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ANIS-E: An Atlas of Marine Non-Indigenous Species in Europe

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ABSTRACT

Motivation: *Non-Indigenous Species (NIS)* pose a major threat to global biodiversity and incur substantial environmental, economic and health costs. Yet, in marine ecosystems, invasion biogeography remains constrained by the limited availability of spatially explicit and consistently documented native range information, which is essential for identifying source regions and interpreting patterns of spread and establishment. In particular, there is no open, standardised resource that systematically links national and regional introduction reports with explicitly sourced native ranges across marine taxa. We developed *Atlas of marine Non-Indigenous Species in Europe* (*ANIS-E*), a publicly available database compiling introduction reports in European seas, with harmonised, spatially explicit native range assignments. We reason that this resource is a key tool for advancing the understanding of marine invasions and informing conservation efforts and policy decisions in Europe.

Main Types of Variables Included: *ANIS-E* includes 6039 introduction reports, encompassing 2016 marine taxa across 18 European marine ecoregions. It provides information on taxonomic rank, identifiers from other databases (e.g., *WoRMS*, *BOLD*), *NIS* or cryptogenic status, and reported introduction pathways. Native range information is available for 1530 taxa.

Spatial Location and Grain: Every known introduction report, based on published national *NIS* inventories, is recorded for the countries bordering European seas, while the native ranges of the introduced species extend across the globe. All spatial data are collated into marine ecoregions using the *Marine Ecoregions of the World* (*MEOW*) classification.

Time Period and Grain: Introduction reports are recorded from 1700 to 2024.

Major Taxa and Level of Measurement: Marine taxa are identified to the species level or below in rank, spanning six kingdoms plus viruses and encompassing 34 phyla.

Software Format: The database is available in '.csv' format. A user-friendly interface providing access to the same data, powered by an R *Shiny app* included in an R package, is also available.

1 | Introduction

The spread of *Non-Indigenous Species* (*NIS*) in marine ecosystems has accelerated in recent decades, under the combined effect of many human activities, such as globalisation, increased trade and global climate change (Roy et al. 2024). These *NIS* pose significant threats to native biodiversity by competing with local species, sometimes driving them to extinction locally (Ricciardi 2004), by introducing new pathogens in the environment (Chinchio et al. 2020), or by acting as ecosystem engineers that alter habitat structure and function (Rilov et al. 2024). Such impacts are often extensive and enduring, affecting not only ecosystem structure and function but also the services these ecosystems provide (Nie et al. 2017).

Species introductions are a global phenomenon. However, managing and eradicating invasive species is both costly (Diagne et al. 2020) and extremely challenging (Pluess et al. 2012), particularly in marine ecosystems (Booy et al. 2017). In fact, eradication is virtually impossible in marine ecosystems due to the open nature of the environment, its dispersive properties, and the logistical difficulties inherent to detecting *NIS*, as well as implementing and assessing the responses of *NIS* to management actions (Simberloff 2021). Hence, prevention is widely recognised as the most effective strategy for limiting the impact of *NIS* to marine environments (Hewitt and Campbell 2007).

Such prevention requires coordinated policy and governance efforts at both national and international levels. Organisations such as the *Convention on Biological Diversity* (*CBD*) and the *International Union for Conservation of Nature* (*IUCN*) support these efforts by promoting international cooperation, providing risk assessment tools and developing guidance for early detection and management of *NIS* (Kumschick et al. 2024). Within Europe, this commitment is reflected in policies such as the EU Regulation 1143/2014 on the prevention and management of the introduction and spread of invasive alien species and the *Marine Strategy Framework Directive* (*MSFD*, 2008/56/EC), which emphasise prevention, reporting early detection and coordinated action among Member States.

Europe is considered one of the global hotspots for *NIS*, with particularly high numbers recorded in both terrestrial and marine ecosystems (Bailey et al. 2020; Dawson et al. 2017). In particular, the Mediterranean Sea stands out as one of the most invaded marine regions worldwide (Bailey et al. 2020). This biogeographic context, combined with strong regional governance and data availability, makes Europe a particularly valuable case study for understanding *NIS* dynamics and developing comprehensive, standardised resources to support research and management.

Given the large number of marine *NIS* recorded by EU members states (i.e., more than 950 marine NIS had been reported by 2021, of which 82% were introduced since 1970; European Environment Agency (2024)), analysing their introduction dynamics can provide valuable insights for anticipating future invasions. For instance, by monitoring species that are already established in one region, it is possible to identify high-risk zones for further spread, in particular areas that are accessible via natural or human-mediated dispersal pathways (Essl et al. 2015). In parallel, knowing the native range of *NIS* enables the use of environmental matching, for instance through machine learning approaches, to predict where similar conditions may favour future establishment (Broennimann et al. 2021).

