia	Rodentia	Sciuridae	<i>Callosciurus erythraeus</i> Pallas, 1779		Mammal	10.15468/dl.5bdcca	10618	6653	109	109	2700	48	0.41	0.44	0.02
Chordata	Mammalia	Rodentia	Sciuridae	<i>Callosciurus finlaysonii</i> (Horsfield, 1823)		Mammal	10.15468/dl.52kr6k	2772	2260	43	43	690	30	0.31	0.70	0.04
Arthropoda	Insecta	Lepidoptera	Gracillariidae	<i>Cameraria ohridella</i> Deschka & Dimić, 1986	Romania	Insect (moth)	10.15468/dl.bz7r95	250937	11257	11240	10571	7279	6886	0.65	0.65	0.95
Tracheophyta	Magnoliopsida	Sapindales	Sapindaceae	<i>Cardiospermum grandiflorum</i> Sw.		Climber/Vine	10.15468/dl.taabd2	5336	3780	596	590	2202	242	0.58	0.41	0.11
Tracheophyta	Magnoliopsida	Caryophyllales	Aizoaceae	<i>Carpobrotus edulis</i> (L.) N.E.Br.	Portugal	Succulent groundcover	10.15468/dl.f6wm8k	32673	24394	13872	12625	9413	4909	0.39	0.39	0.52
Chordata	Mammalia	Rodentia	Castoridae	<i>Castor canadensis</i> Kuhl, 1820		Mammal	10.15468/dl.8gvvy44	82830	77418	180	170	28179	131	0.36	0.77	0.00





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Tracheophyta	Magnoliopsida	Celastrales	Celastraceae	<i>Celastrus orbiculatus Thunb.</i>		Climber/Vine	10.15468/dl.e3nsjg	38376	34560	186	177	18238	133	0.53	0.75	0.01
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Cenchrus setaceus (Forssk.) Morrone</i>		Grass	10.15468/dl.8n5mxt	20385	17804	2420	2328	7379	1400	0.41	0.60	0.19
Chordata	Mammalia	Artiodactyla	Cervidae	<i>Cervus nippon Temminck, 1838</i>		Mammal	10.15468/dl.j7tw4f	12195	5838	2859	2760	2436	1465	0.42	0.53	0.60
Tracheophyta	Magnoliopsida	Cornales	Cornaceae	<i>Cornus sericea L.</i>	Finland	Shrub	10.15468/dl.cpze7m	72982	59800	21051	20255	29914	9224	0.50	0.46	0.31
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Cortaderia jubata (Lemoine ex Carrière) Stapf</i>		Grass	10.15468/dl.dkta6t	11127	10733	1	1	1278	1	0.12	1.00	0.00
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Cortaderia selloana (Schult. & Schult.f.) Asch. & Graebn.</i>	United Kingdom	Grass	10.15468/dl.sqjsrk	37563	22873	12213	11942	13721	7108	0.60	0.60	0.52
Chordata	Aves	Passeriformes	Corvidae	<i>Corvus splendens Viellot, 1817</i>		Bird	10.15468/dl.m4y53t	1498637	272182	3170	45	107756	16	0.40	0.36	0.00
Arthropoda	Insecta	Hemiptera	Tingidae	<i>Corythucha arcuata (Say, 1832)</i>	Romania	Insect (true bug)	10.15468/dl.6tt5gu	3939	3303	3093	3010	2222	1969	0.67	0.65	0.89
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Cotula coronopifolia L.</i>	Portugal	Herbaceous plant	10.15468/dl.2xztpx	27510	15783	5661	5251	7487	1613	0.47	0.31	0.22
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Cyclachaena xanthiifolia (Nutt.) Fresen.</i>	Romania	Herbaceous plant	10.15468/dl.bbf6t	7543	6641	5318	2655	4942	2137	0.74	0.80	0.43
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Delairea odorata Lem.</i>		Climber/Vine	10.15468/dl.vn5hry	10394	9148	1779	1612	4270	943	0.47	0.58	0.22
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Ehrharta calycina Sm.</i>		Grass	10.15468/dl.y72dpy	9906	7783	17	17	3909	14	0.50	0.82	0.00
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Ehrharta erecta Lam.</i>	United Kingdom	Grass	10.15468/dl.xm9nwt	16519	14425	89	77	7955	51	0.55	0.66	0.01
Tracheophyta	Magnoliopsida	Rosales	Elaeagnaceae	<i>Elaeagnus angustifolia L.</i>	Romania	Tree/shrub	10.15468/dl.fxrsym	40809	29707	19175	16814	16221	8408	0.55	0.50	0.52
Chordata	Squamata		Colubridae	<i>Elaphe taeniura (Cope, 1861)</i>	Belgium	Reptile (snake)	10.15468/dl.ey3mkg	1304	1121	172	172	778	17	0.69	0.10	0.02





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Tracheophyta	Magnoliopsida	Fagales	Fagaceae	<i>Fagus orientalis</i> Lipsky	Belgium	Tree	10.15468/dl.j3vvfn	2169	1366	1359	387	914	292	0.67	0.75	0.32
Tracheophyta	Magnoliopsida	Gunnerales	Gunneraceae	<i>Gunnera tinctoria</i> (Molina) Mirbel		Herbaceous Plant	10.15468/dl.qkdn4h	18187	16425	14582	14467	5600	4321	0.34	0.30	0.77
Tracheophyta	Magnoliopsida	Proteales	Proteaceae	<i>Hakea sericea</i> Schrad. & J.C.Wendl.		Shrub	10.15468/dl.bhmtxu	10381	9256	351	350	5223	282	0.56	0.81	0.05
Tracheophyta	Magnoliopsida	Apiales	Apiaceae	<i>Heracleum mantegazzianum</i> Sommier & Levier		Herbaceous Plant	10.15468/dl.762t4w	206118	101684	100638	99691	33130	32250	0.33	0.32	0.97
Tracheophyta	Magnoliopsida	Apiales	Apiaceae	<i>Heracleum persicum</i> Fischer		Herbaceous Plant	10.15468/dl.njau9t	4709	3703	3703	3496	1729	1644	0.47	0.47	0.95
Tracheophyta	Magnoliopsida	Apiales	Apiaceae	<i>Heracleum sosnowskyi</i> Mandenova		Herbaceous Plant	10.15468/dl.c8ncuu	30074	26797	25415	2479	9181	1330	0.34	0.54	0.14
Chordata	Mammalia	Carnivora	Herpestidae	<i>Herpestes javanicus</i> (É.Geoffroy Saint-Hilaire, 1818)		Mammal	10.15468/dl.d2jyek	9849	8291	93	83	1130	42	0.14	0.51	0.04
Tracheophyta	Magnoliopsida	Rosales	Cannabaceae	<i>Humulus scandens</i> (Lour.) Merr.		Climber/Vine	10.15468/dl.66mwdj	12735	11085	327	327	7556	198	0.68	0.61	0.03
Tracheophyta	Magnoliopsida	Ericales	Balsaminaceae	<i>Impatiens capensis</i> Meerb.	Belgium	Herbaceous plant	10.15468/dl.4dqrbp	87889	73240	4990	4988	38709	2140	0.53	0.43	0.06
Tracheophyta	Magnoliopsida	Ericales	Balsaminaceae	<i>Impatiens glandulifera</i> Royle		Herbaceous Plant	10.15468/dl.eresb8	612571	365880	355635	347365	111540	103490	0.30	0.30	0.93
Arthropoda	Insecta	Hymenoptera	Sphecidae	<i>Isodontia mexicana</i> (de Saussure, 1867)	Belgium	Insect (wasp)	10.15468/dl.etgsge	13836	6424	4489	4482	4342	2934	0.68	0.65	0.68
Tracheophyta	Magnoliopsida	Caryophyllales	Polygonaceae	<i>Koenigia polystachya</i> (Wall. ex Meisn.) T.M.Schust. & Reveal		Herbaceous Plant	10.15468/dl.hf22cj	4729	2213	2022	2016	1180	1026	0.53	0.51	0.87
Tracheophyta	Magnoliopsida	Lamiales	Lamiaceae	<i>Lamium galeobdolon</i> subsp. <i>argentatum</i> (Smejkal) J.Duvign.	United Kingdom	Herbaceous plant	10.15468/dl.uzehkf	105154	53414	46880	46734	27194	22638	0.51	0.48	0.83





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Chordata	Squamata		Colubridae	<i>Lampropeltis getula</i> (Linnaeus, 1766)		Reptile	10.15468/dl.hc5jdv	2753	2259	4	4	1999	4	0.88	1.00	0.00
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Lespedeza cuneata</i> (Dum.Cours.) G.Don		Herbaceous Plant	10.15468/dl.v6ugxa	19327	16908	0	0	11432	0	0.68	NA	0.00
Tracheophyta	Magnoliopsida	Lamiales	Linderniaceae	<i>Lindernia dubia</i> (L.) Pennell	Belgium	Herbaceous plant	10.15468/dl.3c5g43	15044	5844	1320	1315	4634	786	0.79	0.60	0.17
Arthropoda	Insecta	Hymenoptera	Formicidae	<i>Linepithema humile</i> (Mayr, 1868)	United Kingdom	Insect (ant)	10.15468/dl.hhd63j	16346	10926	1411	1349	5408	772	0.49	0.57	0.14
Tracheophyta	Polypodiopsida	Schizaeales	Lygodiaceae	<i>Lygodium japonicum</i> (Thunb.) Sw.		Fern	10.15468/dl.yrcu8y	18165	16149	1	1	9748	1	0.60	1.00	0.00
Tracheophyta	Liliopsida	Alismatales	Araceae	<i>Lysichiton americanus</i> Hultén and St. John		Herbaceous Plant	10.15468/dl.6r83sc	36225	29433	9309	9280	8584	2777	0.29	0.30	0.32
Tracheophyta	Magnoliopsida	Ericales	Primulaceae	<i>Lysimachia nummularia</i> L.	Finland	Herbaceous plant	10.15468/dl.6tzv9f	278985	115710	96026	85913	75411	56996	0.65	0.66	0.76
Arthropoda	Insecta	Hemiptera	Flatidae	<i>Metcalfa pruinosa</i> (Say, 1830)	Romania	Insect (planthopper)	10.15468/dl.96h654	19512	14743	3756	3644	8983	2389	0.61	0.66	0.27
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Microstegium vimineum</i> (Trin.) A. Camus		Grass	10.15468/dl.32xr9m	21742	19369	41	9	12410	8	0.64	0.89	0.00
Tracheophyta	Magnoliopsida	Caryophyllales	Polygonaceae	<i>Muehlenbeckia complexa</i> (A.Cunn.) Meisn.	United Kingdom	Woody vine	10.15468/dl.ww2n6d	9189	8224	3453	3439	5067	2342	0.62	0.68	0.46
Chordata	Mammalia	Artiodactyla	Cervidae	<i>Muntiacus reevesi</i> Ogilby, 1839		Mammal	10.15468/dl.8c438d	131860	19925	17550	17530	10949	9976	0.55	0.57	0.91
Chordata	Mammalia	Rodentia	Myocastoridae	<i>Myocastor coypus</i> Molina, 1782		Mammal	10.15468/dl.7ajwuf	139563	43098	33063	30624	16874	12310	0.39	0.40	0.73
Chordata	Mammalia	Carnivora	Procyonidae	<i>Nasua nasua</i> Linnaeus, 1766		Mammal	10.15468/dl.bf4djy	7028	3944	7	7	2055	7	0.52	1.00	0.00
Chordata	Mammalia	Carnivora	Mustelidae	<i>Neogale vison</i> (Schreber, 1777)		Mammal	10.15468/dl.dyaqkb	53641	16856	15742	14542	12979	11358	0.77	0.78	0.88
Chordata	Mammalia	Carnivora	Canidae	<i>Nyctereutes procyonoides</i> Gray, 1834		Mammal	10.15468/dl.mgtr84	35954	20091	6298	5925	16426	4849	0.82	0.82	0.30





