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# A global dataset of taxa to support calibration of invasion risk screening applications

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In invasion science, risk analysis tools are widely used to support the prevention and management of non-native species introductions. Many decision-support frameworks, including those derived from Weed Risk Assessment methodologies such as the Invasiveness Screening Kit (ISK) family of tools, require calibration of outcome scores to distinguish between higher- and lower-risk species. A prerequisite for such calibration is the *a priori* categorisation of screened species as invasive or non-invasive based on evidence from their introduced range, when applicable. This paper provides a curated global dataset comprising 1,926 taxa identified from 209 applications of the ISK tools across 266 risk assessment areas worldwide, spanning over 21 years. The taxa were assigned *de novo a priori* invasion-status categorisations through a standardised verification workflow using authoritative databases and scientific literature. All verification steps and categorisation-evidence sources are recorded in the dataset, ensuring reproducibility of the evidence supporting each final taxon-level categorisation. This dataset provides a standardised reference resource to support calibration and comparative analyses of invasion risk screening applications.

## Background & Summary

Biological invasions constitute one of the major drivers of global environmental change and biodiversity loss<sup>1–3</sup>. The introduction and establishment of species outside their native ranges can alter ecosystem functioning, disrupt ecological communities, and generate substantial economic impacts<sup>4–7</sup>. Because eradication or control after establishment is often difficult and costly, preventive approaches have become a central component of modern biosecurity policy<sup>8–11</sup>. Consequently, structured frameworks have been developed to evaluate the risks posed by non-native species (*sensu* Soto *et al.*<sup>12</sup>, Vilizzi *et al.*<sup>13</sup>) before or after introduction. Risk analysis in invasion science provides such a framework and typically consists of three sequential steps: risk identification (or screening), risk assessment, and risk management<sup>14–16</sup>. Risk identification determines whether a non-native species is likely to establish, spread, and cause ecological or socio-economic impacts in a predefined area; risk assessment evaluates the likelihood and magnitude of those risks in detail; risk management considers and informs the implementation of appropriate actions in response to the species' likelihood of invasiveness.

To assist scientists and environmental managers in applying risk analysis to non-native species, a variety of decision-support tools have been developed<sup>17–22</sup>. Among the risk screening tools, those derived from the Weed Risk Assessment (WRA) model<sup>23</sup> have been particularly influential in shaping contemporary screening methodologies<sup>24–26</sup>. The original WRA, developed for terrestrial plants and later adapted to aquatic plants, consists of a structured questionnaire implemented as a semi-automated spreadsheet that generates weighted risk scores based on responses to a series of questions addressing a species' biological traits, invasion history, and environmental suitability. Building on this framework, a family of Invasiveness Screening Kit (ISK) tools was developed to extend the WRA approach to a range of aquatic organisms. The first generation of ISK tools included the freshwater Fish Invasiveness Screening Kit (FISK)<sup>14,15</sup>, later followed by several taxon-specific derivatives comprising the Amphibian Invasiveness Screening Kit (AmphISK), the Freshwater Invertebrate Screening Kit (FI-ISK), the Marine Fish Invasiveness Screening Kit (MFISK), and the Marine Invertebrate Invasiveness Screening Kit (MI-ISK)<sup>27</sup>. Subsequent developments led to the second generation of ISK tools, beginning with the Aquatic Species Invasiveness Screening Kit (AS-ISK)<sup>28</sup>, applicable to all aquatic organisms from freshwater, brackish, and marine habitats, and later expanded with the Terrestrial Animal Species Invasiveness Screening

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| Domain                      | Applications (n) | Share of dataset (%) | References         |
|-----------------------------|------------------|----------------------|--------------------|
| Aquatic organisms           | 196 <sup>a</sup> | 93.8                 | 15,25,28,33–224    |
| Terrestrial animals         | 9 <sup>b</sup>   | 4.3                  | 29,225–230         |
| Terrestrial plants          | 4                | 1.9                  | 30,231–233         |
| Total (unique applications) | 209              | 100.0                | 15,25,28–30,33–233 |

**Table 1.** Applications of the Invasiveness Screening Kit (ISK) family of decision-support tools included in the dataset, grouped by organismal domain. Tools comprise: (i) for aquatic organisms, the freshwater Fish Invasiveness Screening Kit (FISK), Amphibian Invasiveness Screening Kit (AmphISK), Freshwater Invertebrate Invasiveness Screening Kit (FI-ISK), Marine Fish Invasiveness Screening Kit (MFISK), Marine Invertebrate Invasiveness Screening Kit (MI-ISK), Aquatic Species Invasiveness Screening Kit (AS-ISK); (ii) for terrestrial animals, the Terrestrial Animal Species Invasiveness Screening Kit (TAS-ISK); and (iii) for terrestrial plants, the Terrestrial Plant Species Invasiveness Screening Kit (TPS-ISK). Applications correspond to independent risk-screening applications or risk assessment areas (RAAs) in which taxa were evaluated. Reference numbers correspond to the numbered reference list. Applications are grouped by organismal domain and, within each domain, ordered chronologically by year and, within year, alphabetically by first author. Under the journal's sequential citation format, references<sup>15,25,28–30</sup> are cited earlier in the Background & Summary and therefore necessarily retain their earlier numbering. This table is provided for transparency and documents the global ISK application corpus used to identify taxa for inclusion in the dataset and to summarise the worldwide extent of ISK use (Figs. 1–5). The references listed here are not the evidence sources used to assign the final *a priori* invasive/non-invasive categorisations. <sup>a</sup>Includes one application based on unpublished screening data incorporated here to improve taxonomic coverage; these data are not listed in the reference list because the corresponding study is not yet published. <sup>b</sup>Includes two applications based on unpublished screening data incorporated here to improve taxonomic coverage; these data are not listed in the reference list because the corresponding studies are not yet published.

Kit (TAS-ISK)<sup>29</sup> and the Terrestrial Plant Species Invasiveness Screening Kit (TPS-ISK)<sup>30</sup>. These taxon-generic decision-support tools are implemented as standalone applications with substantially improved graphical interfaces relative to the first-generation ISK tools and, especially, the WRA, provide enhanced data exchangeability and multilingual support<sup>31</sup>, and include additional questions addressing potential effects of climate change on invasion risk<sup>21,28</sup>. They comply with the 'minimum standards' for screening non-native species under European Community Regulation No. 1143/2014 on the prevention and management of the introduction and spread of invasive alien species<sup>18</sup> and are widely used resources in invasion science<sup>19,32</sup> as a suite of screening instruments applied globally across multiple taxa and ecosystems<sup>15,25,28–30,33–233</sup> (Table 1). The number of ISK applications has increased markedly through time (Fig. 1), reflecting the widespread adoption of these tools for invasion risk identification. Among them, AS-ISK has become by far the most widely implemented decision-support tool for the risk screening of non-native aquatic organisms<sup>15,25,28,33–224</sup> (Table 1).

A critical step in applying WRA-type screening tools involves calibrating outcome scores so that species posing high invasion risks can be distinguished from those posing lower risk<sup>234</sup>. Calibration is commonly performed using receiver operating characteristic (ROC) curve analysis<sup>235</sup>, which evaluates the discriminatory performance of outcome scores for the screened species based on their known invasion status in areas where they have been introduced. For ROC curve calibration, species must first be assigned to *a priori* invasive or non-invasive categories<sup>234</sup>. This means that each species is classified independently of its screening score before calibration is performed, so that the ROC curve analysis can test how well the scores distinguish species with documented impacts in introduced ranges from those without such evidence. The invasive category is operationally defined as species for which documented evidence exists of measurable environmental or economic impacts in at least one introduced range. Here, 'introduced range' refers to any area outside the native range of the species, irrespective of political boundaries. It may therefore include translocated populations within a country where the species is native to one region but has been introduced beyond its native range elsewhere in the same country. This definition follows established practice within ISK applications<sup>16,234,236</sup> and is used here to ensure consistency in ROC-based calibration, without implying a universal or context-independent definition of invasiveness across the broader invasion-science literature<sup>12</sup>.