Since the late 1990s, several tools have been developed to document marine *NIS* at global and regional scales. These include the *World Register of Introduced Marine Species* (*WriMS*) (Costello et al. 2021), the information system on aquatic non-indigenous and cryptogenic species *AquaNIS* (Olenin et al. 2014), *NEMESIS* (Fofonoff et al. 2018) for marine *NIS* in the United States, and the *European Alien Species Information Network* (*EASIN*; Katsanevakis et al. 2012) for Europe. In addition, the outcomes of the *Delivering Alien Invasive Species Inventories for Europe* (*DAISIE*) project (ended in 2005) are available via the *Global Biodiversity Information Facility* (*GBIF*). Complementing these broad-scale initiatives, a number of regional resources provide more focused syntheses, such as the *CIESM Atlas of Exotic Species* in the Mediterranean, a four-volume series compiling information on non-indigenous fishes, crustaceans, molluscs and macrophytes. Finally, several thematic databases target specific taxonomic groups and provide more detailed, georeferenced occurrence records, such as *ORMEF* (*Occurrence Records of Mediterranean Exotic Fishes*; Azzurro et al. 2022).

These various platforms sometimes also provide valuable information on introduction reports, species traits, native ranges and regulatory frameworks. However, the introduction reports' resources often lack standardised, spatially explicit sourced information on the native range of species (only 2%–29% of taxa include native range information in *AquaNIS*, *DAISIE* or *EASIN*, respectively; see Table S1.1 in Appendix S1 for a comparison between pan-European datasets). In addition, gathering native range information across all these platforms is not easy. These constraints limit the ability to rapidly check the non-indigenous versus native status in specific seas and conduct robust biogeographic comparisons. Here, we propose *Atlas of marine Non-Indigenous Species in Europe* (*ANIS-E*), an information system focused on providing native ranges of NIS at the pan-European scale. In *ANIS-E*, each introduction report is defined as a unique combination of species, country and marine ecoregion, ensuring consistent standardisation of spatial information across all underlying data sources. *ANIS-E* is built by consolidating dispersed information, drawn from existing published national NIS inventories and native range sources, into a single standardised framework, with the added value of providing explicitly sourced native-range information and a mapping interface.

2 | Methods

2.1 | *Marine Ecoregions of the World* as a Biogeographic Framework

Compiling a comprehensive database containing biogeographic information on *NIS* introduction reports together with their native ranges requires a harmonised framework across heterogeneous data sources. We chose the *Marine Ecoregions of the World* (*MEOW*) system (Spalding et al. 2007), one of the most used classification framework in marine systems. The rationale for choosing this system is three-fold: (1) this is a hierarchical system, with ecoregions, the smallest-scale units being strongly cohesive from an ecological perspective, (2) European seas are spread over a large number of ecoregions (i.e., 18 marine ecoregions), from the North and East Iceland to the Levantine Sea (Spalding et al. 2007), (3) the same system can be used for native and introduction range, and for every taxa reported in the database, allowing for comparative analyses. Precise coordinates for either introduction events or native ranges are not systematically available in the literature; most national listing reports indicate broad locations (e.g., country, region or even oceanographic basin). As a result, *ANIS-E* does not provide spatial coordinates. These coordinates can however, be retrieved from high-resolution occurrence databases (e.g., *OBIS*, *GBIF* or *ORMEF*) specifically designed for such purposes. Besides not replicating these databases, *ANIS-E* provides complementary (bio)geographical information in the standardised and hierarchical *MEOW* classification system that allows the harmonisation of native and introduction range information. Our data product is therefore conceptually similar to the *IUCN Red List* assessment maps (IUCN 2025), but specifically targets marine *NIS*.

2.2 | Compilation of Marine *NIS* in European Marine Ecoregions

To consolidate *ANIS-E* for EU Member States, we used the national listing datasets that they submit under Descriptor 2 of the *MSFD* and which are hosted by the European Commission's *Joint Research Centre* (*JRC*; European Commission 2022). As the *MSFD* datasets were last updated in 2022 and follow a six-year reporting cycle, we supplemented these national inventories with relevant publications giving updated lists of *NIS* from Member States' research institutions in anticipation of the next reporting period. For non-EU countries bordering European seas, introduction reports are also included in *ANIS-E*, provided by their respective national competent authorities. First records of *NIS* in European seas published individually since 2022 were not included. A full list of data sources used to compile introduction reports is provided in Table S2.1 in Appendix S2.

Following compilation, we undertook a thorough data cleaning process focusing mainly on taxonomy. First, from the 2138 taxa listed, we removed taxa identified at the genus level or above (30 taxa) with uncertain status but kept taxa reported as cryptogenic (41 taxa), non-marine species (48 taxa) and *NIS* introduced prior to the Columbian Exchange (i.e., pre 1492 see Crosby 1972; 3 taxa). Then, we retrieved the full taxonomic classification for each of 2016 remaining taxa reported using the *WoRMS* database via the R package *worrms* (Chamberlain and Vanhoorne 2023), and standardised all names to their valid form as of 25 March 2026. Our database includes taxa from six kingdoms—Animalia, Plantae, Chromista, Fungi, Bacteria and Protozoa—as well as Viruses, all identified to the lowest possible taxonomic level (species, subspecies, variety or form). However, due to challenges in detection and identification, the reports made by each country for Fungi, Bacteria, Protozoa and Viruses remain incomplete and should be interpreted with caution.