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Platyhelminthes		Tricladida	Geoplanidae	<i>Obama nungara</i> Carbayo, Álvarez-Presas, Jones & Riutort, 2016		Flatworm	10.15468/dl.xvdsnqp	3010	1703	1544	1537	1348	1221	0.79	0.79	0.91
Chordata	Mammalia	Rodentia	Cricetidae	<i>Ondatra zibethicus</i> Linnaeus, 1766		Mammal	10.15468/dl.npsdrz	1014124	316224	289187	286505	38567	23845	0.12	0.08	0.62
Chordata	Aves	Anseriformes	Anatidae	<i>Oxyura jamaicensis</i> Gmelin, 1789		Bird	10.15468/dl.s3whmx	2989908	251091	5391	5298	107682	2408	0.43	0.45	0.02
Arthropoda	Insecta	Hymenoptera	Formicidae	<i>Pachycondyla chinensis</i> (Emery, 1895)		Insect	10.15468/dl.yhjyh4	3288	2130	8	8	1254	4	0.59	0.50	0.00
Tracheophyta	Magnoliopsida	Buxales	Buxaceae	<i>Pachysandra terminalis</i> Siebold & Zucc.	Belgium	Evergreen groundcover	10.15468/dl.85685j	13454	11532	4627	4610	8052	3355	0.70	0.73	0.42
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Parthenium hysterophorus</i> L.		Herbaceous plant	10.15468/dl.e352cw	28141	23640	209	7	14544	4	0.62	0.57	0.00
Tracheophyta	Magnoliopsida	Lamiales	Paulowniaceae	<i>Paulownia tomentosa</i> (Thunb.) Steud.	United Kingdom	Tree	10.15468/dl.7hut27	51431	44837	30405	30313	20753	12731	0.46	0.42	0.61
Tracheophyta	Magnoliopsida	Caryophyllales	Polygonaceae	<i>Persicaria perfoliata</i> (L.) H. Gross		Climber/Vine	10.15468/dl.4zbbq6	12473	10943	90	87	6376	57	0.58	0.66	0.01
Tracheophyta	Magnoliopsida	Asterales	Asteraceae	<i>Petasites pyrenaicus</i> (L.) G.López	United Kingdom	Herbaceous plant	10.15468/dl.zm4nww	28627	15826	15525	15217	9129	8785	0.58	0.58	0.96
Tracheophyta	Magnoliopsida	Caryophyllales	Phytolaccaceae	<i>Phytolacca americana</i> L.	Portugal	Herbaceous plant	10.15468/dl.cbehzx	160981	132822	38080	37066	74432	22008	0.56	0.59	0.30
Platyhelminthes		Tricladida	Geoplanidae	<i>Platydemus manokwari</i> de Beauchamp, 1963		Flatworm	10.15468/dl.3rd9aa	1089	999	1	1	737	1	0.74	1.00	0.00
Chordata	Mammalia	Carnivora	Procyonidae	<i>Procyon lotor</i> Linnaeus, 1758		Mammal	10.15468/dl.n3v6er	142266	96388	15640	15530	52553	9922	0.55	0.64	0.19
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Prosopis juliflora</i> (Sw.) DC.		Tree	10.15468/dl.r4dp5r	20699	15011	559	11	3231	3	0.22	0.27	0.00
Chordata	Aves	Psittaciformes	Psittacidae	<i>Psittacula krameri</i> (Scopoli, 1769)	United Kingdom	Bird (parakeet)	10.15468/dl.zq6kdn	1912328	373756	169474	150818	119583	22439	0.32	0.15	0.19
Tracheophyta	Magnoliopsida	Fagales	Juglandaceae	<i>Pterocarya fraxinifolia</i> (Poir.) Spach	Belgium	Tree	10.15468/dl.u932wg	9367	1302	1290	1262	884	851	0.68	0.67	0.96





D5.1 Predicted maps of Invasive Alien Species

Phylum	Class	Order	Family	Scientific name	Living Lab country	Taxonomic group	DOI	# raw total	# total global	# total Europe (bbox)	# total Europe	# unique global	# unique Europe	Rat. Uniq. Glob.	Rat. Uniq. Europe	Rat. Conc. Eur.
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Pueraria montana</i> (Lour.) Merr. var. <i>lobata</i> (Willd.)		Climber/Vine	10.15468/dl.tnbf62	17782	15300	380	346	10290	98	0.67	0.28	0.01
Chordata	Aves	Passeriformes	Pycnonotidae	<i>Pycnonotus cafer</i> (Linnaeus, 1766)		Bird	10.15468/dl.uc9uux	1423879	263562	644	548	117161	72	0.44	0.13	0.00
Chordata	Aves	Passeriformes	Pycnonotidae	<i>Pycnonotus jocosus</i> (Linnaeus, 1758)		Bird	10.15468/dl.zat5tr	941375	148193	476	472	57547	163	0.39	0.35	0.00
Tracheophyta	Magnoliopsida	Caryophyllales	Polygonaceae	<i>Reynoutria × bohemica</i> Chrtek & Chrtková		Herbaceous Plant	10.15468/dl.jpkc4s	21158	10482	9628	7689	6539	4680	0.62	0.61	0.72
Tracheophyta	Magnoliopsida	Caryophyllales	Polygonaceae	<i>Reynoutria japonica</i> Houtt.		Herbaceous Plant	10.15468/dl.w64yrk	429124	250887	218293	216783	93087	75175	0.37	0.35	0.81
Tracheophyta	Magnoliopsida	Caryophyllales	Polygonaceae	<i>Reynoutria sachalinensis</i> (F. Schmidt) Nakai		Herbaceous Plant	10.15468/dl.2bmtdr	25585	15600	13998	13655	10673	9184	0.68	0.67	0.86
Tracheophyta	Magnoliopsida	Fabales	Fabaceae	<i>Robinia pseudoacacia</i> L.	Portugal	Tree	10.15468/dl.8aju9h	366293	158828	123609	121067	79429	58259	0.50	0.48	0.73
Chordata	Mammalia	Rodentia	Sciuridae	<i>Sciurus carolinensis</i> Gmelin, 1788		Mammal	10.15468/dl.vy7v68	548321	308213	128206	127953	79822	34554	0.26	0.27	0.43
Chordata	Mammalia	Rodentia	Sciuridae	<i>Sciurus niger</i> Linnaeus, 1758		Mammal	10.15468/dl.6xjnmv	98457	86459	18	18	21907	13	0.25	0.72	0.00
Arthropoda	Insecta	Hymenoptera	Formicidae	<i>Solenopsis geminata</i> (Fabricius, 1804)		Insect	10.15468/dl.5xs4tw	14404	4383	0	0	2258	0	0.52	NA	0.00
Arthropoda	Insecta	Hymenoptera	Formicidae	<i>Solenopsis invicta</i> Buren, 1972		Insect	10.15468/dl.aa8wab	21589	14408	8	8	7791	4	0.54	0.50	0.00
Arthropoda	Insecta	Hymenoptera	Formicidae	<i>Solenopsis richteri</i> Forel, 1909		Insect	10.15468/dl.cgyaw8	682	110	0	0	93	0	0.85	NA	0.00
Tracheophyta	Magnoliopsida	Rosales	Rosaceae	<i>Spiraea × billardii</i> Hérincq	Finland	Shrub	10.15468/dl.grkk63	7722	4794	4783	4703	4020	3948	0.84	0.84	0.98
Tracheophyta	Magnoliopsida	Rosales	Rosaceae	<i>Spiraea alba</i> Du Roi	Finland	Shrub	10.15468/dl.qwncqh	26764	23973	927	848	15220	740	0.63	0.87	0.05
Tracheophyta	Magnoliopsida	Boraginales	Boraginaceae	<i>Symphytum officinale</i> L.	Finland	Herbaceous plant	10.15468/dl.a5a38a	353542	111965	109053	106817	67164	63396	0.60	0.59	0.94





D5.1 Predicted maps of Invasive Alien Species

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Chordata	Mammalia	Rodentia	Sciuridae	<i>Tamias sibiricus</i> Laxmann, 1769		Mammal	10.15468/dl.tynaxx	18620	14395	2839	2781	8522	152	0.59	0.05	0.02
Arthropoda	Insecta	Lepidoptera	Notodontidae	<i>Thaumetopoea processionea</i> (Linnaeus, 1758)	United Kingdom	Insect (moth)	10.15468/dl.kduuk2	35719	6178	6178	6172	3268	3263	0.53	0.53	1.00
Chordata	Aves	Pelecaniformes	Threskiornithidae	<i>Threskiornis aethiopicus</i> Latham, 1790		Bird	10.15468/dl.zyew86	432208	67711	12197	11629	37299	7246	0.55	0.62	0.19
Chordata	Testudines		Emydidae	<i>Trachemys scripta</i> Schoepff, 1792		Reptile	10.15468/dl.8zgg2m	194512	130939	20247	19429	39030	7714	0.30	0.40	0.20
Tracheophyta	Liliopsida	Commelinales	Commelinaceae	<i>Tradescantia fluminensis</i> Vell.	Portugal	Herbaceous vine	10.15468/dl.wg pz7n	25159	21665	7338	7099	10845	3852	0.50	0.54	0.36
Tracheophyta	Magnoliopsida	Malpighiales	Euphorbiaceae	<i>Triadica sebifera</i> (L.) Small		Tree	10.15468/dl.8jnpq2	23976	21307	4	2	11762	2	0.55	1.00	0.00
Arthropoda	Arachnida	Mesostigmata	Varroidae	<i>Varroa destructor</i> Anderson & Trueman, 2000	Romania	Arachnid (mite)	10.15468/dl.zhxcgy	189209	175	57	53	167	52	0.95	0.98	0.31
Arthropoda	Insecta	Hymenoptera	Vespidae	<i>Vespa mandarinia</i> Smith, 1852		Insect	10.15468/dl.ahap kx	3693	1895	0	0	1538	0	0.81	NA	0.00
Arthropoda	Insecta	Hymenoptera	Vespidae	<i>Vespa velutina nigrithorax</i> de Buysson, 1905		Insect	10.15468/dl.4vqzg5	371610	223749	221179	220780	34220	32295	0.15	0.15	0.94
Arthropoda	Insecta	Hymenoptera	Formicidae	<i>Wasmannia auropunctata</i> (Roger, 1863)		Insect	10.15468/dl.gnduzy	13698	5203	203	7	1610	5	0.31	0.71	0.00
Tracheophyta	Liliopsida	Poales	Poaceae	<i>Zizania latifolia</i> (Griseb.) Hance ex F.Muell.	Belgium	Aquatic grass	10.15468/dl.bndkzp	1474	818	574	335	401	102	0.49	0.30	0.25





7.2. List of datasets used in modelling uploaded to Zenodo

Supporting Table 7.2 – Datasets uploaded to Zenodo used in Task 5.1 modelling and data analyses.

Dataset title	URL	DOI
Reclassified Global Land-Cover Plant Functional Type Dataset (1 km) for baseline (2015) and future SSP/RCP scenarios based on Chen et al. (2022, DOI:10.1038/s41597-022-01208-6) — OneSTOP Project Task 5.1	https://zenodo.org/records/17655743	10.5281/zenodo.17655742
Reclassified 3×3 km Moving-Window Percentage Cover derived from the Global Land-Cover Plant Functional Type Dataset (1km resolution) for the 2015 Baseline and Future SSP/RCP Scenarios, Based on Chen et al. (2022; DOI: 10.1038/s41597-022-01208-6) — OneSTOP Project Task 5.1	https://zenodo.org/records/21812339	10.5281/zenodo.21812339
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): SSP5-8.5 Scenario (2071–2100)	https://zenodo.org/records/17655356	10.5281/zenodo.17655355
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): SSP3-7.0 Scenario (2071–2100)	https://zenodo.org/records/17655228	10.5281/zenodo.17655227
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): SSP1-2.6 Scenario (2071–2100)	https://zenodo.org/records/17655051	10.5281/zenodo.17655050
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): SSP5-8.5 Scenario (2041–2070)	https://zenodo.org/records/17654923	10.5281/zenodo.17654922
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): SSP3-7.0 Scenario (2041–2070)	https://zenodo.org/records/17654440	10.5281/zenodo.17654439
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): SSP1-2.6 Scenario (2041–2070)	https://zenodo.org/records/17651614	10.5281/zenodo.17651613
CHELSA Bioclimatic and Environmental Predictors for Species Distribution Models (OneSTOP Project – Task 5.1): Historical Baseline (1981–2010)	https://zenodo.org/records/17644815	10.5281/zenodo.17644814





7.3. Description of wiSDM 2.0 modifications under OneSTOP and project folders

7.3.1. Alterations to wiSDM 2.0 workflow in the OneSTOP fork

Check wiSDM OneSTOP Task 5.1 – version 2.1.0: <https://github.com/OneSTOP-CIBIO/risk-modelling-and-mapping/releases/tag/onestop-v2.1.0>

URL: <https://zenodo.org/records/21880434>

DOI: 10.5281/zenodo.21880434

The adapted framework keeps the core wiSDM 2.0 modelling logic, including two levels of modelling: (i) global climate model and (ii) European-level habitat/land cover model, followed by a combination of both. Cross-validation is performed, if feasible, at all levels and the combined model.

The main changes to the wiSDM 2.0 workflow make it more flexible for OneSTOP's project-specific inputs, more robust for large batches of species, and easier to monitor, validate, retry, and merge across multiple runs or machines. The most relevant additions are:

- i. Support for user-supplied climate and land-cover raster data.
- ii. Support for custom Europe and country boundaries.
- iii. A functional cross-validation stage integrated into the main workflow.
- iv. A chunked multi-species execution framework with logging, recovery, and a Shiny dashboard.
- v. Several robustness improvements for raster alignment, pseudoabsence selection, failed model predictions, and batch reruns.

Main alterations

User-specific environmental input data

The stock workflow was mainly wired to the default downloadable CHELSA climate layers and default land-cover predictors (from Copernicus/CORINE Land cover which do not offer future scenarios). The adapted version adds optional manifest-driven inputs:

- `user_specific_climate_data` allows the climate model to use a CSV manifest of user-provided climate rasters instead of the default CHELSA inputs.
- ``user_specific_landcover_data`` allows the habitat model to use a CSV manifest of user-provided land-cover or habitat rasters instead of the default downloaded land-cover stack.
- New template files document the required manifest structure
- The framework validates period/scenario combinations, predictor names, file paths, CRS consistency, raster alignment, and single-layer raster assumptions.
- User-specific climate inputs support current and future combinations for the standard periods and scenarios.
- User-specific land-cover inputs support either current-only habitat predictors or dynamic future habitat predictors for all future period/scenario combinations.

This is one of the most relevant adaptations because it decouples the framework from the hard-coded/stock input data and enables project-specific IAS distribution modelling with any environmental layers.