In practice, these categorisations are usually compiled independently within individual screening applications and are generally repeated when the same species is evaluated for different risk assessment areas (Fig. 2). Consequently, information on *a priori* invasion status remains fragmented across applications and may in some cases be inconsistent when the same species is screened for different risk assessment areas<sup>237</sup>. This fragmentation can bias the ranking of species according to their estimated invasion risk through the computation of an incorrect ROC-calibrated threshold separating medium- and high-risk species (noting that a fixed threshold of 1 is used to distinguish between low- and medium-risk species)<sup>234</sup>, with cascading effects on the subsequent stages of risk assessment and risk management<sup>23,237</sup>.

The absence of a consolidated dataset of species' invasion-status categorisations has limited consistency and reusability across screening applications, as researchers conducting new screening exercises often need to reconstruct calibration datasets from multiple sources, leading to duplication of effort and potential inconsistencies in categorisation criteria<sup>237</sup>. To address this issue, this paper presents a curated global dataset comprising 1,926 taxa with *a priori* invasion status categorisations compiled from 209 applications of the ISK tools to date across 266 risk assessment areas on all inhabited continents, spanning over 21 years, and assigned *de novo a priori*

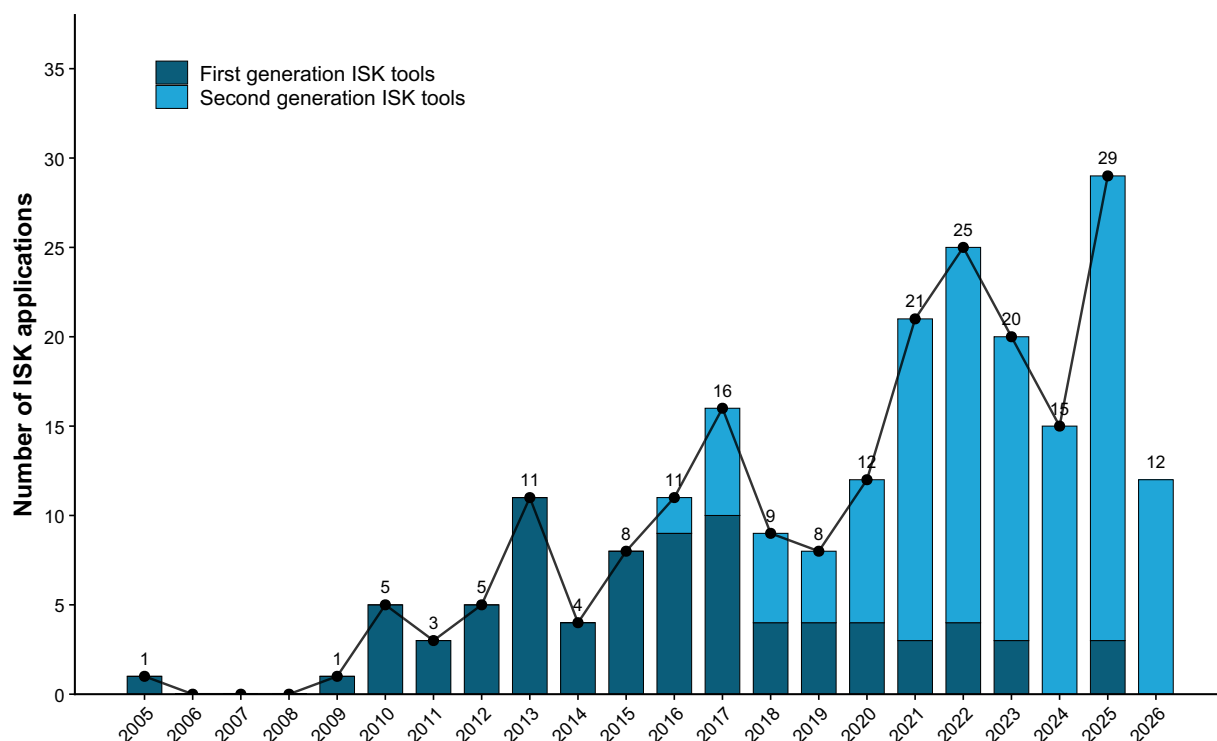


**Fig. 1** Temporal growth in applications of the Invasiveness Screening Kit (ISK) tools from 2005 to March 2026. Stacked bars show the annual number of applications using first-generation (ISK I) and second-generation (ISK II) tools. The black line with points indicates the total number of applications per year up to 2025 and is not extended to 2026 because the year was still in progress at the time of data compilation.

invasion-status categorisation through a standardised verification workflow. The full list of ISK applications is provided for transparency and to document the global extent of ISK use across taxa, habitats, and risk assessment areas (Figs. 1–5). This application source corpus defines the taxonomic scope from which taxa were identified for inclusion in the dataset. Therefore, these application references should not be interpreted as the evidence base for the final *a priori* invasive/non-invasive categorisations. These were assigned *de novo* in the present study through a standardised four-step verification workflow using current species databases and the scientific literature, with all categorisation-evidence sources recorded in the dataset. This study also refines the original *a priori* categorisation protocol<sup>234</sup> by replacing previous reference data sources with more comprehensive and accessible databases.

Although this *a priori* categorisation protocol is applicable to WRA-type screening frameworks more broadly<sup>234</sup>, the present dataset focuses on species screened with the ISK family of tools because these have undergone continuous methodological development and versioned releases, enabling comparability and transferability of screening outcomes and ROC-calibrated thresholds across applications, taxa, and risk assessment areas (Table 1). In addition, the WRA framework for terrestrial plants has recently been extended through the development of the TPS-ISK<sup>30</sup>. Because many taxa included in the dataset have been screened repeatedly across multiple applications and risk assessment areas (Fig. 2), this repeated occurrence highlights the importance of maintaining a consolidated reference dataset that supports the consistent application of their *a priori* invasion status categorisation across applications and facilitates harmonised interpretation of future screening analyses. The resulting dataset provides a consolidated taxon-level reference resource designed to support calibration of invasion risk screening analyses based on the ISK family of tools and a pool of taxa with verified *a priori* invasion status that can be incorporated into new screening analyses and updated as additional screening applications become available. In line with the source literature, throughout ‘species’ is used when referring to the general risk-analysis framework and categorisation protocol, whereas ‘taxon’ is used for the dataset because it includes entities not restricted to the species rank.

## Methods

**Compilation of records.** The dataset was compiled using records for 1,926 taxa derived from 209 applications of the ISK tools for 266 risk assessment areas globally distributed across all inhabited continents (Fig. 3). Notably, the ‘surrogate’ AS-ISK application by Kopecký *et al.*<sup>238</sup> was excluded from the dataset because it provisionally applied only the Biology/Ecology section of the AS-ISK questionnaire<sup>28</sup> to screen terrestrial reptiles, a non-aquatic organismal group outside the intended scope of AS-ISK (and noting that development of the TAS-ISK occurred later<sup>30</sup>). These taxa were compiled from the lists reported in each screening application. Each taxon was represented once in the dataset, even if it had been screened across multiple applications for multiple risk