Using the unique *WoRMS* identifiers (i.e., *AphiaID*), we extracted corresponding identifiers from other major taxonomic databases to enhance interoperability through the *worrms* and *taxize* R packages (Chamberlain et al. 2020; Chamberlain and Vanhoorne 2023). The other unique identifiers integrated from other databases are the *Integrated Taxonomic Information System* (*ITIS*, via *TSN*), *FishBase*, *AlgaeBase*, *National Center for Biotechnology Information* (*NCBI*), and *Barcode of Life* (*BOLD*).

2.3 | Determination of Species Native Range

The native range of *NIS* was determined manually using a multi-step approach. First, we consulted several major taxonomic databases such as *WoRMS*, *WRiMS*, *FishBase*, *AlgaeBase* and reviewed the original sources cited within them manually. For those introduction reports where native range information was not provided by these databases, we expanded our search to academic platforms such as *Scopus*, *Web of Science*, *ScienceDirect*, *Google Scholar* and *JSTOR*. If no relevant data were found on these platforms, we consulted the publications that originally described the species directly, when available. A full list of data sources used to determine native ranges is provided in Table S3.1 in Appendix S3. This methodology enabled us to identify native ranges for 1530 taxa. After excluding 189 cryptogenic species (i.e., species whose native or introduced status cannot be confidently determined sensu Carlton (1996)) from the 2016 taxa in our dataset, we obtained native range data for 84% of all *NIS* listed in *ANIS-E*.

To ensure the quality of the native ranges entered in *ANIS-E*, we compared the native ranges we identified with those provided in *DAISIE*, *AquaNIS* and *EASIN* for species common to all three databases; full details are provided in Appendix S1. This comparison demonstrates a high level of concordance between the native areas reported independently in these databases, guaranteeing the high quality of *ANIS-E* data.

In total, *ANIS-E* includes 6039 introduction reports, comprising 5633 *NIS* introduction reports and 406 cryptogenic introduction reports, representing 2016 taxa, identified at the species level or below, across 42 countries and spanning the time period 1700–2024. Each introduction report corresponds to a unique combination of species × country × *MEOW* ecoregion, standardising spatial information consistently across all underlying data sources.

3 | Data Records

ANIS-E is a relational database structured as a set of linked tables and stored in comma-separated values format (.csv). To support interoperability and reuse, the database follows *FAIR* principles (Wilkinson et al. 2016) by using *Darwin Core* (*DwC*; Darwin Core Maintenance Group (2025)) terms and relevant *DwC* extensions where applicable, and by providing rich machine-readable metadata in *Ecological Metadata Language* format (*EML*; Jones et al. (2019)). The *EML* metadata describes the structure of the *ANIS-E database*, including field definitions, units and controlled vocabularies where relevant. Where a direct *DwC* term is not available, we use *DwC* extensions when relevant. When no suitable *DwC* extension exists, we retain project-specific fields and vocabulary and document them in the *EML* metadata. *ANIS-E* comprises six main files: *introduction.csv*, *taxonomy.csv*, *taxonomy_identifiers.csv*, *origin.csv*, *pathway.csv* and *meow.csv*, each described in detail in the *EML Metadata xml* file (available in the Dryad repository, see Data Availability Statement) and in Appendix S4.

The file '*introduction.csv*' contains information on the introduction reports. It contains 6039 rows and 10 columns (see Table S4.1 and S4.2 in Appendix S4 for a detailed description of the information contained in that file). The file '*taxonomy.csv*' contains information on the taxonomy of the taxa listed in the '*introduction.csv*' file. It contains 2016 rows and 8 columns (see Table S4.3 in Appendix S4 for a detailed description of the information contained in that file). The file '*taxonomy_identifiers.csv*' contains information linking taxa names of the '*taxonomy.csv*' to different taxonomical databases. It contains 5889 rows and 5 columns (see Table S4.4 in Appendix S4 for a detailed description of the information contained in that file). The table '*origin.csv*' contains information about the native range of taxa listed in '*introduction.csv*'. It contains 46,010 rows and 5 columns (see Table S4.5 and S4.6 in Appendix S4 for a detailed description of the information contained in that file). The table '*pathway.csv*' contains information about the *CBD* standardised introduction pathways related to the introduction events containing in the '*introduction.csv*' file. It contains 9003 rows and 3 columns (see Tables S4.7 and S4.8 in Appendix S4). Finally, '*meow.csv*' contains information about the *Marine Ecoregions of the World* described by Spalding et al. (2007), a nested system of realms, provinces and ecoregions. It contains 232 rows and columns (see Table S4.9 and S4.10 in Appendix S4 for a detailed description of the information contained in that file).