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Custom spatial boundaries and raster alignment

The stock workflow assumed the default Europe/country spatial setup. The adapted version adds:

- A ``custom_eu_boundary_path`` for a user-defined European modelling boundary.
- Continued support for ``custom_country_boundary_path``, with broader use across the climate, habitat, and validation scripts.
- Helper functions to load, transform, crop, mask, and align boundary layers to the active raster CRS.
- Logic to handle user-specific rasters whose CRS, extent, and resolution may differ from the stock rasters.

These changes are important for project deployments that need a different geographic definition of Europe, a filtered set of countries, or input rasters in a non-stock projection.

Functional cross-validation integrated into the workflow

The cross-validation stage was expanded to:

- Validate climate-only, habitat-only, and combined climate-habitat suitability outputs.
- Work with both stock and user-specific climate and land-cover inputs.
- Work with custom Europe boundaries.
- Produce per-fold and summary validation outputs.
- Use a “robust” version of the Boyce-index and threshold-independent validation.
- Fall back to climate-only validation where habitat or combined validation is not possible.
- Reuse saved model metadata, including input mode, manifest path, predictor CRS, and selected predictors.

This materially improves the internal evidence base for IAS distribution outputs, especially when modelling many species or comparing stock versus custom input data.

Chunked multi-species execution framework

A new chunk runner was added in ``src/_run_wisdm_by_chunks.R`` to support large species batches. Key features include:

- Species-list driven execution from an user-defined list.
- Manual chunk assignment for running multiple RStudio background jobs in parallel.
- Automatic per-species project naming with sanitised and shortened names.
- Registry, event, completed-species, and log files
- Retry controls for failed or skipped species.
- Optional verification that completed outputs still exist before skipping reruns.
- Optional reuse of successful previous stages on retry attempts.
- Classification of completed models as full models or climate-only outputs.
- Dry-run and preflight modes for checking configuration before running.

This is a major operational adaptation. It turns the stock single/batch workflow into a more resilient production-style system for many IAS models.

Monitoring dashboard and import/merge workflow

The dashboard reads the chunk-control files and provides:

- Progress monitoring by chunk, species, stage, status, and model outcome.
- Log inspection from the browser.
- Detection of active, completed, failed, skipped, stale, and partial climate-only runs.
- A detached launcher so monitoring does not interfere with RStudio background jobs.
- An Imports / Merge workflow for combining run outputs from different machines or transfer batches.





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- A no-overwrite merge strategy that merges control CSVs/logs into a master control folder and adopts large species project folders by moving them into `data/projects/`. This is especially relevant for internal delivery because it supports distributed or long-running IAS modelling campaigns and creates a clearer audit trail.

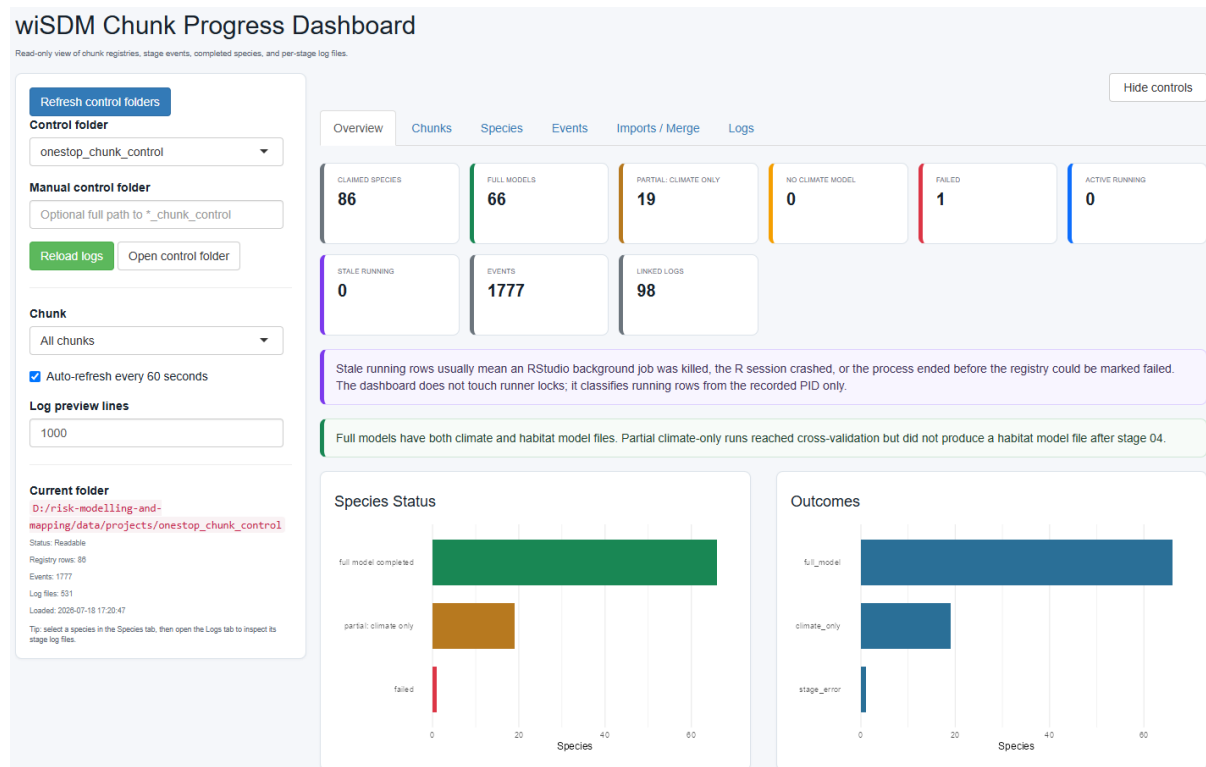


Figure 47 – Print screen of the model control dashboard (developed for the OneSTOP fork version) and used for assessing the state of model runs for the wiSDM-2.0 batch runner.

Model robustness improvements

Several targeted changes make the workflow less prone to errors during runs:

- K-means occurrence and pseudoabsence thinning now uses a fallback that reduces cluster centers when the requested number is not feasible.
- Climate and habitat prediction code is more defensive around failed algorithms and raster prediction blocks.
- Cross-validation can use a safe median-favourability function that tolerates individual method prediction failures, while requiring a minimum number of successful methods.
- Habitat modelling can optionally drop near-zero-variance predictors before fitting, reducing instability from low-information moving-window land-cover variables.
- Bias grids are better aligned to the active climate/habitat raster grid and CRS.
- When a taxon-specific bias grid is unavailable, the workflow can fall back to a neutral bias-grid approach.
- Additional metadata is saved with model objects so downstream stages can check input modes, manifests, CRS, and predictor names.
- Cross-validation is now more defensive: it adapts spatial block size and fold count, can fall back to grouped stratified k-fold validation, keeps duplicate locations in the same fold, records why data or partitions are not evaluable, and tolerates individual algorithm prediction failures.





D5.1 Predicted maps of Invasive Alien Species

New configuration options control the number of folds, candidate block sizes, and whether the non-spatial fallback is enabled.

- Raster outputs now use portable, deterministic species stems and fortified file paths.
- Stage 04 now exits cleanly when a species has no European occurrences.
- Climate and habitat variable-importance and response-curve generation now isolates failures by model and diagnostic type.

Overall, these changes mainly reduce batch failures and improve reproducibility when species have sparse records, unusual predictor values, or custom raster inputs.

Practical implications

Compared with stock wiSDM 2.0, the adapted OneSTOP fork is better suited to internal IAS distribution modelling where:

- input rasters are supplied by the project instead of downloaded from stock sources;
- the modelling region differs from the default wiSDM 2.0 Europe definition;
- many species need to be processed in parallel or across machines;
- interrupted or partial runs must be retried without losing previous successful stages;
- validation outputs are required as part of the modelling deliverable;
- an execution audit trail through registries, logs, and dashboard summaries.

The core modelling structure remains structurally wiSDM 2.0, but the surrounding data-ingestion, execution, validation, and monitoring layers have been substantially strengthened for operational IAS modelling.

7.3.2. Description of wiSDM 2.0 project folders

This annex describes the directory and file conventions used by the species modelling pipeline. It is based on the verified contents of the example project ``onestop_01_acacia_mearnsii``.

Names, paths, file counts, and filename patterns below were verified against the example project. Text explaining the likely role of each output is a brief pipeline-informed interpretation.

Naming conventions

The project directory follows this pattern:

```
`[project]_[two-digit chunk]_[genus]_[species]`
```

For this example, the project directory is ``onestop_01_acacia_mearnsii``. Its species output directory, ``Acacia_mearnsii_2979775``, combines the underscored species name with its GBIF accepted taxon key.

Model outputs are divided into three main branches:

- ``Climate``: climate-only favourability models.
- ``Habitat``: habitat or land-cover favourability models.
- ``Combined``: outputs that combine climate and habitat favourability.

``Current`` contains baseline outputs. ``2041-2070`` and ``2071-2100`` are future projection periods. Each future period is split into three Shared Socioeconomic





D5.1 Predicted maps of Invasive Alien Species

Pathways: `ssp126` (SSP1-2.6), `ssp370` (SSP3-7.0), and `ssp585` (SSP5-8.5).

Complete directory tree

The tree below includes all 229 directories in the example. Files are documented separately because most output filenames repeat systematically.

```
onestop_01_acacia_mearnsii/
|-- Acacia_mearnsii_2979775/
|   |-- Climate/           # Climate-only model outputs
|   |   |-- 2041-2070/      # Mid-century future projections
|   |   |   |-- ssp126/    # SSP1-2.6: low-emissions scenario
|   |   |       |-- Diagnostics/
|   |   |           |-- Confidence_maps/
|   |   |               |-- PDFs/
|   |   |               |-- PNGs/
|   |   |               |-- Rasters/
|   |   |       |-- Predictions/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |-- ssp370/        # SSP3-7.0: high-emissions scenario
|   |   |   |-- Diagnostics/
|   |   |       |-- Confidence_maps/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |       |-- Predictions/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |-- ssp585/        # SSP5-8.5: very-high-emissions scenario
|   |   |   |-- Diagnostics/
|   |   |       |-- Confidence_maps/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |       |-- Predictions/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |-- 2071-2100/        # Late-century future projections
|   |   |-- ssp126/        # SSP1-2.6: low-emissions scenario
|   |   |   |-- Diagnostics/
|   |   |       |-- Confidence_maps/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |       |-- Predictions/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |-- ssp370/        # SSP3-7.0: high-emissions scenario
|   |   |   |-- Diagnostics/
|   |   |       |-- Confidence_maps/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |       |-- Predictions/
|   |   |           |-- PDFs/
|   |   |           |-- PNGs/
|   |   |           |-- Rasters/
|   |   |-- ssp585/        # SSP5-8.5: very-high-emissions scenario
|   |   |   |-- Diagnostics/
|   |   |       |-- Confidence_maps/
|   |   |           |-- PDFs/
```





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```
| | | | | |-- PDFs/
| | | | | |-- PNGs/
| | | | | `-- Rasters/
| | | |-- ssp585/      # SSP5-8.5: very-high-emissions scenario
| | | | |-- Diagnostics/
| | | | | |-- Confidence_maps/
| | | | | | |-- PDFs/
| | | | | | |-- PNGs/
| | | | | | `-- Rasters/
| | | | |-- Predictions/
| | | | | |-- PDFs/
| | | | | |-- PNGs/
| | | | | `-- Rasters/
| | |-- Current/      # Baseline/current-condition outputs
| | | |-- Diagnostics/
| | | | |-- Confidence_maps/
| | | | | |-- PDFs/
| | | | | |-- PNGs/
| | | | | `-- Rasters/
| | | |-- Model_validation/
| | |-- Predictions/
| | | |-- PDFs/
| | | |-- PNGs/
| | | `-- Rasters/
|-- Habitat/          # Habitat-only model outputs
| |-- 2041-2070/      # Mid-century future projections
| |-- ssp126/         # SSP1-2.6: low-emissions scenario
| | |-- Diagnostics/
| | | |-- Confidence_maps/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | `-- Rasters/
| | |-- Predictions/
| | | |-- PDFs/
| | | |-- PNGs/
| | | `-- Rasters/
| |-- ssp370/         # SSP3-7.0: high-emissions scenario
| | |-- Diagnostics/
| | | |-- Confidence_maps/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | `-- Rasters/
| | |-- Predictions/
| | | |-- PDFs/
| | | |-- PNGs/
| | | `-- Rasters/
| |-- ssp585/         # SSP5-8.5: very-high-emissions scenario
| | |-- Diagnostics/
| | | |-- Confidence_maps/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | `-- Rasters/
| | |-- Predictions/
| | | |-- PDFs/
| | | |-- PNGs/
| | | `-- Rasters/
|-- 2071-2100/        # Late-century future projections
| |-- ssp126/         # SSP1-2.6: low-emissions scenario
| | |-- Diagnostics/
| | | |-- Confidence_maps/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | `-- Rasters/
| | |-- Predictions/
| | | |-- PDFs/
| | | |-- PNGs/
| | | `-- Rasters/
|-- ssp370/          # SSP3-7.0: high-emissions scenario
| |-- Diagnostics/
| | |-- Confidence_maps/
```





D5.1 Predicted maps of Invasive Alien Species