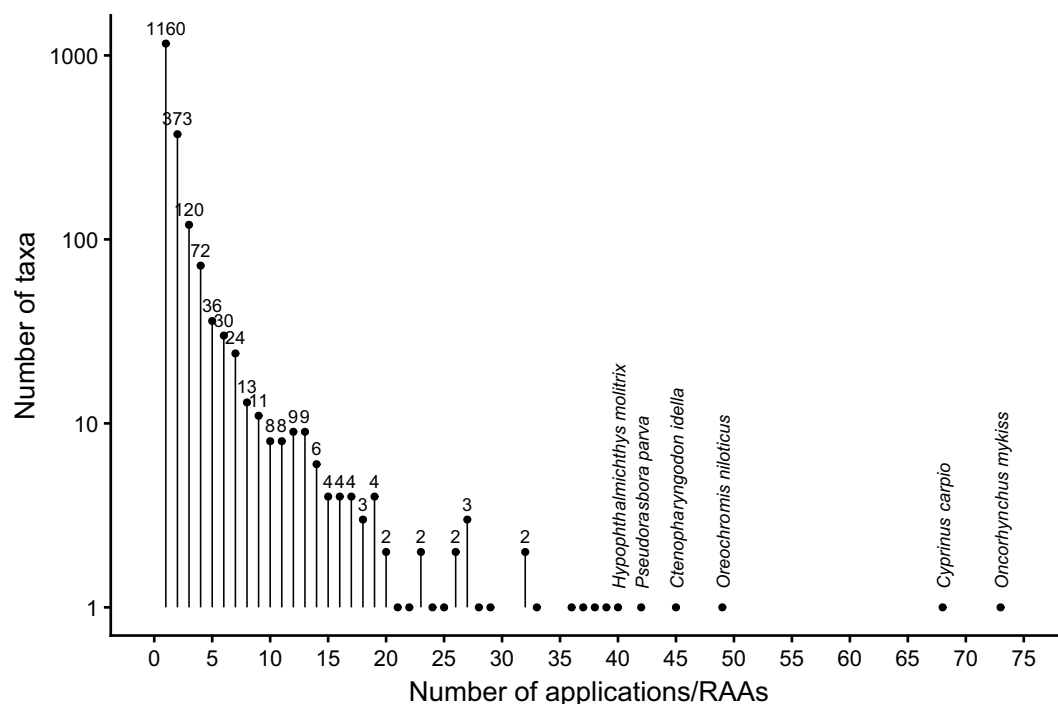


**Fig. 2** Distribution of taxa according to the number of ISK instances (application/risk assessment area combinations) in which they have been evaluated. Points indicate the number of taxa screened across different numbers of screening instances (log scale), with vertical segments connecting each value to the baseline. Species screened in the largest numbers of instances are labelled.

assessment areas or, in some cases, organismal groups; in the latter case, information from multiple screening contexts was used only to characterise the diversity of organismal groups represented in the ISK applications.

Because of the taxon-level structure of the dataset, the original ISK applications were not recorded as row-level sources for each taxon. Many taxa have been screened in multiple applications across several risk assessment areas (Fig. 2), and listing all such applications against each deduplicated taxon record would create a screening-history database, which is outside the scope of the present paper. Instead, the complete list of ISK applications was provided for transparency and to document the worldwide extent of ISK use, including temporal development, geographic coverage, toolkit coverage, and taxonomic breadth (Table 1; Figs. 1–5). These applications define the source corpus from which taxa were identified, whereas the evidence supporting the final *a priori* status categorisation was recorded through the verification-step fields described below.

Of the 209 applications used to define the taxon-inclusion corpus, 204 had been published between 2005 and March 2026, two were available as preprints, and three were unpublished ISK screening datasets included to avoid unnecessary loss of taxonomic coverage (Table 1). These unpublished screenings were used to identify additional taxa that had been screened with ISK tools. For all taxa, irrespective of whether they were identified from published applications, preprints or unpublished screening datasets, the final *a priori* categorisation was assigned independently in the present study through the same standardised four-step verification workflow described below. No unpublished third-party evidence was used to support the final *a priori* status categorisations.

The taxa comprise six genera, 1,896 species, five subspecies, and 19 hybrids, and span five kingdoms (Animalia, Plantae, Fungi, Chromista and Bacteria), 23 phyla, 55 classes, 196 orders and 566 families (Fig. 4). Among these taxa, 1,639 (85.0%) have been screened as aquatic organisms using first-generation ISK tools or AS-ISK, 179 (9.2%) as terrestrial animals using TAS-ISK, and 111 (5.8%) as terrestrial plants using TPS-ISK. Three mammals have been screened both as aquatic organisms (AS-ISK) and as terrestrial animals (TAS-ISK). Of the 1,639 aquatic organisms, 50 species have been screened for two aquatic habitats (i.e. freshwater/marine, freshwater/brackish or brackish/marine), and one for three aquatic habitats (freshwater/brackish/marine). Accounting for taxa screened in two or three habitat contexts, the resulting 1,690 aquatic screening records comprise 16 of the 27 organismal group categories supported by AS-ISK<sup>31</sup>. The 179 terrestrial animals comprise 10 of the 12 organismal group categories supported by TAS-ISK<sup>29</sup> and the 111 terrestrial plants comprise five of the seven organismal group categories supported by TPS-ISK<sup>30</sup> (Fig. 5).

The applications from which taxa were compiled are listed in Table 1 and provide the source corpus underlying the taxonomic scope and descriptive summaries of ISK use presented in this study. The resulting dataset is a standardised, re-verified, taxon-level reference resource for calibration and related comparative applications of the ISK family of tools. It is not intended to reproduce the full history of individual screenings, scores, thresholds or application-specific outcomes across risk assessment areas, which would require a separate taxon-by-application data structure.

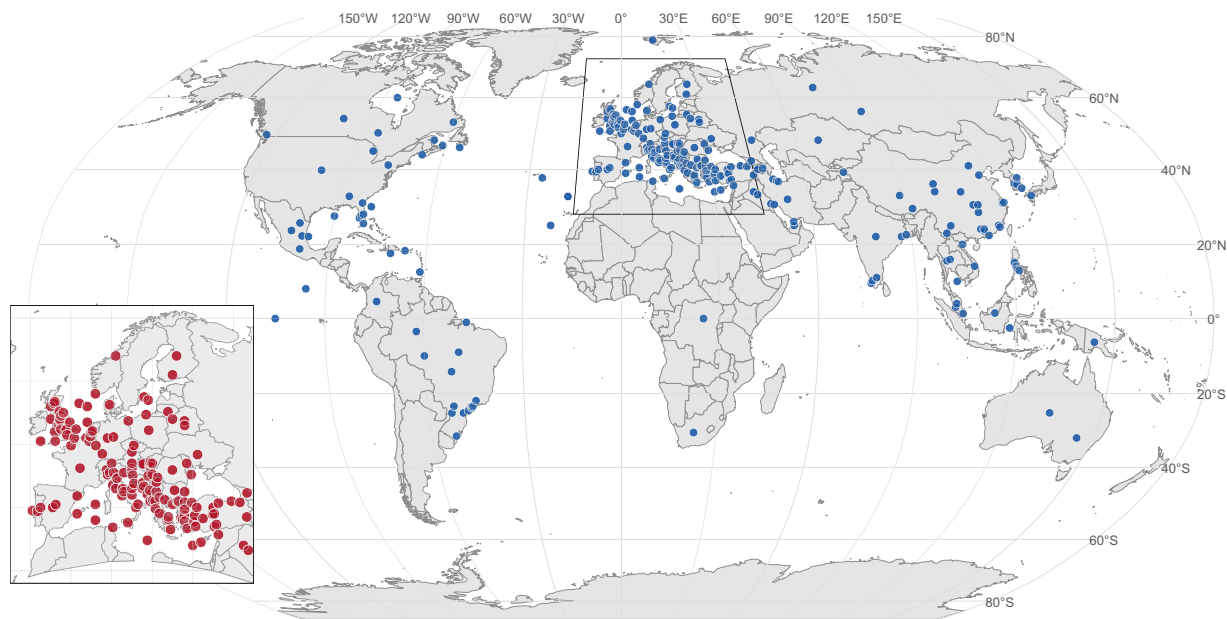


**Fig. 3** Global distribution of ISK applications. Geographic locations of the 266 risk assessment areas contributing records for the 1,926 taxa included in the global dataset with *a priori* invasion status used for calibration of risk screening outcomes, derived from 209 applications of the ISK family of decision-support tools conducted worldwide between 2005 and March 2026. Blue points represent the approximate centroid of each risk assessment area. The inset enlarges Europe to improve visibility of the dense cluster of screening applications in this region.