With this linked table structure, *ANIS-E* preserves full provenance for each record by retaining source references and identifiers that allow users to trace information back to the original dataset or publication. *ANIS-E* is a harmonised compilation and does not aim to independently verify or correct introduction reports from the original sources; with the exception of native range assignments and taxonomic harmonisation, all information is reproduced as reported in the source of the introduction reports (listed in Table S3.1 in Appendix S3). Consequently, any errors or uncertainties regarding introduction dates, introduction pathway present in the original data sources are also reflected in *ANIS-E*. Because *ANIS-E* is a versioned compilation, future releases can incorporate new or updated national inventories and propagate corrections (e.g., taxonomic updates, revised establishment status and amended native-range assignments) while maintaining clear version history and source traceability.

4 | Usage Notes

Users can access *ANIS-E* data in several ways. The dataset is available for direct download as individual '.csv' files from Dryad. Alternatively, users can access *ANIS-E* through the R package anise, which can be installed from GitHub, after installing the package using *devtools::install_github ('clementviolet/ANIS-E')* and loading it with library (anise). Users can load each table individually using the *data ('xx')* function—replacing xx with the table name (excluding the '.csv' extension) or load all tables at once using the *data_anise ()* function. This enables seamless integration of the dataset with users' preferred tools within the R environment.

For a user-friendly and quick visualisation of the data (including maps), the anise package also includes an interactive self-hosted R *Shiny* web interface, which can be launched via the *shiny_anise ()* function (Figure 1a). On the *European Introduction Map* page, users can select one or more European ecoregions (Figure 1b), and download all information regarding the *NIS* inhabiting them, using the COPY, CSV or EXCEL buttons. On the *Species Explorer page*, users can browse information on all taxa included in the *ANIS-E* database (Figure 1c,d). When the input selection mode is set to text (Figure 1d), users can enter either accepted species or higher rank names (following *WoRMS* nomenclature) or *WoRMS taxon identifiers* (*AphiaID*) into the text box. Each input must be entered on a separate line and must correspond to an accepted species or higher rank name in *WoRMS*. If the input selection mode is set to table (Figure 1c), users can filter the table by clicking on the column headers and/or select one or multiple rows by clicking on them. In both input modes, users can download information about the introduction ranges (Figure 1c) or native ranges (Figure 1d) of the selected species by clicking the COPY, CSV or EXCEL buttons. A more detailed presentation of the application is available in the vignette included with the R package.

4.1 | Usage Examples

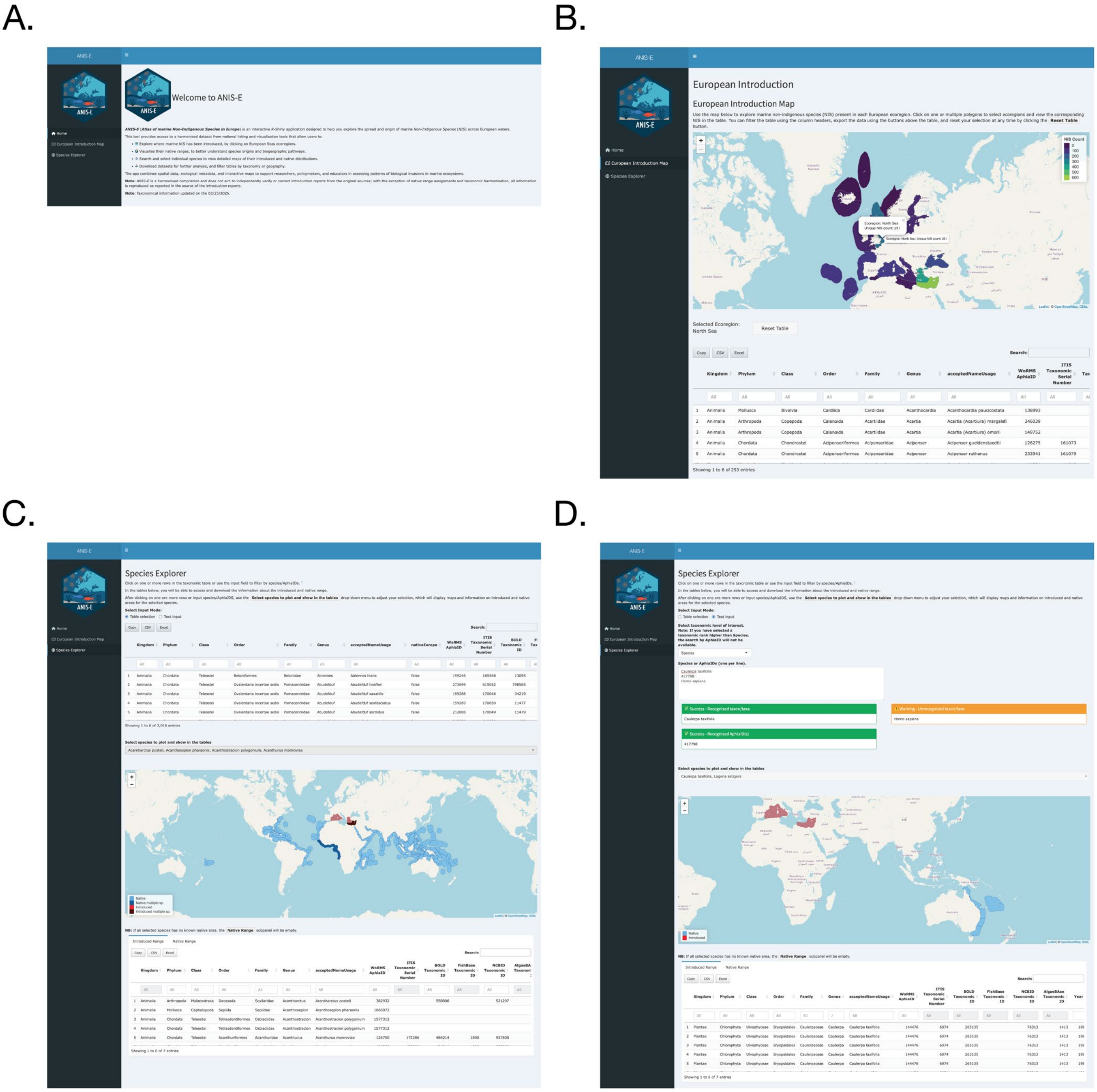
4.1.1 | Biogeographic Origins of Marine *NIS* Across European Seas