```
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | |-- Rasters/
| | | |-- Predictions/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | |-- Rasters/
| | |-- ssp585/ # SSP5-8.5: very-high-emissions scenario
| | | |-- Diagnostics/
| | | | |-- Confidence_maps/
| | | | | |-- PDFs/
| | | | | |-- PNGs/
| | | | | |-- Rasters/
| | | |-- Predictions/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | |-- Rasters/
| |-- Current/ # Baseline/current-condition outputs
| | |-- Diagnostics/
| | | |-- Confidence_maps/
| | | | |-- PDFs/
| | | | |-- PNGs/
| | | | |-- Rasters/
| | | |-- Model_validation/
| | | |-- Response_curves/
| | | |-- Variable_importance/
| | |-- Predictions/
| | | |-- PDFs/
| | | |-- PNGs/
| | | |-- Rasters/
|-- Model_validation/ # Cross-validation summaries
```

Directory descriptions

Supporting Table 7.3 – Description of main directories under wiSDM 2.0 projects.

Directory	Verified contents and interpreted purpose
Project root	Species metadata and processed occurrence data, plus the species output and project-level validation directories.
Acacia_mearnsii_2979775	All model products for GBIF taxon key 2979775.
Climate	Climate-only fitted model, diagnostics, baseline predictions, and future projections.
Habitat	Habitat-only fitted model, diagnostics, baseline predictions, and future projections.
Combined	Combined climate-habitat predictions and validation products; no separate serialized model is present in this example.
Current	Baseline predictions and the fullest set of model diagnostics. The climate branch also stores interim rasters here.
2041-2070, 2071-2100	Mid-century and late-century future projections, respectively.





Directory	Verified contents and interpreted purpose
ssp126, ssp370, ssp585	Projection branches for SSP1-2.6, SSP3-7.0, and SSP5-8.5.
Predictions	Final continuous ensemble and thresholded binary favourability products.
Diagnostics	Model evaluation and uncertainty products. Future branches contain confidence maps only.
Confidence_maps	Ensemble uncertainty maps. Each branch has display copies and analysis-ready rasters.
Model_validation	Per-fold and summary validation metrics, including AUC, Boyce, TSS, sensitivity, and specificity.
Response_curves	Plots of fitted response to predictor variables; present for current climate and habitat models.
Variable_importance	Predictor-importance plots; present for current climate and habitat models.
Interim	Climate ensemble means used downstream, plus the occurrence-sampling bias grid.
PDFs	Vector-page map products intended for reports or printing.
PNGs	Raster-image map products intended for previews, documents, or presentations.
Rasters	Georeferenced GeoTIFF outputs intended for GIS and quantitative analysis.
Project-level Model_validation	Consolidated validation summary across model types and regions.

Unique and project-level files

Project root

- ``onestop_01_acacia_mearnsii_taxa_info.csv`` — accepted GBIF taxon, scientific name, occurrence date range, GBIF download identifier, and project name.
- ``onestop_01_acacia_mearnsii_processed_occurrences.qs`` — serialized processed occurrence data used by the modelling workflow.
- ``Model_validation/Validation_summary.csv`` — consolidated model-validation summary for the species.

Serialized fitted models

- ``Climate/Climate_model_Acacia_mearnsii_2979775.qs`` — serialized fitted climate model object.





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- ``Habitat/Habitat_model_Acacia_mearnsii_2979775.qs`` — serialized fitted habitat model object.

No corresponding serialized file occurs directly under ``Combined`` in this example.

Current model validation

Climate validation contains four files, separating the partial models for the European level (i.e., habitat model) and the global level (i.e., climate model) results:

- ``Acacia_mearnsii_eu_climate_validation_per_fold.csv``
- ``Acacia_mearnsii_eu_climate_validation_summary.csv``
- ``Acacia_mearnsii_global_climate_validation_per_fold.csv``
- ``Acacia_mearnsii_global_climate_validation_summary.csv``

Habitat validation contains:

- ``Acacia_mearnsii_habitat_validation_per_fold.csv``
- ``Acacia_mearnsii_habitat_validation_summary.csv``

Combined-model validation contains:

- ``Acacia_mearnsii_combined_validation_per_fold.csv``
- ``Acacia_mearnsii_combined_validation_summary.csv``

Files ending in ``_per_fold.csv`` record metrics for individual cross-validation folds. Files ending in ``_summary.csv`` record means and standard deviations across folds.

Current response and importance plots

- ``Climate/Current/Diagnostics/Response_curves/Acacia_mearnsii_Climate_response_curves.png``
- ``Climate/Current/Diagnostics/Variable_importance/Acacia_mearnsii_Climate_variable_importance.png``
- ``Habitat/Current/Diagnostics/Response_curves/Acacia_mearnsii_Habitat_response_curves.png``
- ``Habitat/Current/Diagnostics/Variable_importance/Acacia_mearnsii_Habitat_variable_importance.png``

The spaces before ``response_curves`` and ``variable_importance`` are present in the verified filenames.

Climate interim rasters

``Climate/Current/Interim`` contains eight GeoTIFFs:

- ``Biasgrid_Acacia_mearnsii_2979775.tif`` — spatial bias grid used when sampling or weighting occurrence/background data.
- ``Acacia_mearnsii_Climate_current_ensemble_mean.tif`` — current ensemble mean.
- ``Acacia_mearnsii_Climate_[period]_[ssp]_ensemble_mean.tif`` — six future ensemble means, covering both future periods and all three SSPs.

For the last pattern, ``[period]`` is ``2041-2070`` or ``2071-2100``, and the future scenario ``[ssp]`` is ``ssp126``, ``ssp370``, or ``ssp585``.





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Repeated prediction products

Every `Predictions` directory contains 20 files: four GeoTIFFs, eight PNGs, and eight PDFs. There are 21 prediction directories, accounting for 420 files.

Raster predictions: four files per directory

The analysis-ready GeoTIFF names use these exact templates:

- Current:

Acacia_mearnsii_[Model]_current_[variant].tif

- Future:

Acacia_mearnsii_[Model]_[period]_[ssp]_[variant].tif

`[Model]` is `Climate`, `Habitat`, or `Combined`. `[variant]` is one of:

- `ensemble` — continuous ensemble favourability.
- `binary1pct` — binary favourability using a 1% omission threshold.
- `binary5pct` — binary favourability using a 5% omission threshold.
- `binary10pct` — binary favourability using a 10% omission threshold.

PNG and PDF predictions: eight files per format and directory

Each raster prediction has a PNG and PDF map. Each map also has an `\_occ` version that overlays occurrence records. Thus each format contains four base variants and four occurrence-overlay variants.

The binary map names follow the raster ordering:

- Acacia_mearnsii_[Model]_current_binary[1|5|10]pct[_occ].[png|pdf]
- Acacia_mearnsii_[Model]_[period]_[ssp]_binary[1|5|10]pct[_occ].[png|pdf]

The continuous ensemble display files use a different future ordering that is present in the verified outputs:

- Acacia_mearnsii_[Model]_current_ensemble[_occ].[png|pdf]
- Acacia_mearnsii_[Model]_[ssp]_[period]_ensemble[_occ].[png|pdf]

Repeated confidence-map products

There are 21 `Confidence\_maps` directories, each divided into `PDFs`, `PNGs`, and `Rasters`.

- Every branch contains one ensemble standard-deviation map in each format: `Acacia\_mearnsii\_[Model]\_[period-or-current]\_[ssp-if-future]\_ensemble\_SD` with the appropriate `.pdf`, `.png`, or `.tif` extension.
- Climate and Combined branches contain three files per confidence-map directory: one PDF, one PNG, and one GeoTIFF.
- Current Habitat also contains three files.
- Each future Habitat branch contains four files because its `Rasters`





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directory additionally includes

`Acacia\_mearnsii\_Habitat\_[period]\_[ssp]\_ensemble\_mean.tif`.

These directories account for 69 files: 21 PDFs, 21 PNGs, and 27 GeoTIFFs. Standard deviation (`SD`) represents spatial disagreement or uncertainty among ensemble members; ensemble mean rasters represent average predicted favourability.

File-format glossary

Format	Description
CSV (.csv)	Plain-text tabular metadata or validation results. The taxon metadata file uses semicolon delimiters; validation files use commas.
QS (.qs)	Compressed serialization format for R objects. These files require compatible R tooling and package versions to inspect.
GeoTIFF (.tif)	Georeferenced raster suitable for GIS display, overlay, and quantitative spatial analysis.
PNG (.png)	Portable raster image used for quick viewing and embedding in documents or presentations.
PDF (.pdf)	Page-oriented map output suited to printing, reports, and scalable document rendering.





7.4. EASIN species-country records

Supporting Table 7.4 – Matrix of the 120 OneSTOP target species and their officially recorded presence (orange dots in filled cells) in each EU-27 Member State plus the United Kingdom, based on the EASIN database. (*) species flagged with an asterisk were not matched against the EASIN database. (**) species matched in EASIN database but without country records.

EASIN ID	EASIN Species name	Austria	Belgium	Bulgaria	Croatia	Cyprus	Czechia	Denmark	Estonia	Finland	France	Germany	Greece	Hungary	Ireland	Italy	Latvia	Lithuania	Luxembourg	Malta	Netherlands	Poland	Portugal	Romania	Slovakia	Slovenia	Spain	Sweden	United Kingdom
R00039	Acacia dealbata		●		●						●	●	●		●	●							●	●		●	●		●
R00044	Acacia longifolia										●		●			●							●				●		
R00046	Acacia mearnsii		●								●					●							●				●		
R00047	Acacia melanoxylon										●					●							●				●		●
R00053	Acacia saligna				●	●		●			●		●			●				●			●				●		
R00210	Acridotheres cristatellus	●	●								●	●									●		●				●		●
R00212	Acridotheres tristis	●	●			●		●			●	●	●			●						●	●	●			●	●	●
R00409	Agrilus planipennis																											●	
R00460	Ailanthus altissima	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●			●	●		●	●	●	●	●	●	●	●
R00502	Alchemilla mollis	●	●				●	●	●	●				●	●	●	●		●			●	●		●	●	●		●
R00609	Alnus cordata	●	●					●			●	●			●	●						●		●					●
R00644	Alopochen aegyptiaca	●	●	●	●	●	●	●			●	●	●	●	●	●			●	●		●	●	●	●	●	●	●	●
R00818	Ambrosia artemisiifolia	●	●	●	●		●	●	●	●	●	●	●	●	●	●	●	●	●			●	●	●	●	●	●	●	●
R00820	Ambrosia tenuifolia										●					●								●			●		
R00821	Ambrosia trifida	●	●				●	●	●	●	●	●		●	●	●	●	●	●			●	●		●	●	●	●	●
R00859	Amorpha fruticosa	●	●	●	●		●				●	●	●	●		●	●	●	●			●	●	●	●	●	●	●	●
R00994	Andropogon virginicus										●																		
	Apis florea Fabricius, 1787 (*)																												
R01414	Arion vulgaris	●	●	●	●		●	●	●	●	●	●	●	●	●	●	●	●	●			●	●	●	●	●	●	●	●
R01506	Arthurdendylus triangulatus							●							●													●	●