**Taxonomic standardization.** Taxon names extracted from the source publications were verified against recognised taxonomic reference databases to ensure consistency across records originating from different screening applications. This step was necessary because species lists compiled from publications sometimes contain spelling errors, outdated synonyms or inconsistencies in taxonomic nomenclature. Taxonomic verification was conducted in February–March 2026 using current taxonomic backbones as described below.

During this process, taxon names were compared against authoritative taxonomic references and corrected where necessary to match currently accepted scientific names. Taxonomic verification was performed using the World Register of Marine Species (WoRMS; [www.marinespecies.org](http://www.marinespecies.org)) and the Global Biodiversity Information Facility taxonomic backbone (GBIF; [www.gbif.org](http://www.gbif.org)). WoRMS was consulted when the taxon was listed in that database, whereas GBIF was used when the taxon was not present in WoRMS. This applied mainly to terrestrial animals and plants, although in a few cases aquatic taxa were also verified using GBIF when no corresponding entry was available in WoRMS.

Spelling errors in scientific names present in the original reference sources were corrected during this verification step, with the corrected accepted names retained in the final dataset. Because the dataset is designed as a verified taxon-level reference resource rather than a reconstruction of source-specific nomenclatural changes, original misspellings and their corresponding corrections were not retained as separate fields. Where taxa were reported under outdated or unaccepted names, these were updated to the currently accepted names according to the reference database used for verification (i.e. WoRMS or GBIF), and the accepted names were retained in the dataset. In cases where taxa were reported as morphs or haplotypes that are not currently recognised as valid taxonomic entities, these records were pooled under the corresponding valid taxon name to ensure consistency across the dataset.

Higher-level taxonomy (kingdom, phylum, class, order, and family fields in the dataset) was standardised using authoritative taxonomic sources, including GBIF and WoRMS, with manual completion or verification where classifications were incomplete or taxon names did not match reliably.

***A priori* categorisation protocol.** The *a priori* invasion status of each taxon in the dataset was determined using an enhanced version of the categorisation protocol developed by Vilizzi *et al.*<sup>234</sup> to support calibration of WRA-type decision-support tools. This structured, rule-based protocol categorises species as invasive or non-invasive on the basis of verifiable evidence from authoritative databases and, where necessary, peer-reviewed literature. A species is categorised as invasive when documented impact is identified in at least one introduced range; otherwise, it is classified as non-invasive after completion of all verification steps. All decisions are supported by explicitly recorded sources to ensure transparency and reproducibility of the categorisation workflow. The dataset therefore preserves categorisation provenance at the taxon level, namely the evidence used to assign the final *a priori* status, rather than screening provenance in the form of taxon-by-application histories and associated screening outcomes. The protocol comprises four sequential verification steps of which the first three are applied to all species irrespective of outcome under a redundancy principle, whereas the literature search (Step 4) is undertaken only for species not categorised as invasive after Steps 1–3 (Fig. 6).

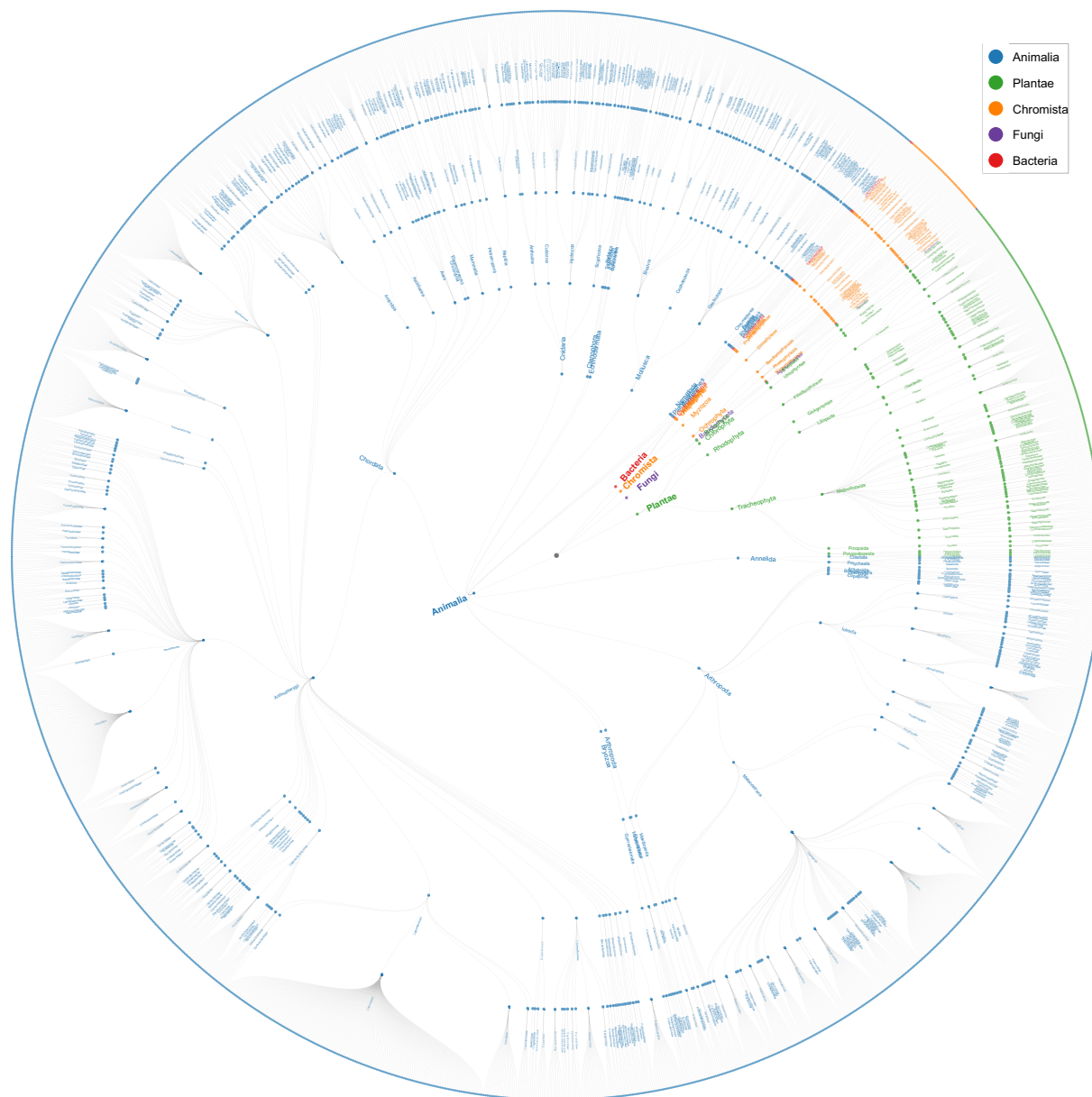


**Fig. 4** Taxonomic scope of the database of taxa with *a priori* invasion status used for calibration of risk screening outcomes. The radial hierarchical tree illustrates the taxonomic distribution of the 1,926 taxa included in the dataset. These taxa span five kingdoms (Animalia, Plantae, Chromista, Fungi and Bacteria), comprising 23 phyla, 55 classes, 196 orders and 566 families. Colours indicate kingdoms and terminal nodes represent the individual taxa included in the database. Kingdom-level counts (taxa): Animalia, 1,662; Plantae, 211; Chromista, 51; Fungi, 1; Bacteria, 2.