A primary aim of *ANIS-E* is to enable the examination of large-scale introduction patterns across European marine regions. A comparison between the Mediterranean Sea and the Northern European Seas illustrates distinct patterns in *NIS* composition and origin (Figure 2). In the Mediterranean Sea, the majority of *NIS* with available native range information are fish (21%) and gastropods (16%), both predominantly originating from the Western and Central Indo-Pacific. In contrast, Northern European Seas are primarily characterised by non-indigenous bivalve introductions (16%), with native ranges in the Temperate Northern Atlantic and Tropical Atlantic. Red algae (10%) from the Temperate Northern Pacific comprise the second most represented group.

These patterns reveal clear contrasts in both the taxonomic composition and native origins of *NIS* between southern and northern European seas. The dominance of Indo-Pacific taxa in the Mediterranean reflects long-standing introduction pathways, notably via the Suez Canal (Spanier and Galil 1991), whereas introductions in Northern European Seas are more closely tied to trans-Atlantic shipping and temperate water affinities (Bailey et al. 2020). This comparison underscores the importance of regional context in understanding marine invasions and highlights the value of biogeographically structured data in detecting patterns and informing prevention strategies.

4.1.2 | Detecting Intra-European *NIS* Transfers

Another example of application of *ANIS-E* is the rapid exploration of *NIS* distributions across Europe, supporting the identification of species recorded in multiple countries. The database distinguishes between species native to certain European marine regions but introduced to others, and species not native to Europe that have been recorded multiple times, either through repeated primary introductions or secondary spread within European seas. For example, it documents the introduction of the brown alga *Cutleria multifida* into the western Mediterranean, the Ionian Sea and the Black Sea during the 19th and 20th centuries. Similarly, it records the expansion of the gastropod *Hexaplex*



Welcome to ANIS-E

ANIS-E (***Atlas of marine Non-Indigenous Species in Europe***) is an interactive *R-Shiny* application designed to help you explore the spread and origin of marine *Non-Indigenous Species* (*NIS*) across European waters.

This tool provides access to a harmonised dataset from national listing and visualisation tools that allow users to:

- Explore where marine NIS has been introduced, by clicking on European Seas ecoregions.
- Visualise their native ranges, to better understand species origins and biogeographic pathways.
- Search and select individual species to view detailed maps of their introduced and native distributions.
- Download datasets for further analysis, and filter tables by taxonomy or geography.

The app combines spatial data, ecological metadata, and interactive maps to support researchers, policymakers, and educators in assessing patterns of biological invasions in marine ecosystems.

Note: *ANIS-E* is a harmonised compilation and does not aim to independently verify or correct introduction reports from the original sources; with the exception of native range assignments and taxonomic harmonisation, all information is reproduced as reported in the source of the introduction reports.

Note: Taxonomical information updated on the 03/25/2026.

European Introduction

European Introduction Map

Use the map below to explore marine non-indigenous species (NIS) present in each European ecoregion. Click on one or multiple polygons to select ecoregions and view the corresponding NIS in the table. You can filter the table using the column headers, export the data using the buttons above the table, and reset your selection at any time by clicking the **Reset Table** button.