R01512	Aruncus dioicus	●	●		●		●	●	●	●	●	●		●		●	●	●	●			●	●	●	●	●	●	●	●
R01515	Arundo donax		●		●	●					●		●			●				●		●		●		●	●		
R01529	Asclepias syriaca	●	●	●	●		●	●		●	●	●		●		●	●	●				●	●		●	●	●	●	●
R01772	Australoplane sanguinea														●													●	●
R01815	Axis axis				●			●			●	●						●				●				●		●	
R01830	Baccharis halimifolia		●								●					●						●		●			●		●
R19995	Baccharis spicata																						●						
R02029	Bipalium kewense	●	●				●	●		●	●	●			●	●						●	●	●		●	●	●	●
R02356	Broussonetia papyrifera	●	●	●	●	●	●				●	●	●	●	●	●				●		●		●	●	●	●		●
R02410	Buddleja davidii	●	●	●	●		●	●			●	●	●	●	●	●		●	●			●	●	●	●	●	●	●	●
R02573	Callosciurus erythraeus		●								●					●						●						●	
R02574	Callosciurus finlaysonii		●		●			●								●						●							
R02635	Cameraria ohridella	●	●	●	●		●	●	●	●	●	●	●	●	●	●	●	●	●			●	●		●	●	●	●	●
R02783	Cardiospermum grandiflorum		●								●					●				●			●				●		



D5.1 Predicted maps of Invasive Alien Species



EASIN ID	EASIN Species name	Austria	Belgium	Bulgaria	Croatia	Cyprus	Czechia	Denmark	Estonia	Finland	France	Germany	Greece	Hungary	Ireland	Italy	Latvia	Lithuania	Luxembourg	Malta	Netherlands	Poland	Portugal	Romania	Slovakia	Slovenia	Spain	Sweden	United Kingdom
R02862	<i>Carpobrotus edulis</i>		•		•	•					•	•	•		•	•				•	•		•				•		•
R02919	<i>Castor canadensis</i>	•	•							•	•	•		•					•			•	•					•	
R02976	<i>Celastrus orbiculatus</i>	•	•	•			•	•	•	•	•	•	•	•			•	•			•	•		•	•			•	•
R03000	<i>Cenchrus setaceus</i>		•	•		•					•	•	•			•			•	•			•				•	•	
R03227	<i>Cervus nippon</i>	•	•		•		•	•	•	•	•	•		•	•	•		•	•		•	•			•			•	•
R04084	<i>Cornus sericea</i>	•	•				•	•	•	•	•	•			•	•	•	•	•		•	•			•	•		•	•
R19708	<i>Cortaderia selloana</i> subsp. <i>jubata</i>		•								•																•		
R04105	<i>Cortaderia selloana</i>	•	•		•	•		•			•	•	•	•	•	•					•		•			•	•		•
R04121	<i>Corvus splendens</i>		•					•			•			•	•	•	•	•			•	•					•	•	•
R04152	<i>Corythucha arcuata</i>	•		•	•		•				•	•	•	•	•	•						•	•	•	•	•	•		
R04264	<i>Cotula coronopifolia</i>	•	•					•		•	•	•	•		•	•					•		•				•	•	•
R18196	<i>Iva xanthiifolia</i>	•	•	•	•		•	•	•	•	•	•		•				•	•		•	•			•	•		•	•
R04874	<i>Delairea odorata</i>	•			•			•		•	•	•			•	•					•		•				•		•
R05435	<i>Ehrharta calycina</i>																						•				•		
R05436	<i>Ehrharta erecta</i>					•					•				•	•					•		•						•
R05455	<i>Elaeagnus angustifolia</i>	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•
R19499	<i>Orthriophis taeniurus</i>		•																			•							
	<i>Fagus orientalis</i> Lipsky (*)																												
R06923	<i>Gunnera tinctoria</i>		•					•			•	•			•						•		•				•	•	•
R07005	<i>Hakea sericea</i>		•						•		•					•						•					•		
R07248	<i>Heracleum mantegazzianum</i>	•	•	•	•		•	•	•	•	•	•	•	•	•	•	•	•	•		•	•		•	•	•	•	•	•
R07250	<i>Heracleum persicum</i>						•	•	•	•											•							•	•
R07252	<i>Heracleum sosnowskyi</i>						•	•	•	•		•		•		•	•	•	•		•	•	•	•	•	•		•	
R07276	<i>Urva auropunctata</i>				•																						•		
R18922	<i>Humulus scandens</i>	•	•		•		•	•			•	•		•		•						•		•	•	•	•	•	•
R07717	<i>Impatiens capensis</i>		•					•		•	•	•							•		•	•						•	•
R07719	<i>Impatiens glandulifera</i>	•	•	•	•		•	•	•	•	•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•
R07831	<i>Isodontia mexicana</i>	•	•	•	•		•	•			•	•		•		•			•		•	•	•	•	•	•	•		•
R11145	<i>Koenigia polystachya</i>	•	•				•	•			•	•			•	•					•	•				•		•	•
R18403	<i>Lamium galeobdolon</i> subsp. <i>argentatum</i>	•	•				•	•		•	•				•	•					•		•		•	•		•	•
R20061	<i>Lamprolaxis getula</i>	•	•					•			•				•														
R19709	<i>Lespedeza cuneata</i>		•																										
R08605	<i>Lindernia dubia</i>	•	•	•	•		•				•	•	•	•		•					•		•	•		•	•		
R08610	<i>Linepithema humile</i>	•	•	•							•	•	•		•	•					•	•	•				•	•	•
R19710	<i>Lygodium japonicum</i>																											•	
R08915	<i>Lysichiton americanus</i>	•	•				•	•		•	•	•			•				•		•	•				•		•	•
R08922	<i>Lysimachia nummularia</i>	•	•	•	•		•	•	•	•	•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•
R09406	<i>Metcalfa pruinosa</i>	•	•	•	•		•				•	•	•	•		•					•	•	•	•	•	•	•		
R09459	<i>Microstegium vimineum</i>		•																										
R09627	<i>Muehlenbeckia complexa</i>		•								•				•						•		•				•	•	•
R09640	<i>Muntiacus reevesi</i>		•				•	•			•	•			•						•							•	•
R09952	<i>Neogale vison</i>	•	•	•			•	•	•	•	•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•
R09720	<i>Myocastor coypus</i>	•	•	•	•		•	•		•	•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•
R09857	<i>Nasua nasua</i>		•					•			•	•		•							•						•	•	•



D5.1 Predicted maps of Invasive Alien Species



EASIN ID	EASIN Species name	Austria	Belgium	Bulgaria	Croatia	Cyprus	Czechia	Denmark	Estonia	Finland	France	Germany	Greece	Hungary	Ireland	Italy	Latvia	Lithuania	Luxembourg	Malta	Netherlands	Poland	Portugal	Romania	Slovakia	Slovenia	Spain	Sweden	United Kingdom	
R10085	<i>Nyctereutes procyonoides</i>	•	•	•	•		•	•	•	•	•	•	•	•		•	•	•	•		•	•	•	•	•	•	•	•	•	
R19398	<i>Obama nungara</i>	•	•	•	•		•	•		•	•	•	•	•	•	•				•	•		•		•	•	•	•	•	
R10336	<i>Ondatra zibethicus</i>	•	•	•	•		•	•	•	•	•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•	
R10652	<i>Oxyura jamaicensis</i>	•	•			•	•	•		•	•	•		•	•	•					•	•	•		•	•	•	•	•	
R20177	<i>Brachyponera chinensis</i>				•							•				•														
R10673	<i>Pachysandra terminalis</i>	•	•		•		•	•		•	•	•		•		•	•		•		•	•			•	•		•	•	
R10890	<i>Parthenium hysterophorus</i>		•								•											•								
R10951	<i>Paulownia tomentosa</i>	•	•	•	•		•				•	•	•	•	•	•			•		•		•	•	•	•	•	•	•	
R19287	<i>Persicaria perfoliata</i>		•																		•									
R19025	<i>Petasites pyrenaicus</i>		•					•				•			•	•					•		•				•		•	
R11485	<i>Phytolacca americana</i>	•	•	•	•	•	•				•	•	•	•		•		•	•	•	•	•	•	•	•	•	•	•	•	
R19511	<i>Platydemus manokwari</i>										•																		•	
R12260	<i>Procyon lotor</i>	•	•		•		•	•		•	•	•	•	•	•	•			•	•		•	•	•	•	•	•	•	•	
R12278	<i>Neltuma juliflora</i>										•			•													•			
R12477	<i>Psittacula krameri</i>	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•		•	•		•	•	•	•	•		•	•	•	
R12505	<i>Pterocarya fraxinifolia</i>	•	•					•	•	•	•	•			•	•			•		•	•	•	•	•		•		•	
R12644	<i>Pueraria montana</i> (Lour.) Merr. var. <i>lobata</i>				•											•										•				
R12684	<i>Pycnonotus cafer</i>		•					•				•	•						•		•						•		•	
R12685	<i>Pycnonotus jocosus</i>		•									•	•			•					•						•		•	
R18189	<i>Reynoutria x bohemica</i>	•	•		•	•	•	•	•	•	•	•		•	•	•			•		•	•		•	•	•	•	•	•	
R18201	<i>Reynoutria japonica</i>	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•		•	•	•		•	•	•	•	•	
R18205	<i>Reynoutria sachalinensis</i>	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•		•	•		•	•	•	•	•	•	
R13059	<i>Robinia pseudoacacia</i>	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•		•	•	•	•	•	•	•	•	•	
R13698	<i>Sciurus carolinensis</i>		•								•	•			•	•					•		•				•	•	•	
R19317	<i>Sciurus niger</i>		•									•									•						•	•	•	
R14285	<i>Solenopsis geminata</i>					•					•		•								•						•		•	
R20064	<i>Solenopsis invicta</i>										•					•					•						•	•	•	
R20063	<i>Solenopsis richteri</i> (**)																													
R14469	<i>Spiraea x billardii</i>	•	•					•	•	•		•			•				•			•				•	•		•	•
R14439	<i>Spiraea alba</i>	•	•				•	•	•	•	•	•			•		•	•	•		•	•						•	•	
R18722	<i>Symphytum officinale</i> subsp. <i>uliginosum</i>											•																		
R14882	<i>Tamias sibiricus</i>	•	•					•				•			•	•					•							•	•	•
R15085	<i>Thaumetopoea processionea</i>	•	•					•			•	•		•		•			•		•		•				•	•	•	
R15136	<i>Threskiornis aethiopicus</i>	•	•		•		•	•			•	•		•		•	•				•	•	•		•	•	•	•	•	
R18154	<i>Trachemys scripta</i>	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•			•	•	•	•	•	•	•	•	•	•	
R15301	<i>Tradescantia fluminensis</i>		•		•					•	•		•		•	•					•		•	•			•	•	•	
R15336	<i>Triadica sebifera</i>										•	•				•					•		•				•		•	
R15826	<i>Varroa destructor</i>	•	•				•	•	•		•	•			•	•			•		•	•			•			•	•	
R20231	<i>Vespa mandarinia</i>									•																		•		
R15970	<i>Vespa velutina nigrithorax</i>	•	•				•	•			•	•		•	•	•			•		•		•		•		•		•	
R20062	<i>Wasmannia auropunctata</i>					•					•																•			
R16316	<i>Zizania latifolia</i>		•						•							•	•	•	•											





7.5. Changes in environmental favourability by species

Supporting Table 7.5 – Projected change in mean environmental favourability for the 120 OneSTOP target IAS across EU27 + UK, by future period and emission scenario (Malta was excluded due to the absence of land cover projection data and therefore no SDM predictions). Rows are the 120 target species; columns are the six future period × scenario combinations. Each value is the percentage change in area-weighted mean environmental favourability relative to that species' own historical baseline, computed over the same footprint. Mean favourability is derived from the continuous wiSDM-2.0 favourability projections as $\Sigma(\text{country mean favourability} \times \text{country area}) / \Sigma(\text{country area})$ over the 27 in-scope countries. Values span -77.1% to +219.5%; 63 of 120 species increase on average. SDM-based environmental favourability (climate and land cover predictors) is reported here. Dispersal, propagule pressure, biotic interactions or management drivers are not considered. Scenario spread is a range, not a confidence interval.

Species name	Taxonomic group	Baseline average favourability	2041-2070_SSP1-2.6	2041-2070_SSP3-7.0	2041-2070_SSP5-8.5	2071-2100_SSP1-2.6	2071-2100_SSP3-7.0	2071-2100_SSP5-8.5
<i>Acacia dealbata</i>	Vascular plant – tree	0.402	-7.6	-11.1	-14.9	-3.9	-20.6	-25.6
<i>Acacia longifolia</i>	Vascular plant – tree/shrub	0.180	-16.3	-21.8	-22.8	-12.6	-28.0	-29.1
<i>Acacia mearnsii</i>	Vascular plant – tree	0.163	-16.8	-22.5	-30.7	-10.3	-39.1	-48.2
<i>Acacia melanoxylon</i>	Vascular plant – tree	0.257	-13.8	-17.6	-23.4	-7.8	-27.1	-30.2
<i>Acacia saligna</i>	Vascular plant – tree/shrub	0.313	-3.6	-3.7	-8.0	4.3	-14.6	-26.6
<i>Acridotheres cristatellus</i>	Vertebrate – bird	0.105	34.0	22.3	30.3	38.5	18.9	17.7
<i>Acridotheres tristis</i>	Vertebrate – bird	0.244	10.6	12.2	11.2	14.4	13.7	11.2
<i>Agrilus planipennis</i>	Invertebrate – insect	0.088	58.2	54.2	65.5	37.3	84.9	113.0
<i>Ailanthus altissima</i>	Vascular plant – tree	0.436	5.5	4.1	5.4	4.9	-0.1	-1.2
<i>Alchemilla mollis</i>	Vascular plant – herbaceous	0.401	-19.8	-23.1	-28.3	-15.1	-40.8	-48.6
<i>Alnus cordata</i>	Vascular plant – tree	0.345	0.4	4.3	0.7	5.8	-1.6	-10.6
<i>Alopochen aegyptiaca</i>	Vertebrate – bird	0.437	-12.9	-9.8	-10.5	-9.1	-17.1	-21.3
<i>Ambrosia artemisiifolia</i>	Vascular plant – herbaceous	0.463	1.9	0.4	2.3	2.0	-4.0	-3.4
<i>Ambrosia tenuifolia</i>	Vascular plant – herbaceous	0.290	20.1	28.9	25.4	28.6	30.7	19.6