In this study, the *a priori* invasion status of each taxon was systematically re-evaluated using current and free-access invasion databases and the scientific literature to ensure consistent application of categorisation criteria across the entire dataset. In cases of conflicting evidence among regions, priority was given to documented impact in any introduced range, consistent with the objective of distinguishing taxa capable of producing measurable impacts under suitable conditions. For this purpose, only records reporting observed or otherwise explicitly documented ecological or economic impacts were accepted as supporting evidence, whereas statements referring only to potential, possible, predicted or suspected impacts were not considered sufficient. Searches across all protocol steps also considered known taxonomic synonyms to ensure that relevant invasion records were not overlooked. All database queries and literature searches were conducted between January–March 2026. The protocol implemented here represents a refined and updated version of the original framework, incorporating modifications to data sources, decision rules, and verification procedures to improve transparency, reproducibility and consistency across taxa, regions, and data sources.

1. *Species-specific databases.* This first step involves a search in species-specific biodiversity databases relevant to the species being evaluated. GBIF served as the primary reference database for 1,914 of the 1,926 taxa in

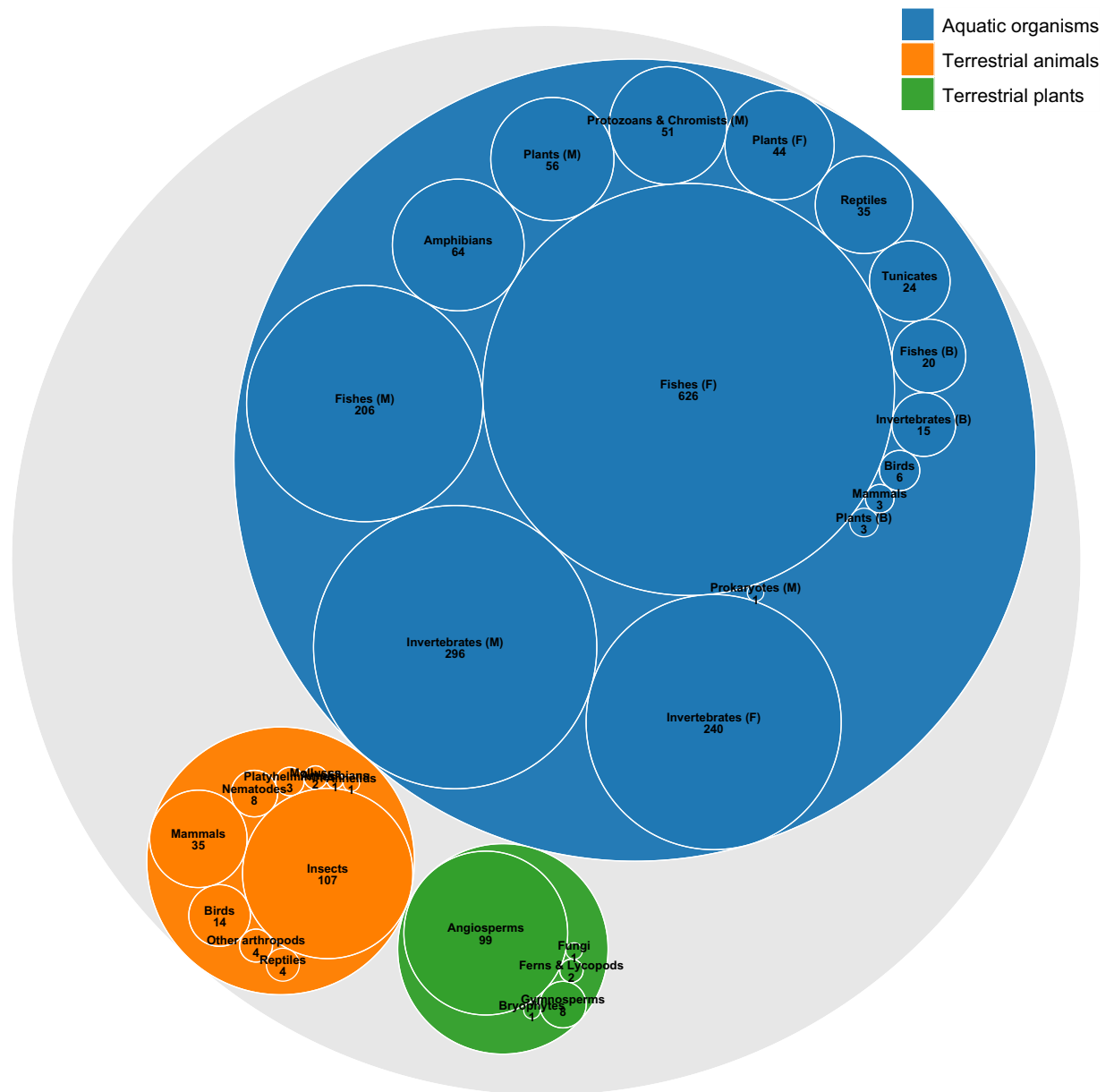


**Fig. 5** Distribution of taxa across organismal group categories in the dataset of taxa with *a priori* invasion status used for calibration of risk screening outcomes. Circle-packing diagram showing the number of taxa assigned to organismal groups within three domains: aquatic organisms, terrestrial animals and terrestrial plants. Circle size is proportional to the number of taxa in each group, and colours correspond to the three domains. The figure includes 1,980 category assignments derived from 1,926 unique taxa in the dataset. The higher number of assignments reflects taxa occurring in more than one organismal group (see text for explanation). Bubble size is proportional to the number of taxa assigned to each organismal group; very small bubbles therefore indicate groups represented by few taxa. Kingdom-level counts as per Fig. 4.

the dataset, whereas for the 12 species not listed in GBIF the database AlgaeBase ([www.algaebase.org](http://www.algaebase.org)) was used. In GBIF, a taxon was categorised as (i) invasive (Y) if documented evidence of impact was reported for one or more countries or islands where it has been recorded as introduced, (ii) non-invasive (N) if no evidence of impact was reported for one or more countries or islands where it has been recorded as introduced, and (iii) not evaluated (–) if no records of introduction were available. Because the Global Register of Introduced and Invasive Species (GRIIS: <https://griis.org/>) is available through GBIF as a checklist resource, GRIIS-derived information on introduced and invasive species was incorporated within this step rather than treated as a separate verification step. This was particularly relevant because GBIF records derived from GRIIS include information on whether a taxon is recorded as invasive based on evidence of impact in the introduced range. Thus, GRIIS contributed to the GBIF evidence base used here for identifying introduced-range status and documented impacts where available. In AlgaeBase, a taxon was categorised as (i) invasive (Y) if listed as ‘harmful’, (ii) non-invasive (N) if not listed as harmful, and (iii) not evaluated