Selected Ecoregion:
North Sea

	Kingdom	Phylum	Class	Order	Family	Genus	acceptedNameUsage	WoRMS AphiaID	ITIS Taxonomic Serial Number	Tax
	All	All	All	All	All	All	All	All	All	Al
1	Animalia	Mollusca	Bivalvia	Cardiida	Cardiidae	Acanthocardia	Acanthocardia paucicostata	138993		
2	Animalia	Arthropoda	Copepoda	Calanoida	Acartiidae	Acartia	Acartia (Acartiura) margalefi	346039		
3	Animalia	Arthropoda	Copepoda	Calanoida	Acartiidae	Acartia	Acartia (Acartiura) omorii	149752		
4	Animalia	Chordata	Chondrostei	Acipenseriformes	Acipenseridae	Acipenser	Acipenser gueldenstaedtii	126275	161073	
5	Animalia	Chordata	Chondrostei	Acipenseriformes	Acipenseridae	Acipenser	Acipenser ruthenus	233941	161079	

Showing 1 to 6 of 253 entries

Species Explorer

Click on one or more rows in the taxonomic table or use the input field to filter by species/AphiaIDs. ¹

In the tables below, you will be able to access and download the information about the introduced and native range.

After clicking on one ore more rows or input species/AphiaIDS, use the **Select species to plot and show in the tables** drop-down menu to adjust your selection, which will display maps and information on introduced and native areas for the selected species.

Select Input Mode:
● Table selection ○ Text input

	Kingdom	Phylum	Class	Order	Family	Genus	acceptedNameUsage	nativeEurope	WoRMS AphiaID	ITIS Taxonomic Serial Number	BOLD Taxonomic ID	F Tax
	All	All	All	All	All	All	All	All	All	All	All	Al
1	Animalia	Chordata	Teleostei	Beloniformes	Belonidae	Ablennes	Ablennes hians	false	159246	165548	13055	
2	Animalia	Chordata	Teleostei	Ovalentaria incertae sedis	Pomacentridae	Abudefduf	Abudefduf hoefleri	false	273699	615052	798565	
3	Animalia	Chordata	Teleostei	Ovalentaria incertae sedis	Pomacentridae	Abudefduf	Abudefduf saxatilis	false	159288	170046	34219	
4	Animalia	Chordata	Teleostei	Ovalentaria incertae sedis	Pomacentridae	Abudefduf	Abudefduf sexfasciatus	false	159289	170050	11477	
5	Animalia	Chordata	Teleostei	Ovalentaria incertae sedis	Pomacentridae	Abudefduf	Abudefduf sordidus	false	212888	170049	11479	

Showing 1 to 6 of 2,016 entries

Select species to plot and show in the tables
Acantharctus posteli, Acanthosepion pharaonis, Acanthostracion polygonium, Acanthurus monroviae

NB: If all selected species has no known native area, the **Native Range** subpanel will be empty.

Introduced Range | Native Range

	Kingdom	Phylum	Class	Order	Family	Genus	acceptedNameUsage	WoRMS AphiaID	ITIS Taxonomic Serial Number	BOLD Taxonomic ID	FishBase Taxonomic ID	NCBID Taxonomic ID	AlgaeBA Taxonom
	All	All	All	All	All	All	All	All	All	All	All	All	All
1	Animalia	Arthropoda	Malacostraca	Decapoda	Scyllaridae	Acantharctus	Acantharctus posteli	382932		558906		521297	
2	Animalia	Mollusca	Cephalopoda	Sepiida	Sepiidae	Acanthosepion	Acanthosepion pharaonis	1666972					
3	Animalia	Chordata	Teleostei	Tetraodontiformes	Ostraciidae	Acanthostracion	Acanthostracion polygonium	1577312					
4	Animalia	Chordata	Teleostei	Tetraodontiformes	Ostraciidae	Acanthostracion	Acanthostracion polygonium	1577312					
5	Animalia	Chordata	Teleostei	Acanthuriformes	Acanthuridae	Acanthurus	Acanthurus monroviae	126750	172286	484214	1800	927808	

Showing 1 to 6 of 7 entries

Species Explorer

Click on one or more rows in the taxonomic table or use the input field to filter by species/AphiaIDs. ¹

In the tables below, you will be able to access and download the information about the introduced and native range.

After clicking on one ore more rows or input species/AphiaIDS, use the **Select species to plot and show in the tables** drop-down menu to adjust your selection, which will display maps and information on introduced and native areas for the selected species.

Select Input Mode:
○ Table selection ● Text input

Select taxonomic level of interest.
Note: If you have selected a taxonomic rank higher than Species, the search by AphiaID will not be available.

Species

Species or AphiaIDs (one per line).
Caulerpa taxifolia
417798
Homo sapiens

✓ Success - Recognised taxon/taxa
Caulerpa taxifolia

⚠ Warning - Unrecognised taxon/taxa
Homo sapiens

✓ Success - Recognised AphiaID(s)
417798

Select species to plot and show in the tables
Caulerpa taxifolia, Lagena setigera

NB: If all selected species has no known native area, the **Native Range** subpanel will be empty.