<i>Ambrosia trifida</i>	Vascular plant – herbaceous	0.185	43.9	52.1	64.4	35.5	75.1	91.9
<i>Amorpha fruticosa</i>	Vascular plant – shrub	0.354	19.4	21.7	26.5	17.5	24.4	29.2
<i>Andropogon virginicus</i>	Vascular plant – grass	0.265	43.3	52.6	57.2	41.6	68.2	67.9
<i>Apis florea</i>	Invertebrate – insect	0.049	66.1	96.8	107.4	61.5	150.9	168.3
<i>Arion vulgaris</i>	Invertebrate – gastropod	0.458	-13.3	-18.0	-22.2	-10.8	-32.5	-41.1
<i>Arthurdendyus triangulatus</i>	Invertebrate – flatworm	0.175	-35.0	-38.6	-44.7	-31.4	-56.0	-62.3
<i>Aruncus dioicus</i>	Vascular plant – herbaceous	0.446	-13.3	-20.3	-23.6	-11.1	-34.7	-40.3
<i>Arundo donax</i>	Vascular plant – grass	0.480	7.7	5.1	5.2	10.5	1.7	-3.8
<i>Asclepias syriaca</i>	Vascular plant – herbaceous	0.262	12.9	7.8	11.9	8.7	5.1	11.5
<i>Australoplane sanguinea</i>	Invertebrate – flatworm	0.169	2.6	11.1	8.9	3.7	10.9	9.4
<i>Axis axis</i>	Vertebrate – mammal	0.203	34.2	66.3	76.7	41.7	106.8	115.2
<i>Baccharis halimifolia</i>	Vascular plant – shrub	0.237	13.4	21.7	21.8	15.0	30.8	27.4
<i>Baccharis spicata</i>	Vascular plant – shrub	0.200	75.0	83.0	89.3	71.7	105.9	95.6
<i>Bipalium kewense</i>	Invertebrate – flatworm	0.388	-1.8	0.1	7.3	7.5	4.7	0.9
<i>Broussonetia papyrifera</i>	Vascular plant – tree	0.334	22.8	22.7	27.2	24.4	22.1	23.3
<i>Buddleja davidii</i>	Vascular plant – shrub	0.464	-12.0	-11.4	-13.0	-10.8	-19.6	-23.9
<i>Callosciurus erythraeus</i>	Vertebrate – mammal	0.162	23.8	27.5	31.0	24.9	33.8	30.0
<i>Callosciurus finlaysonii</i>	Vertebrate – mammal	0.100	13.2	23.7	29.3	14.6	39.3	34.6
<i>Cameraria ohridella</i>	Invertebrate – insect	0.387	-13.7	-15.9	-19.2	-12.0	-29.5	-35.5
<i>Cardiospermum grandiflorum</i>	Vascular plant – climber/vine	0.159	-11.7	-0.2	-8.2	-0.9	-7.8	-31.5
<i>Carpobrotus edulis</i>	Vascular plant – herbaceous	0.357	-14.3	-17.1	-22.2	-7.0	-30.4	-41.6
<i>Castor canadensis</i>	Vertebrate – mammal	0.291	7.8	8.8	7.7	7.1	12.7	12.2
<i>Celastrus orbiculatus</i>	Vascular plant – climber/vine	0.173	27.2	22.2	25.5	24.9	20.0	20.8
<i>Cenchrus setaceus</i>	Vascular plant – grass	0.303	-0.6	1.5	0.1	3.4	2.9	-0.4
<i>Cervus nippon</i>	Vertebrate – mammal	0.421	0.1	2.0	0.6	-0.6	-1.7	-8.2
<i>Cornus sericea</i>	Vascular plant – shrub	0.435	-11.0	-17.2	-19.2	-9.5	-31.3	-37.8
<i>Cortaderia jubata</i>	Vascular plant – grass	0.303	-35.9	-39.3	-47.6	-25.8	-56.6	-66.7
<i>Cortaderia selloana</i>	Vascular plant – grass	0.483	-6.5	-7.5	-8.7	-3.8	-13.2	-17.1
<i>Corvus splendens</i>	Vertebrate – bird	0.054	22.9	32.3	35.6	25.8	44.7	44.0





D5.1 Predicted maps of Invasive Alien Species

Species name	Taxonomic group	Baseline average favourability	2041-2070_SSP1-2.6	2041-2070_SSP3-7.0	2041-2070_SSP5-8.5	2071-2100_SSP1-2.6	2071-2100_SSP3-7.0	2071-2100_SSP5-8.5
<i>Corythucha arcuata</i>	Invertebrate – insect	0.421	7.3	6.1	7.8	7.5	3.8	1.1
<i>Cotula coronopifolia</i>	Vascular plant – herbaceous	0.376	-20.5	-20.0	-23.6	-16.0	-32.2	-40.1
<i>Cyclachaena xanthiifolia</i>	Vascular plant – herbaceous	0.273	-10.9	-21.1	-20.3	-12.8	-36.6	-39.9
<i>Delairea odorata</i>	Vascular plant – climber/vine	0.183	9.0	18.1	15.7	16.9	20.0	11.6
<i>Ehrharta calycina</i>	Vascular plant – grass	0.223	-24.8	-19.5	-30.6	-16.1	-37.2	-53.5
<i>Ehrharta erecta</i>	Vascular plant – grass	0.145	-9.0	-16.4	-19.7	-3.3	-26.6	-31.8
<i>Elaeagnus angustifolia</i>	Vascular plant – tree/shrub	0.365	3.4	3.0	5.5	3.6	-2.5	-1.4
<i>Elaphe taeniura</i>	Vertebrate – reptile	0.099	29.5	31.5	34.1	35.6	34.7	25.8
<i>Fagus orientalis</i>	Vascular plant – tree	0.336	3.8	-5.3	-8.2	4.7	-16.6	-27.2
<i>Gunnera tinctoria</i>	Vascular plant – herbaceous	0.224	-23.9	-25.4	-32.4	-16.8	-42.0	-48.9
<i>Hakea sericea</i>	Vascular plant – shrub	0.245	-0.8	-1.6	-8.4	7.0	-11.2	-27.4
<i>Heracleum mantegazzianum</i>	Vascular plant – herbaceous	0.424	-23.4	-29.8	-36.2	-17.2	-50.6	-59.2
<i>Heracleum persicum</i>	Vascular plant – herbaceous	0.278	1.6	-9.7	-11.6	1.4	-19.1	-24.7
<i>Heracleum sosnowskyi</i>	Vascular plant – herbaceous	0.251	42.0	36.3	37.5	41.0	32.7	35.4
<i>Herpestes javanicus</i>	Vertebrate – mammal	0.243	14.5	15.6	15.0	15.3	20.0	15.6
<i>Humulus scandens</i>	Vascular plant – climber/vine	0.191	29.7	25.6	31.2	27.4	26.5	26.4
<i>Impatiens capensis</i>	Vascular plant – herbaceous	0.263	-0.8	1.0	3.1	-2.1	-1.2	1.7
<i>Impatiens glandulifera</i>	Vascular plant – herbaceous	0.502	-17.3	-21.3	-25.3	-15.2	-36.5	-45.2
<i>Isodontia mexicana</i>	Invertebrate – insect	0.334	5.2	5.3	6.4	6.5	2.3	1.5
<i>Koenigia polystachya</i>	Vascular plant – herbaceous	0.399	-21.7	-23.6	-30.6	-17.1	-41.9	-50.8
<i>Lamium galeobdolon subsp. argentatum</i>	Vascular plant – herbaceous	0.452	-13.7	-15.8	-18.1	-11.4	-27.7	-32.4
<i>Lamprolittis getula</i>	Vertebrate – reptile	0.154	70.2	108.9	118.1	62.1	177.4	214.9
<i>Lespedeza cuneata</i>	Vascular plant – herbaceous	0.114	68.4	73.6	83.3	58.4	101.4	114.6
<i>Lindernia dubia</i>	Vascular plant – herbaceous	0.372	21.0	25.5	28.9	19.5	30.9	34.5
<i>Linepithema humile</i>	Invertebrate – insect	0.365	-1.7	-3.3	-2.4	3.8	-7.1	-12.2
<i>Lygodium japonicum</i>	Vascular plant – fern	0.085	120.6	149.2	170.7	97.7	204.7	219.5
<i>Lysichiton americanus</i>	Vascular plant – herbaceous	0.337	-16.0	-22.8	-25.7	-12.6	-39.3	-47.9
<i>Lysimachia nummularia</i>	Vascular plant – herbaceous	0.477	-5.2	-6.6	-7.4	-5.4	-14.0	-18.9
<i>Metcalia pruinosa</i>	Invertebrate – insect	0.243	39.2	42.9	48.8	36.1	48.3	51.3
<i>Microstegium vimineum</i>	Vascular plant – grass	0.081	90.1	96.0	104.2	69.3	123.7	131.8
<i>Muehlenbeckia complexa</i>	Vascular plant – climber/vine	0.273	-5.0	-4.2	-6.8	0.5	-14.2	-19.1
<i>Muntiacus reevesi</i>	Vertebrate – mammal	0.210	-18.6	-16.5	-20.9	-14.5	-26.8	-26.6
<i>Mustela vison</i>	Vertebrate – mammal	0.471	-12.8	-13.1	-16.3	-11.5	-21.8	-27.4
<i>Myocastor coypus</i>	Vertebrate – mammal	0.451	-5.6	-3.3	-2.8	-3.5	-8.0	-9.5
<i>Nasua nasua</i>	Vertebrate – mammal	0.089	30.9	30.3	35.0	38.9	28.0	22.2
<i>Nyctereutes procyonoides</i>	Vertebrate – mammal	0.378	-16.6	-20.1	-23.0	-13.2	-31.8	-39.3
<i>Obama nungara</i>	Invertebrate – flatworm	0.411	-5.3	0.6	-0.2	0.7	-2.1	-2.9
<i>Ondatra zibethicus</i>	Vertebrate – mammal	0.388	-6.3	-5.2	-5.2	-6.4	-8.9	-7.7
<i>Oxyura jamaicensis</i>	Vertebrate – bird	0.335	4.8	8.5	12.0	4.1	9.2	15.0
<i>Pachycondyla chinensis</i>	Invertebrate – insect	0.092	114.7	140.8	152.5	79.6	148.8	160.1
<i>Pachysandra terminalis</i>	Vascular plant – herbaceous	0.281	1.1	-3.2	-3.2	0.4	-12.6	-14.3
<i>Parthenium hysterophorus</i>	Vascular plant – herbaceous	0.237	29.0	40.5	45.0	31.8	56.4	51.7
<i>Paulownia tomentosa</i>	Vascular plant – tree	0.437	2.1	0.5	0.6	3.4	-5.3	-7.8
<i>Persicaria perfoliata</i>	Vascular plant – climber/vine	0.161	44.1	37.4	39.1	42.4	42.4	40.5
<i>Petasites pyrenaicus</i>	Vascular plant – herbaceous	0.348	7.2	10.8	12.0	7.7	9.6	10.4
<i>Phytolacca americana</i>	Vascular plant – herbaceous	0.397	17.0	16.5	18.5	16.1	16.8	16.4
<i>Platydemus manokwari</i>	Invertebrate – flatworm	0.121	85.6	100.2	117.6	76.9	142.0	143.8
<i>Procyon lotor</i>	Vertebrate – mammal	0.443	4.4	6.4	7.6	3.6	7.0	8.6
<i>Prosopis juliflora</i>	Vascular plant – tree/shrub	0.062	15.4	30.0	32.5	16.5	52.4	51.8
<i>Psittacula krameri</i>	Vertebrate – bird	0.251	-4.3	-0.7	-0.5	-2.0	-3.3	-1.3
<i>Pterocarya fraxinifolia</i>	Vascular plant – tree	0.333	-3.0	-3.9	-3.2	-0.7	-11.4	-15.2
<i>Pueraria montana</i>	Vascular plant – climber/vine	0.169	37.0	39.1	46.1	32.5	49.8	54.2
<i>Pycnonotus cafer</i>	Vertebrate – bird	0.029	18.3	14.5	17.3	19.8	20.0	19.3
<i>Pycnonotus jocosus</i>	Vertebrate – bird	0.099	16.7	18.9	23.2	26.0	20.9	21.2
<i>Reynoutria japonica</i>	Vascular plant – herbaceous	0.481	-9.6	-11.5	-13.6	-8.8	-21.5	-27.5
<i>Reynoutria sachalinensis</i>	Vascular plant – herbaceous	0.465	-8.7	-12.9	-15.1	-6.7	-25.8	-34.1
<i>Reynoutria × bohemica</i>	Vascular plant – herbaceous	0.483	-10.1	-15.7	-18.5	-8.2	-29.9	-36.4
<i>Robinia pseudoacacia</i>	Vascular plant – tree	0.498	-3.7	-5.5	-4.7	-3.8	-11.9	-13.2
<i>Sciurus carolinensis</i>	Vertebrate – mammal	0.281	-0.7	5.9	8.1	-0.8	6.4	7.7
<i>Sciurus niger</i>	Vertebrate – mammal	0.222	67.7	86.1	98.2	55.6	121.4	127.8
<i>Solenopsis geminata</i>	Invertebrate – insect	0.102	42.7	60.3	70.1	41.0	101.6	123.8
<i>Solenopsis invicta</i>	Invertebrate – insect	0.137	79.1	104.1	120.2	67.2	160.2	173.3
<i>Solenopsis richteri</i>	Invertebrate – insect	0.172	72.7	79.3	90.3	68.9	110.5	101.9



D5.1 Predicted maps of Invasive Alien Species



Species name	Taxonomic group	Baseline average favourability	2041-2070_SSP1-2.6	2041-2070_SSP3-7.0	2041-2070_SSP5-8.5	2071-2100_SSP1-2.6	2071-2100_SSP3-7.0	2071-2100_SSP5-8.5
<i>Spiraea alba</i>	Vascular plant – shrub	0.292	3.8	1.8	1.1	2.2	-2.1	-1.5
<i>Spiraea × billardii</i>	Vascular plant – shrub	0.330	-32.8	-44.3	-51.8	-25.8	-68.1	-77.1
<i>Symphytum officinale</i>	Vascular plant – herbaceous	0.492	-14.1	-16.6	-18.6	-11.9	-28.8	-34.3
<i>Tamias sibiricus</i>	Vertebrate – mammal	0.137	9.1	4.0	3.9	7.6	-3.1	-6.6
<i>Thaumetopoea processionea</i>	Invertebrate – insect	0.368	-14.4	-15.4	-21.8	-11.3	-31.3	-36.6
<i>Threskiornis aethiopicus</i>	Vertebrate – bird	0.331	-1.0	-2.6	-2.0	9.0	-11.8	-16.9
<i>Trachemys scripta</i>	Vertebrate – reptile	0.396	4.5	5.4	7.6	4.2	5.7	7.6
<i>Tradescantia fluminensis</i>	Vascular plant – herbaceous	0.358	1.7	-0.7	-4.5	5.4	-9.2	-16.8
<i>Triadica sebifera</i>	Vascular plant – tree	0.128	72.4	92.5	106.5	63.1	153.3	178.0
<i>Varroa destructor</i>	Invertebrate – arachnid	0.591	0.6	-0.3	-0.1	1.7	-2.8	-4.0
<i>Vespa mandarinia</i>	Invertebrate – insect	0.040	70.2	65.1	79.7	77.8	73.5	69.2
<i>Vespa velutina</i>	Invertebrate – insect	0.383	-8.0	-6.3	-8.9	-3.4	-16.1	-23.8
<i>Wasmannia auropunctata</i>	Invertebrate – insect	0.069	63.6	89.5	102.7	64.6	151.4	181.1
<i>Zizania latifolia</i>	Vascular plant – grass	0.348	8.9	3.2	4.8	6.6	-4.9	-7.3



D5.1 Predicted maps of Invasive Alien Species



Supporting Table 7.6 – Percentage change in environmentally favourable area over EU27 + UK for 120 target IAS, by future period and scenario, relative to each species' historical baseline favourable area (in km²). Favourable area is the count of 1 km equal-area cells above the 10 % minimum-training-presence threshold, summed over the 27 in-scope countries (Malta excluded). Favourable area increases in 379 of the 720 cells and in 60 of the 120 species averaged over the six futures. (*) Three species recorded some issues in the basal area for calculations, which are considered valid but unstable regarding the magnitude of change. SDM-based environmental favourability (climate and land cover predictors) is reported here. Dispersal, propagule pressure, biotic interactions or management drivers are not considered. Scenario spread is a range, not a confidence interval.

