World of Crayfish™: A web platform towards real-time global mapping of freshwater crayfish and their pathogens (#95689)

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World of Crayfish™: A web platform towards real-time global mapping of freshwater crayfish and their pathogens

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In many regions across the globe, freshwater crayfish and their pathogens alter freshwater communities and cause economic damages. Resulting management decisions and conservation interventions require accurate and up-to-date distribution data and mapping tools. Such data are currently patchily distributed with limited accessibility and are rarely up to date. To address these challenges, we developed a versatile *e*-portal dedicated for freshwater crayfish and their pathogens, populated with expert data and operating in near real-time, including *Aphanomyces astaci*, the causative agent of the crayfish plague. we introduce *World of Crayfish*™, a living, publicly available database providing worldwide distributional data sourced by experts in the field. The database offers open access to the data through specialized standard geospatial services (Web Map Service, Web Feature Service) enabling users to view, embed, and download customizable outputs for various applications. The platform is designed to support technical enhancements in the future, with the potential to eventually incorporate various additional features. This tool intends to be a step forward towards a modern era of conservation planning and management of freshwater biodiversity.

Title

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Abstract

In many regions across the globe, freshwater crayfish and their pathogens alter freshwater communities and cause economic damages. Resulting management decisions and conservation interventions require accurate and up-to-date distribution data and mapping tools. Such data are currently patchily distributed with limited accessibility and are rarely up to date. To address these challenges, we developed a versatile *e*-portal dedicated for freshwater crayfish and their pathogens, populated with expert data and operating in near real-time, including *Aphanomyces astaci*, the causative agent of the crayfish plague. we introduce *World of Crayfish*™, a living, publicly available database providing worldwide distributional data sourced by experts in the field. The database offers open access to the data through specialized standard geospatial services (Web Map Service, Web Feature Service) enabling users to view, embed, and download customizable outputs for various applications. The platform is designed to support technical enhancements in the future, with the potential to eventually incorporate various additional features. This tool intends to be a step forward towards a modern era of conservation planning and management of freshwater biodiversity.

Introduction

Accurate mapping of species distributions is essential for enhancing and improving conservation efforts and decision-making regarding both native and non-native species (Gonzalez et al., 2023). Data derived models, such as species distribution models, are generally helpful for predicting various scenarios of current and future distributions but require specific expertise and quality data for model training and calibration (Liu et al., 2020; Guareschi et al., 2024). Large, globally open access datasets are a priceless resource for tracking changes in the world's biodiversity (Liang & Gamarra, 2020) as easy-to-use and trustworthy platforms increase the capacity of prompt data collection and adequate assessments of growing pressures on many species in a variety of ecosystems (Pyšek et al., 2020). Meanwhile, the computation of global data descriptors for geo-physical, climate, and environmental parameters with high resolution data has increased in availability, with software even designed to provide time series spanning from the past to the present day (Soto et al., 2023). When high quality environmental and biological data are combined, the potential for highly powerful modelling approaches can be realized (Domisch, Amatulli & Jetz, 2015; Beck et al., 2018; Kaufman et al., 2020). For example, spatially explicit conservation assessment and planning, predicting future trajectories of biological invasions and monitoring disease outbreaks across landscapes.

The reliability and power of these approaches are highly dependent on accurate and precise species distribution data (Rocchini et al., 2011; Brooks et al., 2019; Li, Bearup & Liao, 2020). Data found in publicly available databases have to be treated with great care due to e.g., the recent incline in data collected by citizen scientists as the varying levels of expertise and methodologies among participants can introduce biases and inconsistencies that challenge the reliability and comparability of the data sets (Kosmala et al., 2016; Callaghan et al., 2020). Moreover, inaccuracies in species identification and potential disturbances to legally protected or vulnerable species by untrained individuals can compromise data quality and further contribute to conservation concerns, such as proliferation of pathogens through improper biosecurity during monitoring (Barve et al., 2011; Robinson et al., 2020; Lipták et al., 2024).