Introduced Range | Native Range

	Kingdom	Phylum	Class	Order	Family	Genus	acceptedNameUsage	WoRMS AphiaID	ITIS Taxonomic Serial Number	BOLD Taxonomic ID	FishBase Taxonomic ID	NCBID Taxonomic ID	AlgaeBAse Taxonomic ID	Year
	All	All	All	All	All	/	All	All	All	All	All	All	All	
1	Plantae	Chlorophyta	Ulvophyceae	Bryopsidales	Caulerpaceae	Caulerpa	Caulerpa taxifolia	144476	6974	265135		76313	1413	196
2	Plantae	Chlorophyta	Ulvophyceae	Bryopsidales	Caulerpaceae	Caulerpa	Caulerpa taxifolia	144476	6974	265135		76313	1413	196
3	Plantae	Chlorophyta	Ulvophyceae	Bryopsidales	Caulerpaceae	Caulerpa	Caulerpa taxifolia	144476	6974	265135		76313	1413	196
4	Plantae	Chlorophyta	Ulvophyceae	Bryopsidales	Caulerpaceae	Caulerpa	Caulerpa taxifolia	144476	6974	265135		76313	1413	196
5	Plantae	Chlorophyta	Ulvophyceae	Bryopsidales	Caulerpaceae	Caulerpa	Caulerpa taxifolia	144476	6974	265135		76313	1413	196

Showing 1 to 6 of 7 entries

FIGURE 1 | (a) Homepage of the web interface of the self-hosted *ANIS-E* R *Shiny App*. (b) *European introduction map* page, displaying a list of *NIS* recorded in each *MEOW* ecoregion. (c) *Species explorer* page (table mode): Users can browse the entire dataset and select a species of interest. Once a species is selected, the *Introduced Range* table below the map provides the corresponding introduced range(s). (d) *Species explorer* page (text mode): Users can submit a list of taxa and retrieve their attributes. The native range table below the map then provides information on the native range(s) of the selected species. NB: The introduced range and native range tables are both available in both mode of *Species explorer* page.

trunculus from the Mediterranean to Macaronesia, the Bay of Biscay and the North Sea. The spread of *Grateloupia turuturu* is also traceable, with the first record in Macaronesia in 1914, followed by later reports suggesting expansion across Europe during the second half of the 20th century, reaching southern Norway in 2019 and the Black Sea in 2021. This spatio-temporal information can be used in conjunction with geographic profiling tools to identify introduction hotspots and likely propagation routes, thereby informing targeted management measures to reduce the risk of further introductions (Essl et al. 2015).

4.1.3 | Using Metabarcoding to Detect Emerging *NIS*

Another objective of *ANIS-E* is to facilitate the rapid verification of species lists against non-indigenous status at the *MEOW* ecoregion level. This functionality is particularly relevant in the context of the increasing use of metabarcoding of environmental DNA (eDNA), which often generates extensive species inventories, including efforts aimed at detecting *NIS*. While metabarcoding offers high-throughput detection capabilities, it is subject to specific limitations such as false positives and false