Species name	Taxonomic group	Baseline area (km ²)	2041-2070_SSP1-2.6	2041-2070_SSP3-7.0	2041-2070_SSP5-8.5	2071-2100_SSP1-2.6	2071-2100_SSP3-7.0	2071-2100_SSP5-8.5
<i>Acacia dealbata</i>	Vascular plant – tree	1295702	-16.0	-26.7	-34.5	-4.1	-44.7	-51.6
<i>Acacia longifolia</i>	Vascular plant – tree/shrub	316434	-49.8	-59.2	-59.0	-44.7	-68.6	-68.4
<i>Acacia mearnsii</i>	Vascular plant – tree	1225687	-20.5	-27.8	-36.8	-11.1	-43.6	-52.4
<i>Acacia melanoxylon</i>	Vascular plant – tree	776478	-37.4	-47.7	-54.1	-25.2	-65.7	-68.9
<i>Acacia saligna</i>	Vascular plant – tree/shrub	733627	17.0	15.5	2.0	47.9	-16.5	-31.7
<i>Acridotheres cristatellus</i>	Vertebrate – bird	583240	52.0	31.1	50.7	59.5	27.2	29.4
<i>Acridotheres tristis</i>	Vertebrate – bird	1443515	22.5	32.1	20.0	34.7	32.1	8.4
<i>Agrilus planipennis</i>	Invertebrate – insect	3927	298.6	134.3	354.9	128.7	316.2	981.3
<i>Ailanthus altissima</i>	Vascular plant – tree	2152447	3.8	-2.4	-1.6	5.1	-16.1	-17.1
<i>Alchemilla mollis</i>	Vascular plant – herbaceous	1204149	-42.1	-44.9	-52.0	-33.0	-67.2	-73.5
<i>Alnus cordata</i>	Vascular plant – tree	1203190	-5.8	-3.1	-13.7	10.5	-19.1	-36.3
<i>Alopochen aegyptiaca</i>	Vertebrate – bird	1884257	-21.0	-15.1	-15.0	-15.7	-24.1	-28.4
<i>Ambrosia artemisiifolia</i>	Vascular plant – herbaceous	2065254	-8.6	-11.6	-5.3	-7.9	-23.5	-17.5
<i>Ambrosia tenuifolia</i>	Vascular plant – herbaceous	1340865	33.5	49.8	47.4	44.7	58.0	42.5
<i>Ambrosia trifida</i>	Vascular plant – herbaceous	2038434	36.8	46.0	54.9	31.4	68.8	83.5
<i>Amorpha fruticosa</i>	Vascular plant – shrub	1185995	39.9	40.7	55.3	39.6	36.7	53.0
<i>Andropogon virginicus</i>	Vascular plant – grass	844666	78.2	96.6	107.2	76.3	149.4	169.8
<i>Apis florea</i>	Invertebrate – insect	1841 (*)	609.6	1383.8	1247.1	794.7	1468.2	1413.9
<i>Arion vulgaris</i>	Invertebrate – gastropod	1931472	-22.7	-28.3	-35.9	-24.6	-49.7	-58.7
<i>Arthurdendyus triangulatus</i>	Invertebrate – flatworm	355547	-36.6	-40.0	-48.5	-33.9	-66.8	-75.5
<i>Aruncus dioicus</i>	Vascular plant – herbaceous	1855748	-19.9	-31.3	-36.7	-16.8	-50.7	-57.8
<i>Arundo donax</i>	Vascular plant – grass	2274129	17.7	9.9	9.7	28.9	2.6	-10.3
<i>Asclepias syriaca</i>	Vascular plant – herbaceous	987686	29.2	6.7	19.7	16.3	-6.3	16.7
<i>Australoplane sanguinea</i>	Invertebrate – flatworm	323698	7.8	16.9	4.6	6.6	6.4	-2.8
<i>Axis axis</i>	Vertebrate – mammal	98608	120.1	432.5	545.1	235.8	918.8	1048.1
<i>Baccharis halimifolia</i>	Vascular plant – shrub	655952	19.6	36.5	34.3	19.6	49.1	46.7
<i>Baccharis spicata</i>	Vascular plant – shrub	415854	109.4	117.6	123.0	103.3	160.8	174.3
<i>Bipalium kewense</i>	Invertebrate – flatworm	2485090	0.1	7.0	23.2	19.2	23.6	14.3
<i>Broussonetia papyrifera</i>	Vascular plant – tree	1150212	46.8	40.9	51.0	53.7	25.3	29.1
<i>Buddleja davidii</i>	Vascular plant – shrub	1647879	-35.0	-27.7	-26.4	-39.3	-37.7	-39.5
<i>Callosciurus erythraeus</i>	Vertebrate – mammal	2323006	37.5	40.6	45.4	36.8	51.9	45.5
<i>Callosciurus finlaysonii</i>	Vertebrate – mammal	290079	14.2	23.6	33.7	16.4	49.1	36.4
<i>Cameraria ohridella</i>	Invertebrate – insect	1542936	-38.1	-41.9	-44.6	-34.6	-62.5	-66.6
<i>Cardiospermum grandiflorum</i>	Vascular plant – climber/vine	351564	1.5	2.0	-3.5	23.6	-7.0	-28.3
<i>Carpobrotus edulis</i>	Vascular plant – herbaceous	1085373	-22.3	-28.2	-34.6	-6.4	-44.2	-56.7
<i>Castor canadensis</i>	Vertebrate – mammal	917050	19.4	17.1	14.1	18.3	23.9	19.2
<i>Celastrus orbiculatus</i>	Vascular plant – climber/vine	3306762	7.2	4.4	2.7	7.1	-3.5	-8.6
<i>Cenchrus setaceus</i>	Vascular plant – grass	594582	7.5	15.3	11.6	12.1	23.9	15.5
<i>Cervus nippon</i>	Vertebrate – mammal	1643364	5.2	16.6	16.2	-1.2	15.6	4.4
<i>Cornus sericea</i>	Vascular plant – shrub	1582739	-21.1	-28.9	-31.5	-18.5	-55.6	-64.4



D5.1 Predicted maps of Invasive Alien Species



Species name	Taxonomic group	Baseline area (km2)	2041-2070_SSP1-2.6	2041-2070_SSP3-7.0	2041-2070_SSP5-8.5	2071-2100_SSP1-2.6	2071-2100_SSP3-7.0	2071-2100_SSP5-8.5
<i>Cortaderia jubata</i>	Vascular plant – grass	596215	-42.3	-47.9	-55.2	-31.8	-62.8	-70.1
<i>Cortaderia selloana</i>	Vascular plant – grass	1768534	-24.4	-28.7	-33.2	-14.9	-44.7	-52.3
<i>Corvus splendens</i>	Vertebrate – bird	1562 (*)	672.3	1030.0	1011.0	710.3	1340.6	1436.4
<i>Corythucha arcuata</i>	Invertebrate – insect	1258477	33.4	31.9	39.1	20.7	34.9	30.7
<i>Cotula coronopifolia</i>	Vascular plant – herbaceous	1244818	-32.7	-33.1	-36.9	-23.8	-45.8	-53.8
<i>Cyclachaena xanthiifolia</i>	Vascular plant – herbaceous	711710	-24.3	-50.1	-48.2	-27.4	-78.6	-82.2
<i>Delairea odorata</i>	Vascular plant – climber/vine	431429	15.6	17.8	17.9	33.4	11.7	6.8
<i>Ehrharta calycina</i>	Vascular plant – grass	274877	-36.4	-32.9	-36.9	-35.2	-44.4	-52.7
<i>Ehrharta erecta</i>	Vascular plant – grass	192891	-27.3	-46.4	-42.4	-21.4	-58.3	-53.3
<i>Elaeagnus angustifolia</i>	Vascular plant – tree/shrub	1599050	3.8	-0.8	3.5	8.5	-18.6	-18.8
<i>Elaphe taeniura</i>	Vertebrate – reptile	110282	66.6	71.8	86.4	82.0	82.8	73.8
<i>Fagus orientalis</i>	Vascular plant – tree	1229330	28.0	11.9	7.6	27.0	0.3	-15.2
<i>Gunnera tinctoria</i>	Vascular plant – herbaceous	684377	-30.9	-33.2	-41.0	-22.8	-50.3	-56.4
<i>Hakea sericea</i>	Vascular plant – shrub	970891	-0.7	9.1	-6.1	7.4	3.7	-31.7
<i>Heracleum mantegazzianum</i>	Vascular plant – herbaceous	1424513	-53.5	-59.7	-71.7	-43.3	-85.8	-90.3
<i>Heracleum persicum</i>	Vascular plant – herbaceous	1057681	11.8	-1.6	-6.6	12.5	-8.2	-18.3
<i>Heracleum sosnowskyi</i>	Vascular plant – herbaceous	953476	2.2	-18.8	-19.4	1.1	-41.5	-44.7
<i>Herpestes javanicus</i>	Vertebrate – mammal	350180	78.4	111.4	92.2	75.1	161.7	115.0
<i>Humulus scandens</i>	Vascular plant – climber/vine	792991	89.9	89.1	105.4	77.9	94.4	101.0
<i>Impatiens capensis</i>	Vascular plant – herbaceous	888321	1.6	2.2	3.6	1.7	-3.8	-1.8
<i>Impatiens glandulifera</i>	Vascular plant – herbaceous	2304486	-20.8	-25.2	-29.7	-20.7	-42.6	-51.6
<i>Isodontia mexicana</i>	Invertebrate – insect	1140208	-1.9	-6.2	-10.7	7.5	-36.5	-42.0
<i>Koenigia polystachya</i>	Vascular plant – herbaceous	1382121	-28.1	-17.2	-30.3	-22.8	-40.4	-54.9
<i>Lamium galeobdolon subsp. argentatum</i>	Vascular plant – herbaceous	1251933	-34.7	-35.8	-42.9	-31.4	-59.1	-63.3
<i>Lampropeltis getula</i>	Vertebrate – reptile	583141	80.6	138.4	150.8	70.2	223.7	283.3
<i>Lespedeza cuneata</i>	Vascular plant – herbaceous	76069	260.6	281.8	332.9	206.1	387.4	409.9
<i>Lindernia dubia</i>	Vascular plant – herbaceous	1410121	36.8	44.1	53.5	34.7	47.6	58.6
<i>Linepithema humile</i>	Invertebrate – insect	1165903	-2.2	-10.3	-6.4	19.9	-23.7	-28.2
<i>Lygodium japonicum</i>	Vascular plant – fern	62048	309.7	391.5	437.7	275.0	604.2	651.6
<i>Lysichiton americanus</i>	Vascular plant – herbaceous	1126968	-33.5	-38.2	-41.0	-28.4	-50.3	-55.2
<i>Lysimachia nummularia</i>	Vascular plant – herbaceous	1950064	-27.8	-29.0	-30.2	-30.4	-47.2	-52.8
<i>Metcalfa pruinosa</i>	Invertebrate – insect	683808	88.4	92.8	108.5	78.0	96.6	86.2
<i>Microstegium vimineum</i>	Vascular plant – grass	41744	378.2	430.9	448.6	217.6	578.7	624.8
<i>Muehlenbeckia complexa</i>	Vascular plant – climber/vine	751902	-7.6	-10.9	-8.3	3.1	-29.2	-35.2
<i>Muntiacus reevesi</i>	Vertebrate – mammal	455265	-42.8	-44.4	-57.1	-35.4	-71.5	-73.4
<i>Mustela vison</i>	Vertebrate – mammal	1824824	-37.0	-33.5	-40.1	-37.2	-50.1	-57.5
<i>Myocastor coypus</i>	Vertebrate – mammal	1511490	-15.2	-9.3	-9.7	-10.0	-18.5	-17.1
<i>Nasua nasua</i>	Vertebrate – mammal	143106	56.8	56.7	64.2	69.8	54.9	46.0
<i>Nyctereutes procyonoides</i>	Vertebrate – mammal	1587414	-39.8	-48.2	-56.6	-34.8	-75.5	-87.8
<i>Obama nungara</i>	Invertebrate – flatworm	1010459	-9.0	-2.8	0.8	5.7	-2.2	4.2
<i>Ondatra zibethicus</i>	Vertebrate – mammal	848801	-17.9	-15.8	-22.5	-17.8	-27.4	-31.2
<i>Oxyura jamaicensis</i>	Vertebrate – bird	2348488	1.8	6.6	11.6	3.3	5.5	14.5
<i>Pachycondyla chinensis</i>	Invertebrate – insect	13986	377.6	589.3	599.9	448.6	1478.7	1844.2
<i>Pachysandra terminalis</i>	Vascular plant – herbaceous	745178	-28.0	-38.7	-33.1	-35.3	-64.9	-61.2
<i>Parthenium hysterophorus</i>	Vascular plant – herbaceous	129887	148.4	216.5	231.9	157.4	310.5	306.1
<i>Paulownia tomentosa</i>	Vascular plant – tree	1610905	1.5	-4.1	-5.0	7.7	-25.2	-30.3
<i>Persicaria perfoliata</i>	Vascular plant – climber/vine	30477	370.4	305.9	320.2	299.9	333.7	328.4
<i>Petasites pyrenaicus</i>	Vascular plant – herbaceous	1207073	16.6	22.5	25.9	22.4	15.1	16.0
<i>Phytolacca americana</i>	Vascular plant – herbaceous	2059813	38.6	40.7	44.2	36.8	42.1	40.9
<i>Platydemus manokwari</i>	Invertebrate – flatworm	152319	201.6	229.8	303.0	186.5	331.2	333.2
<i>Procyon lotor</i>	Vertebrate – mammal	1401845	8.5	15.5	16.3	4.9	18.0	24.5



D5.1 Predicted maps of Invasive Alien Species



Species name	Taxonomic group	Baseline area (km2)	2041-2070_SSP1-2.6	2041-2070_SSP3-7.0	2041-2070_SSP5-8.5	2071-2100_SSP1-2.6	2071-2100_SSP3-7.0	2071-2100_SSP5-8.5
<i>Prosopis juliflora</i>	Vascular plant – tree/shrub	43796	110.4	179.6	193.9	105.6	285.5	261.6
<i>Psittacula krameri</i>	Vertebrate – bird	780678	-11.8	-9.3	-17.4	-10.1	-24.0	-20.8
<i>Pterocarya fraxinifolia</i>	Vascular plant – tree	1062494	-26.8	-34.9	-35.3	-22.7	-57.1	-61.0
<i>Pueraria montana</i>	Vascular plant – climber/vine	370850	145.8	152.0	173.5	121.1	188.1	208.8
<i>Pycnonotus cafer</i>	Vertebrate – bird	10229	49.6	34.1	54.9	48.5	38.5	52.5
<i>Pycnonotus jocosus</i>	Vertebrate – bird	261859	33.0	24.2	44.7	49.1	29.5	40.7
<i>Reynoutria japonica</i>	Vascular plant – herbaceous	2042677	-23.6	-14.6	-18.5	-27.1	-28.3	-37.5
<i>Reynoutria sachalinensis</i>	Vascular plant – herbaceous	1698553	-15.2	-20.5	-24.4	-10.1	-40.3	-50.1
<i>Reynoutria × bohemica</i>	Vascular plant – herbaceous	2403920	-22.7	-31.6	-34.9	-23.3	-48.3	-55.6
<i>Robinia pseudoacacia</i>	Vascular plant – tree	2500338	-11.6	-15.4	-14.3	-10.2	-30.8	-31.8
<i>Sciurus carolinensis</i>	Vertebrate – mammal	634042	-6.2	11.1	15.2	-12.8	14.2	16.9
<i>Sciurus niger</i>	Vertebrate – mammal	890606	95.7	125.0	152.4	70.9	188.6	199.0
<i>Solenopsis geminata</i>	Invertebrate – insect	53 (*)	2005.7	5988.7	7849.1	2437.7	37849.1	115952.8
<i>Solenopsis invicta</i>	Invertebrate – insect	201672	352.9	449.9	536.4	285.0	720.1	790.6
<i>Solenopsis richteri</i>	Invertebrate – insect	219235	143.8	153.8	185.8	133.3	214.2	208.5
<i>Spiraea alba</i>	Vascular plant – shrub	3123001	1.7	-0.5	-0.9	2.7	-4.5	-5.1
<i>Spiraea × billardii</i>	Vascular plant – shrub	1232292	-32.6	-44.6	-51.9	-28.6	-74.6	-87.8
<i>Symphytum officinale</i>	Vascular plant – herbaceous	1942962	-27.6	-31.5	-34.7	-22.9	-54.1	-59.7
<i>Tamias sibiricus</i>	Vertebrate – mammal	1727689	7.2	-0.5	-0.9	2.0	-7.8	-13.7
<i>Thaumetopoea processionea</i>	Invertebrate – insect	981228	-32.9	-39.0	-47.1	-26.6	-64.8	-69.2
<i>Threskiornis aethiopicus</i>	Vertebrate – bird	1312953	-8.9	-14.3	-14.0	13.6	-29.5	-28.9