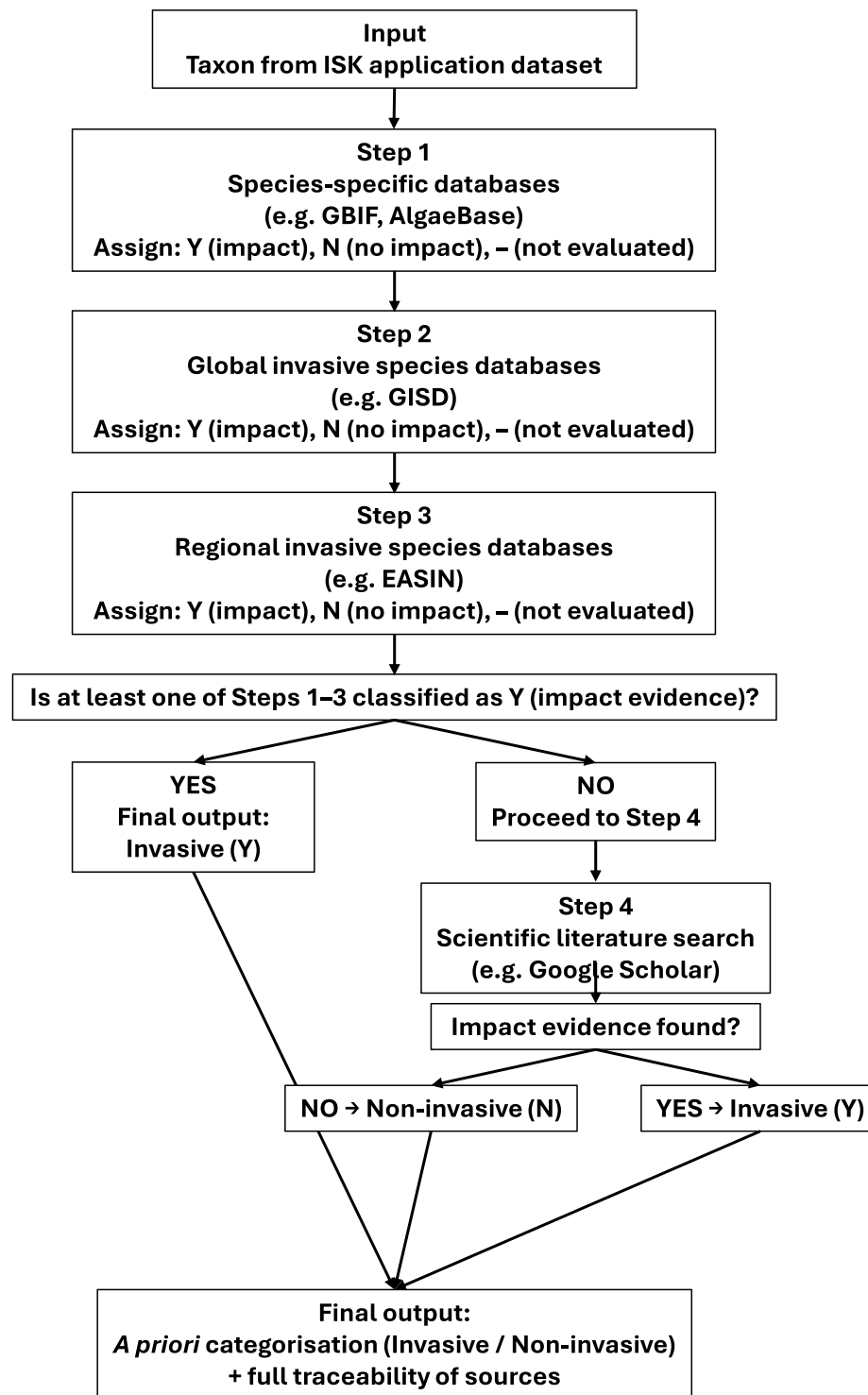


**Fig. 6** Workflow of the *a priori* invasion-status categorisation protocol applied to taxa included in the dataset. Each taxon was sequentially evaluated using: (Step 1) species-specific databases (GBIF or AlgaeBase), (Step 2) a global invasive species database (GISD), and (Step 3) a regional invasive species database (EASIN), with each step assigning a preliminary status of invasive (Y), non-invasive (N), or not evaluated (–) based on the presence or absence of documented impact in introduced ranges. Following these steps, taxa were classified as invasive if at least one of Steps 1–3 provided evidence of impact (Y). Taxa for which no impact evidence was identified in Steps 1–3 were further assessed through (Step 4) targeted searches of the scientific literature (Google Scholar). Documented evidence of ecological or economic impact in introduced regions was considered sufficient for classification as invasive (Y), whereas taxa lacking such evidence were classified as non-invasive (N). All decisions were supported by verifiable sources and recorded within the dataset to ensure transparency, reproducibility, and traceability of the evidence underlying each taxon-level categorisation.

(–) if no relevant information was provided. For hybrids (listed separately as parental species in GBIF), categorisation was assigned as invasive (Y) if documented evidence of impact was reported for either or both parental species, non-invasive (N) if neither parental species had evidence of impact, not evaluated (–) if no introduction records were available for both parental species. GBIF was used in place of FishBase ([www.fishbase.se](http://www.fishbase.se)) and SeaLifeBase ([www.sealifebase.se](http://www.sealifebase.se)) for aquatic organisms, as originally implemented in the protocol<sup>234</sup>, because it provides extensive georeferenced occurrence records and associated metadata on species introductions across regions. By contrast, FishBase and SeaLifeBase classify species only as ‘harmless’ or ‘potential pest’, categories that are often not accompanied by detailed supporting references and are updated irregularly, and SeaLifeBase rarely provides explicit information on documented invasion impacts. Consequently, GBIF allows a more transparent and reproducible identification of introduced occurrences and associated impact evidence for the purposes of *a priori* invasion-status categorisation.

2. *Global invasive species databases.* This second step involves a search in global repositories documenting invasive species and their impacts, which provide curated evidence of invasiveness across multiple regions. The Global Invasive Species Database (GISD; [www.iucngisd.org/gisd/](http://www.iucngisd.org/gisd/)) served as the reference source for this step. For species listed in the GISD, those with documented impacts were categorised as invasive (Y), whereas those without impact information were categorised as non-invasive (N). Species not listed in the GISD were categorised as not evaluated (–) in this step. The CABI Invasive Species Compendium (ISC; <https://www.cabi.org/isc>), originally included in the protocol<sup>234</sup>, was not used in the present study because access to the compendium has since become restricted behind a subscription paywall, limiting its reproducibility and accessibility for users without institutional access.
3. *Regional invasive species databases.* This third step involves a search of regional or country-level inventories of invasive species, which may provide additional evidence of invasiveness in specific geographic contexts not captured by global databases. The European Alien Species Information Network (EASIN; <https://easins.jrc.ec.europa.eu/easin>) served as the reference source for this step. For species listed in EASIN, those reported as causing an impact were categorised as invasive (Y), whereas those listed without reported impacts were categorised as non-invasive (N). Species not listed in EASIN were categorised as not evaluated (–) in this step. The choice of EASIN reflects its extensive taxonomic coverage and its role as an integrated platform compiling data from multiple regional and national invasive species inventories and other authoritative sources, and is therefore an improvement over the previous use in the protocol<sup>234</sup> of the Exotic Species of North America list (IESNA: [www.invasive.org](http://www.invasive.org)).
4. *Scientific literature.* For species not categorised as invasive in the previous steps, targeted literature searches were conducted to identify peer-reviewed publications documenting invasion events or impacts outside the native range. Documented evidence demonstrating ecological or economic impacts in introduced regions was considered sufficient to categorise a species as invasive. Searches were conducted in Google Scholar (<https://scholar.google.com>) using the taxon name in combination with the keywords listed in *Technical validation*. Where multiple relevant publications were identified, the invasion-status categorisation was based on the available body of evidence rather than on a single publication. Specifically, for dataset documentation and traceability, one Step 4 verification source was recorded directly in the relevant taxon row, chosen as the publication providing the clearest and most direct taxon-specific evidence of impact outside the native range, with priority given, where applicable, to the most recent study where this provided equally strong or stronger supporting evidence.

Collectively, these modifications refine the original protocol by improving the consistency, transparency and reproducibility of invasion-status categorisation across species, regions, and data sources.

**Dataset construction.** Following application of the *a priori* categorisation protocol, the outcomes of each verification step were recorded in structured fields together with the corresponding information sources. For each taxon, the dataset contains records documenting the evidence consulted during the categorisation process, including taxonomic reference URL, database-entry URLs, and literature sources where applicable. The dataset was assembled as a harmonised table in which each row corresponds to a single taxon and columns correspond to taxonomic metadata, verification-step outcomes, categorisation-evidence sources, and the final *a priori* status categorisation. This structure preserves the verification workflow and allows the invasion-status categorisation assigned to each taxon to be traced directly to the underlying sources used during the evaluation process. The ISK application source corpus and the categorisation-evidence sources are therefore separate components of the study.