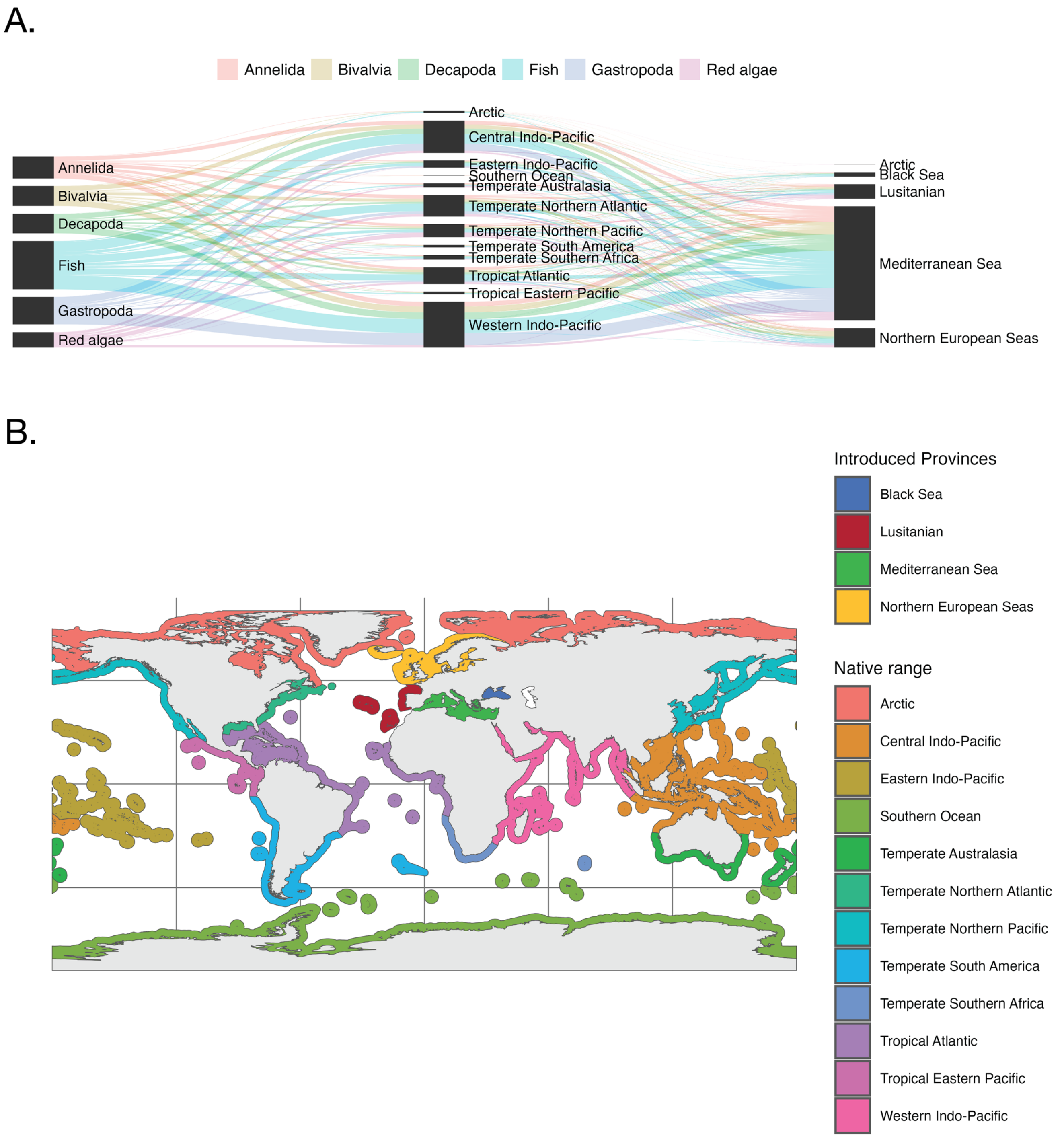


FIGURE 2 | (a) Sankey diagram illustrating the distribution of the six most abundant marine non-indigenous taxonomic groups across European provinces, grouped by their native biogeographic ecoregions (second column) and introduced provinces (third column). (b) World map showing the locations of the biogeographic regions referenced in panel b.

negatives (Couton et al. 2022; Darling et al. 2020). Traditionally, verifying the *NIS* status of taxa detected through metabarcoding required consulting multiple databases (e.g., *AquaNIS*, *NEMESIS*, *WRiMS*), which is time-consuming and may present inconsistencies.

By integrating and standardising information from diverse sources, *ANIS-E* provides a single, harmonised resource for cross-checking metabarcoding outputs against verified *NIS* across Europe. This will likely greatly reduce the time and effort required for data validation and will ensure that assessments are based on a consistent, regionally relevant framework. For example, in a case study involving 538 taxa identified to species level from eDNA samples collected in the Mediterranean Sea (Lilli et al. 2025, submitted), *ANIS-E* enabled fast identification of 41 species as *NIS* for that region, after excluding those native to the Mediterranean but introduced elsewhere in Europe. Coupling *ANIS-E* with metabarcoding thus offers a powerful approach for early detection, monitoring and rapid assessment of marine *NIS*, bridging the gap between molecular observations and policy-relevant reporting.

5 | Perspectives

ANIS-E has a wide spectrum of applications, from operational management to advanced research. For environmental managers, it can facilitate surveillance, early detection and risk assessment of marine *NIS* at regional, national and continental scales. For researchers, it offers a harmonised dataset suitable for ecological analyses, invasion modelling, pathway assessments and biogeographic studies, creating opportunities for cross-disciplinary work. To ensure reliability and long-term usability, the database will be maintained exclusively using information from peer-reviewed and published sources. Its structure allows straightforward updates through the associated *Shiny* application and stable public repositories. Although its initial focus is on Europe, the underlying framework is readily adaptable for expansion to other geographic regions, enabling broader-scale analyses. Building on this foundation, future developments will include the integration of trait data to support functional and ecological analyses, as well as enhanced interoperability with other biodiversity resources (e.g., *GBIF*, *OBIS*). Strengthening connections with genetic databases such as *NCBI* will enable direct linkages between introduction records and molecular data, facilitating genomic studies of invasion processes and supporting emerging tools such as eDNA-based monitoring. In the long term, we hope that *ANIS-E* will complement existing resources and serve as a practical reference for both understanding and managing marine biological invasions.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The *ANIS-E* database is available under a Creative Commons Zero licence from Dryad at: https://doi.org/10.5061/dryad.q2bvq83zr. The *anise* R shiny companion app is available on Zenodo https://doi.org/10.5281/zenodo.17076265 and from Github repository https://github.com/clementviolet/ANIS-E.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Appendix S1: geb70242-sup-0001-AppendixS1.docx** *ANIS-E*, *AquaNIS*, *EASIN* and *DAISIE* comparison. **Appendix S2:** geb70242-sup-0002-AppendixS2.xlsx. Introduction reports data sources. **Appendix S3:** geb70242-sup-0003-AppendixS3.xlsx. Native range data sources. **Appendix S4:** geb70242-sup-0004-AppendixS4.docx. *ANIS-E* controlled vocabulary list.