<i>Trachemys scripta</i>	Vertebrate – reptile	2091814	2.2	3.3	9.5	2.9	0.0	5.7
<i>Tradescantia fluminensis</i>	Vascular plant – herbaceous	785507	1.0	-5.3	-7.4	6.5	-20.6	-30.1
<i>Triadica sebifera</i>	Vascular plant – tree	53211	593.5	817.8	972.7	466.7	1475.4	1798.4
<i>Varroa destructor</i>	Invertebrate – arachnid	2681268	-2.6	1.6	0.3	0.1	-2.2	-8.3
<i>Vespa mandarinia</i>	Invertebrate – insect	39651	161.3	145.0	168.4	167.2	126.0	103.3
<i>Vespa velutina</i>	Invertebrate – insect	1055194	-18.0	-19.3	-22.3	-8.2	-46.5	-48.9
<i>Wasmannia auropunctata</i>	Invertebrate – insect	2838	447.6	735.1	914.3	421.5	2852.8	4682.8
<i>Zizania latifolia</i>	Vascular plant – grass	1273336	18.0	0.1	8.7	7.0	-14.2	-14.0





7.6. SDM Map Gallery full description

This annex describes the OneSTOP Map Gallery, the web-based component through which the potential distribution maps produced by the project's invasive alien species (IAS) species distribution modelling (SDM) work are published and made publicly accessible. It summarises the purpose of the gallery, its position within the modelling workflow, the production chain that generates it, the cartographic content of the maps, and the functionality available to users. Implementation-level detail (parameter values, file paths and code-level configuration) is documented in the software repository and is not reproduced here.

Purpose and scope

The Map Gallery is a public dissemination product. It presents, in a single browsable interface, the potential distribution maps modelled for each IAS addressed in OneSTOP, under current conditions and under a set of future climate scenarios and time horizons. Its objective is to make model outputs accessible to policy makers, managers, researchers and the interested public without requiring GIS software, specialised training, or access to the underlying model files.

The gallery is a presentation and dissemination layer only. It does not fit models, derive suitability thresholds, or perform any spatial analysis. All modelling decisions are taken upstream and are reported in the main body of the deliverable.

Position within the SDM workflow

Model fitting, evaluation and the conversion of continuous suitability surfaces into binary (suitable/unsuitable) projections are carried out in the OneSTOP-adapted wiSDM modelling workflow. The gallery begins where that workflow ends, taking as input, for each species, seven binary projection rasters together with the occurrence records used for model training.

Of the seven projections, one represents the historical/current environmental conditions used for model calibration, and the remaining six project the fitted model onto two future time periods under three shared socioeconomic pathway (SSP/RCP) scenarios, as summarised in Supporting Table 7.7.

Supporting Table 7.7 – Temporal and scenario coverage of the map series published for each species.

Time period	Climate scenarios	Maps per species
Historical / current (1981–2010)	Baseline conditions used for model calibration	1
Mid century: 2041–2070	SSP1/RCP2.6, SSP3/RCP7.0, SSP5/RCP8.5	3
End-century:	SSP1/RCP2.6, SSP3/RCP7.0, SSP5/RCP8.5	3





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Time period	Climate scenarios	Maps per species
2071–2100		
Total		7

Design rationale: a static, low-maintenance website

The gallery is deliberately implemented as a static website. The published site consists of a single generated HTML page, the final map images in PNG format, and the OneSTOP and EU funding logos; it is served through GitHub Pages. There is no application server, database, web-GIS service or server-side map rendering involved at publication time, and the R and Python components described below are authoring tools that are run locally before publication rather than services that run on the site.

This design was chosen for the following reasons:

- Longevity and low maintenance: the published outputs have no runtime dependencies and remain functional beyond the lifetime of the project, without hosting, licence or maintenance costs.
- Robustness and performance: pages load quickly, images are loaded progressively as the user scrolls, and there is no service that can fail or require patching.
- Archivability: the complete site can be copied, mirrored or archived as a simple folder of files, which supports open-science and data-management requirements.

The corresponding trade-off is that the gallery is a collection of pre-rendered map images rather than an interactive web-GIS client. Users can filter, browse and enlarge maps, but cannot toggle spatial layers, query individual cells, or pan and zoom continuously. Where such functionality is required, the underlying rasters remain available through the project's data repositories.

Production workflow

The gallery is produced through a four-stage, reproducible chain that converts model outputs into a publishable website (Table 2). Each stage is scripted, so the full map series can be regenerated whenever models are updated or extended to additional species.

Supporting Table 7.8 – Stages of the map-gallery production chain.

Stage	Component	Function
1. Rendering	R script (terra, sf, ggplot2 and related packages)	Locates the seven binary projections for each species, combines them with country boundaries and occurrence information, and renders publication-quality PNG maps.
2. Standardisation	Python image-processing script	Applies a consistent crop to all rendered maps so that the series is visually uniform.





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Stage	Component	Function
3. Provenance overlay	Python image-processing script	Adds a caption bar carrying the product name, version number and reference date to every image.
4. Gallery generation	Python site generator	Reads the final images, derives their metadata, and writes the complete gallery page, including its styling and interactive behaviour.

The generated page and the final images are then committed to the repository and published automatically through GitHub Pages.

Naming convention as the interface between stages

Image filenames act as the controlled interface between the rendering and publication stages. Each filename encodes the species name, the modelled period and the climate scenario, and the site generator parses these elements to build the gallery metadata: species display name, period label, scenario label and a link to the corresponding GBIF species search. Files that do not follow the convention are not included in the published gallery, so filenames are validated before publication.

Quality control outputs

The rendering stage also produces a summary table reporting, for each species and scenario, the total number of raster cells, the number of valid cells, the number of cells classified as suitable and unsuitable, and the approximate suitable area. These statistics are used internally to verify model outputs and to support the quantitative results reported in the main deliverable; they are not published as part of the gallery.

Cartographic content of the maps

All maps in the series share a common layout and symbology, so that different species, periods and scenarios can be compared directly. Each map contains:

- the binary model projection, with areas predicted as suitable shown in dark green, areas predicted as unsuitable in light grey, and areas without data left blank;
- country boundaries for the European and neighbouring countries covered by OneSTOP, drawn in grey over the projection;
- the occurrence evidence used for model training, represented as the cells of the OneSTOP 20 × 20 km reference grid that contain at least one training record, outlined in blue. Displaying occurrence evidence at grid-cell resolution rather than as individual points generalises sensitive locality information and keeps the maps legible at continental scale;
- a map title giving the species name in italics, a subtitle identifying the time period and climate scenario, and a scale bar;
- a caption bar with the product name, version and reference date, ensuring that every image remains self-describing if it is downloaded or reused independently of the gallery.





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Maps are rendered at 300 dpi on a white background at a size suitable for both on-screen viewing and inclusion in reports and presentations.

Gallery functionality

The published page presents all maps as a grid of thumbnails and offers the following features:

- progressive (hierarchical) filtering: users first select a species, then a time period, and then — for future periods — a climate scenario;
- consistent chronological and scenario ordering of the results, from historical conditions through the two future periods and from the low- to the high-emission scenarios;
- a full-screen viewer in which any map can be enlarged and browsed sequentially, with mouse and keyboard navigation;
- a direct link from each species name to the corresponding GBIF species search, opening in a new tab;
- OneSTOP and EU funding acknowledgement branding in the page header and footer.

An internet connection is required only when a user follows an external link; the gallery interface and all map images are local static assets.

Technical requirements and reproducibility

The authoring tools require an R environment with the spatial and plotting packages used for map rendering (notably *terra*, *sf*, *ggplot2*, *ggspatial* and *rnatrualearth*) and a Python 3 environment with the Pillow imaging library; the site generator itself uses only the Python standard library. Inputs consist of the per-species model output folders produced by the modelling workflow and the OneSTOP 20 × 20 km reference grid.

Rendering is incremental: maps that already exist are not regenerated, so the series can be extended with new species or updated selectively at low computational cost. Because the gallery page is generated rather than hand-written, any change to page text, styling or behaviour is made in the generator and the page is regenerated; the published page should not be edited directly.

Known limitations

- The gallery displays binary suitable/unsuitable projections; the underlying continuous suitability values and the thresholds applied to them are documented upstream and are not conveyed by the maps themselves.
- Input rasters are assumed to be already thresholded to binary values; any correction must be made in the modelling workflow.
- Species links point to GBIF name-based searches rather than to validated taxon identifiers.
- Adding, removing or renaming map images requires the gallery page to be regenerated, since the metadata is embedded at generation time.
- The site is not an interactive GIS, as described in Section 3.