## Data Records

The dataset presented in this study constitutes a consolidated global dataset of taxa identified from applications of the ISK family of tools and assigned *de novo a priori* invasion-status categorisations through the verification workflow described above. The dataset is archived in the Zenodo repository<sup>239</sup> and is provided as a comma-separated values file (.csv) to ensure interoperability with WRA-type decision-support tools commonly used in invasion risk analysis. The dataset is released under a Creative Commons Attribution 4.0 licence (CC-BY 4.0).

The main data file, entitled ‘ISK\_categorisation\_dataset.csv’, contains the complete dataset of taxa included in this study. Each row corresponds to a single taxon and contains the information used to determine its *a priori* invasion status according to the verification workflow described in the *a priori* categorisation protocol. The data file is intended to be used as a standalone taxon-level categorisation resource. Users therefore do not need to reconstruct the categorisation workflow from Table 1, from the ISK application references, or from separate source lists in order to use the dataset. For each taxon, the file provides the accepted taxon name, taxonomic

| Field                | Description                                                                                                                                                                                         | Example                                                                                                                                             |
|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| taxon_id             | Unique identifier assigned to each taxon in the dataset                                                                                                                                             | 7                                                                                                                                                   |
| taxon_name           | Scientific name of the taxon                                                                                                                                                                        | <i>Acanthaster planci</i>                                                                                                                           |
| common_name          | Common name where available                                                                                                                                                                         | crown-of-thorns starfish                                                                                                                            |
| authority            | Taxonomic authority of the scientific name                                                                                                                                                          | (Linnaeus, 1758)                                                                                                                                    |
| kingdom              | Taxonomic kingdom                                                                                                                                                                                   | Animalia                                                                                                                                            |
| phylum               | Taxonomic phylum                                                                                                                                                                                    | Echinodermata                                                                                                                                       |
| class                | Taxonomic class                                                                                                                                                                                     | Asteroidea                                                                                                                                          |
| order                | Taxonomic order                                                                                                                                                                                     | Valvatida                                                                                                                                           |
| family               | Taxonomic family                                                                                                                                                                                    | Acanthasteridae                                                                                                                                     |
| taxon_url            | URL linking to the taxonomic reference used for the taxon                                                                                                                                           | <a href="https://www.marinespecies.org/aphia.php?p=taxdetails&amp;id=213289">https://www.marinespecies.org/aphia.php?p=taxdetails&amp;id=213289</a> |
| step1_species_db     | Evidence from the species-specific database consulted in Step 1 of the <i>a priori</i> categorisation protocol                                                                                      | Y                                                                                                                                                   |
| step1_species_db_url | URL of the species database entry consulted in Step 1                                                                                                                                               | <a href="https://www.gbif.org/species/2271208">https://www.gbif.org/species/2271208</a>                                                             |
| step2_global_db      | Evidence from global invasive-species databases consulted in Step 2                                                                                                                                 | Y                                                                                                                                                   |
| step2_gisd_url       | URL of the Global Invasive Species Database entry consulted in Step 2                                                                                                                               | <a href="https://www.iucngisd.org/gisd/speciesname/Acanthaster+planci">https://www.iucngisd.org/gisd/speciesname/Acanthaster+planci</a>             |
| step3_regional_db    | Evidence from regional invasive-species databases consulted in Step 3                                                                                                                               | Y                                                                                                                                                   |
| step3_easin_url      | URL of the European Alien Species Information Network entry consulted in Step 3                                                                                                                     | <a href="https://easin.jrc.ec.europa.eu/spexplorer/species/factsheet/R16519">https://easin.jrc.ec.europa.eu/spexplorer/species/factsheet/R16519</a> |
| step4_literature     | Literature source recorded directly in the taxon row when Step 4 of the protocol was applied, preferably as a DOI URL where available, or otherwise as a stable URL or full bibliographic reference | n.a.                                                                                                                                                |
| apriori_status       | Final <i>a priori</i> invasive/non-invasive categorisation assigned de novo in the present study from the four-step verification protocol                                                           | Invasive                                                                                                                                            |

**Table 2.** Description of the fields contained in the global dataset of taxa with *a priori* invasion status used for calibration of risk screening outcomes of the ISK family of decision-support tools. The table lists the variables included in the dataset together with their definitions and example entries.

metadata, taxonomic reference URL, verification-step outcomes, source URLs or literature identifiers supporting those steps, and the final *a priori* invasive/non-invasive categorisation. The final categorisation should therefore not be interpreted as having been copied from, or necessarily matching, the original ISK applications. Instead, each categorisation represents the outcome of the standardised verification workflow implemented in the present study.

The structure of the dataset reflects the sequential verification steps used to determine the invasion status of each taxon. Columns correspond to the verification steps of the *a priori* categorisation protocol together with associated taxonomic metadata and the final invasion-status categorisation derived from the protocol. In addition to the final outcome, the dataset retains the intermediate outputs of the verification process together with the associated information sources, thereby preserving the verification workflow and allowing each categorisation to be traced directly to the evidence used during evaluation.

The tabular structure facilitates reproducibility of the categorisation procedure and enables independent verification of the evidence supporting each invasion-status assignment. The variables included in the dataset are described in Table 2.

**Data overview.** To provide a concise overview of the released data file, the dataset contains records for 1,926 taxa compiled from 209 applications of the ISK family of decision-support tools conducted across 266 risk assessment areas worldwide from 2005 to March 2026 (Table 1). The taxa comprise six genera, 1,896 species, five subspecies and 19 hybrids, and span five kingdoms (Animalia, Plantae, Fungi, Chromista and Bacteria), 23 phyla, 55 classes, 196 orders and 566 families. Among these taxa, 1,639 (85.0%) correspond to aquatic organisms screened using first-generation ISK tools or AS-ISK, 179 (9.2%) correspond to terrestrial animals screened using TAS-ISK, and 111 (5.8%) correspond to terrestrial plants screened using TPS-ISK.

The dataset records the outcomes of the four-step *a priori* categorisation protocol together with the corresponding information sources used during the evaluation process. For each taxon, the dataset includes the outputs of the verification steps, links to the database entries consulted during the categorisation workflow, and the final *a priori* invasion-status categorisation derived from the protocol.

## Technical Validation

Multiple quality-control procedures were implemented to ensure the reliability, consistency, and reproducibility of the dataset.

Taxon names extracted from the source publications were verified against recognised taxonomic reference databases to ensure consistency across records originating from different screening applications. This step reduced inconsistencies arising from spelling errors, outdated synonyms, and differing taxonomic conventions.

During taxonomic standardisation of the 1,926 taxa compiled for the dataset, quality control resulted in correction of 17 scientific names for spelling errors, updating of 186 outdated or unaccepted scientific names to currently accepted names, and pooling of 25 taxa reported at morph or haplotype level under accepted taxa. These summary counts are reported here to document the scale of taxonomic standardisation and quality control, but are not included as separate fields in the released dataset, which is designed as a verified taxon-level reference resource rather than a reconstruction of source-specific nomenclatural changes.

The *a priori* invasion status of each taxon was systematically re-evaluated and updated using the four-step verification protocol described above. This validation step was independent of the original *a priori* categorisations, risk ranks, or screening outcomes reported in the source ISK applications. The source applications were used to identify taxa for inclusion, whereas the final categorisation was assigned using the verification evidence recorded in the dataset. This procedure integrates information from authoritative invasion databases and peer-reviewed literature to identify documented evidence of invasiveness outside the native range. Databases consulted during the verification process included GBIF, AlgaeBase, GISD and EASIN. Where database searches did not provide conclusive evidence of invasiveness, targeted Google Scholar searches were conducted using the scientific name of the taxon together with combinations of invasion- and impact-related terms, including “invasive”, “impact”, “non-native”, “alien”, “exotic”, “foreign”, “non-indigenous”, “allochthonous”, “introduced”, “established”, “naturalised/naturalized”, “spread”, as appropriate to the terminology used for different taxonomic groups and invasion contexts<sup>16</sup>. These searches were used to identify peer-reviewed publications documenting invasion events and associated ecological or economic impacts outside the native range of the species. To minimise subjectivity and support reproducibility, categorisations were based on verifiable sources, including curated databases and peer-reviewed literature, and the supporting evidence used to assign each final categorisation is recorded within the dataset to enable independent reassessment.

Higher-level taxonomy was retrieved for 1,536 taxa (80% of all taxa) via WoRMS and for 390 taxa (20%) via GBIF. Under the four-step verification workflow, 677 taxa (35%) were categorised as invasive on the basis of evidence recorded in Steps 1–3, whereas 1,249 taxa (65%) required Step 4 literature searches. Of the 1,249 taxa evaluated at Step 4, 40 (3%) were ultimately categorised as invasive and 1,209 (97%) as non-invasive. Overall, 717 taxa (37%) were categorised as invasive and 1,209 taxa (63%) as non-invasive. This means that just over one-third of the taxa had verified evidence of documented impact in at least one introduced range, whereas the remaining taxa lacked such evidence after completion of the full verification workflow and were therefore treated as non-invasive for calibration purposes. Across the preliminary database-based stages of the workflow, Step 1 assigned Y/N/– to 599 (31%)/642 (33%)/685 (36%) taxa, Step 2 to 193 (10%)/39 (2%)/1,694 (88%) taxa, and Step 3 to 383 (20%)/503 (26%)/1,040 (54%) taxa, illustrating the relative contribution of each evidence source before application of Step 4.

These distributions indicate that the three preliminary database-based stages provided complementary evidence, with Step 2 functioning primarily as an additional source of positive evidence of invasiveness and Step 3 yielding the largest proportion of decisive outcomes before application of Step 4. EASIN was selected as the regional invasive-species database for Step 3 because it is currently the most comprehensive open, harmonised and policy-linked regional platform available for this purpose, integrating non-native species information from multiple sources across terrestrial, freshwater and marine environments in Europe and documenting more than 15,000 non-native species<sup>240</sup>. Other regional resources do exist, but they are generally more limited in geographic coverage, habitat scope, taxonomic breadth or standardisation. Accordingly, Step 3 was designed as a standardised regional confirmation stage based on a single comprehensive source, rather than as a composite search across multiple heterogeneous regional databases, with any remaining unresolved cases addressed through targeted literature searches in Step 4.

The outcomes of all verification steps are recorded directly within the dataset together with the corresponding source URLs. This structure enables each *a priori* invasion-status categorisation to be traced to the underlying evidence used during the categorisation workflow. Maintaining this evidence-level traceability is particularly important because the dataset is intended to support calibration analyses of invasion risk-screening tools.

## Usage Notes

**Intended use.** This dataset provides a taxon-level reference resource for calibration of applications of the ISK tools. Researchers applying ISK tools may use it as a source of *a priori* invasion status for taxa included in their screening exercises. When a screened taxon is present in the dataset, its categorisation can be incorporated directly into the calibration dataset used to determine screening thresholds. For this intended use, the relevant reusable unit is the verified taxon-level categorisation record supported by the evidence captured during the four-step workflow, rather than reconstruction of the full screening history of that taxon across previous applications. For practical reuse, users should search the dataset by accepted taxon name, retrieve the final *a priori* categorisation and, where needed, inspect the verification fields and source URLs to confirm the evidence supporting that categorisation. The ISK application corpus documents why taxa were eligible for inclusion in the dataset; the verification fields document why the final categorisation was assigned.

The dataset can also be used directly in software environments that implement ROC-curve calibration for ISK-based screening applications. This use has been recently implemented in ISK v3.0, which includes a built-in ROC curve computation engine that can use the verified *a priori* invasive/non-invasive categorisations provided here as calibration input<sup>241</sup>. This represents an operational implementation of the dataset as a standalone taxon-level calibration resource, while the dataset itself remains independent of any specific software platform.

The dataset complements the standardised protocol for implementing WRA-type screening tools<sup>234</sup>, which defines the methodological framework for WRA-type screening tools, by providing a globally compiled and standardised reference set of taxon-level *a priori* categorisations for the calibration component of that protocol. In particular, it supports the component concerned with the *a priori* categorisation of species used in

ROC-curve calibration. *A priori* categorisation is relevant only for applications in which calibration of screening outcomes is feasible. ROC-curve calibration requires a representative set of screened species including sufficient numbers of taxa categorised *a priori* as invasive or non-invasive, with a reasonably balanced composition of the two groups and a sample size typically of at least 15–20 species per category<sup>23,24</sup>. Accordingly, in applications in which only one species, or only a few species, are screened, calibration is not possible and a generalised threshold is used instead<sup>25</sup>.

Although developed for ISK applications, the dataset may also be used in comparative analyses of invasion risk, evaluation of screening-tool performance, and investigations of patterns of species invasiveness across taxa and regions. Users should verify invasion-status categorisations for species not included in the dataset and update categorisations where new invasion records become available.

**Limitations.** The dataset is designed as a curated taxon-level reference resource and does not provide reconstruction of taxon-by-application screening histories or application-specific screening outcomes. Its focus is instead on the verified *a priori* categorisation assigned to each taxon through a standardised evidence-based workflow. Users interested in the historical distribution of taxa across individual applications, risk assessment areas or screening outcomes should therefore treat these as separate analytical questions beyond the scope of the present data product. The absence of row-level lists of all ISK applications in which each taxon has appeared is therefore a design choice rather than an omission. Such lists would address a different question, namely the historical distribution of taxa across ISK applications and risk assessment areas. The present dataset instead addresses the calibration-specific question of whether each taxon has verified evidence of documented impact in at least one introduced range.

The dataset is derived from screening applications and associated verification procedures, and therefore reflects the availability and scope of existing assessments. Taxonomic and geographic coverage may consequently be uneven, with some regions and groups better represented than others; however, the use of multiple complementary databases and peer-reviewed literature reduces the likelihood of systematic misclassification.

Invasion-status categorisations are based on the best available evidence at the time of compilation, drawing on authoritative databases and peer-reviewed literature. However, invasion dynamics are time-dependent, and newly documented occurrences may not be immediately reflected. Categorisations should therefore be considered subject to revision as additional evidence becomes available<sup>91,215,223</sup>.

The *a priori* categorisation of species into invasion-status classes simplifies a continuum of invasion processes and impacts. While this is necessary for calibration purposes, users should consider the context dependency of invasiveness when applying categorisations outside the conditions represented in the dataset.

**Future developments.** The dataset is designed to be expandable as new screening applications contribute additional taxa to the source corpus and as new evidence becomes available for taxonomic verification and *a priori* categorisation. Future updates will therefore improve taxonomic coverage and maintain the currency of the evidence base supporting taxon-level categorisations. Expansion of the dataset to address other analytical objectives, including reconstruction of screening histories across applications and risk assessment areas, would require a separate data structure and lies outside the scope of the present Data Descriptor. For species not included in the present dataset, users should follow the same four-step protocol described here in order to assign an *a priori* invasion-status categorisation in a consistent and reproducible manner.

There is also potential for integration with large-scale species inventories, such as those available through EASIN, which include a greater number of taxa. However, such integration would require consistent application of screening and verification procedures and is therefore beyond the scope of the present study. Future work may explore systematic expansion in this direction while maintaining methodological consistency.

## Data availability

The dataset described in this study is publicly available in the Zenodo repository (<https://doi.org/10.5281/zenodo.19240779>). The repository contains the full dataset in CSV format together with metadata describing the structure of the database and the meaning of each field.

## Code availability

No custom scripts are provided with this dataset.

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## Author contributions

The author conceived the study, developed the methodology, compiled and curated the dataset, performed the analyses, and wrote the manuscript.

## Competing interests

The author declares no competing interests.

## Additional information

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