Freshwater crayfish (Crustacea: Decapoda: Astacida) (sensu Scholtz & Richter, 1995; Crandall & De Grave, 2017) naturally occur on all continents except Antarctica and continental Africa and include roughly 700 described species (Crandall & Buhay, 2007; Crandall & De Grave, 2017) with distinct diversity hotspots in southeastern North America and Australasia (Lodge et al., 2012). Crayfish play an integral role in aquatic ecosystems due to their size, longevity, and omnivorous feeding habits (Momot, 1995). Furthermore, crayfish are regarded as a classical conservation conundrum where many are threatened and vulnerable in their native ranges, whereas many are also recognized as damaging biological invaders (Momot, 1995). Understanding the drivers of this conundrum requires global accurate information on their distribution accompanied by environmental mapping. This is especially the case for non-native crayfish, which, once introduced, can become a major pressure on freshwater biota and the functioning of aquatic ecosystems (Emery-Butcher, Beatty & Robson, 2020). They also pose a significant threat to native crayfish species due to competition, predation, and – among other effects – the transmission of the crayfish plague pathogen *Aphanomyces astaci* Schikora (Chucholl & Schrimpf, 2016; Jussila & Edsman, 2020). Yet, as the eradication of non-native crayfish is often deemed impossible (Lidova et al., 2019; Manfrin et al., 2019), early detection of introduced non-native crayfish remains the most meaningful and a crucial step in mitigating their negative effects and for the conservation of native crayfish (Reaser et al., 2019). Tracking native and non-native crayfish distributions is therefore of utmost importance for the conservation of this group, which contains a wide variety of freshwater (including surface and underground streams and lakes) and semi-terrestrial species (Jussila et al., 2021). Without rapid and accessible communication of field observations, along with geo-spatial descriptive information effective early management actions are impossible (Sax & Gaines, 2003; Mcclenachan, Ferretti & Baum, 2012; Salomaki et al., 2020; Miller et al., 2021). Accurate species identification for many crayfish species, both native and non-native, particularly in sympatric areas, however, remains challenging with expert studies and reports remaining the most trustworthy sources for occurrence data (Costello, 2009; Costello et al., 2013; Costello & Wieczorek, 2014). The value of such reliable expert sources may not be maximized unless they are uploaded and made available in centralized databases (Boakes et al., 2010). Indeed, although the distributions of both native and non-native crayfish as well as the crayfish plague pathogen can be scattered in peer-reviewed publications and other verified resources, there is still a lack of combined, coherent and publicly accessible reliable data, ultimately limiting the practical application for researchers and conservation managers. Traditional mapping has been useful for documenting the locations of European and North American crayfish species, including non-native species and the presence of the crayfish plague pathogen (Kouba, Petrusek & Kozák, 2014; Ungureanu et al., 2020). However, these maps quickly become outdated, and the large volume of published work, in combination with varying accessibility, makes collating data difficult, time-consuming, and resource intensive (Thessen, Cui & Mozzherin, 2012). For instance, Oficialdegui et al (Oficialdegui, Sánchez & Clavero, 2020) conducted a comprehensive review concerning the global spread of *Procambarus clarkii* Girard 1852, identifying occurrences in 40 countries. Since then, in four years, besides the increase of non-native populations in already documented countries, more invasive populations have emerged in other countries previously deemed free of this species.

A comprehensive, large-scale and updateable database on crayfish distributions tracking the dynamic ranges of both native and non-native species should be prioritized to enable quick reporting for accurate assessments of, and predictions about, the evolution of the distributions and the conservation status of these species (Reaser, Frey & Meyers, 2019). Such a database could help scientists and stakeholders make more accurate assessments of the native or non-native status of populations by allowing the determination of possible migration patterns and the most plausible scenarios for the range expansions of some species. Moreover, the efforts of analyzing the spread of pathogens to anticipate the direction and speed of their range expansions and their effects on various species are still in the pioneering stage and require accurate mapping through collaborative efforts among researchers from various fields of expertise (Fišer, 2019; Strand et al., 2019; Marques et al., 2021). For this purpose, and to fill these knowledge gaps in the field of astacology, we introduce the *World of Crayfish*™ (WoC™). This *e*-portal provides an overview of the worldwide distribution of freshwater and semi-terrestrial crayfish and their pathogen *A. astaci* (Martínez-Ríos, Martín-Torrijos & Diéguez-Uribeondo, 2023; Strand et al., 2023), laying the groundwork for addressing other problematic crustacean pathogens in the near future.

The WoC database and platform provide a valuable resource to redress current data deficiencies by gathering and curating data from around the world in one location and to deliver distributional maps and centralized data sets. In addition, the platform also provides an alternative repository for data sets from new publications or indeed prior to publication by offering a unique accession code for each available record. In doing so, WoC overcomes the publication lag time in reporting occurrence data. As WoC accumulates larger volumes of both temporal and spatial data, it will become increasingly relevant for agencies (e.g., the *International Union for Conservation of Nature, Cabi Compendium, European Alien Species Information Network*) responsible for assessing and updating the conservation status of crayfish species and the changing distributions of native and non-native crayfish. Moreover, WoC is built to enable the implementation of additional features and improvements as data availability increases, opening new opportunities for state-of-the-art approaches to ecological modelling of crayfish and crayfish plague occurrences. This initiative is expected to boost and assist research and the publication of faunistic-focused studies on crayfish to contribute to their conservation and management.

Methods

Description

World of Crayfish is a platform that can be accessed at https://world.crayfish.ro/. The platform has an interface that welcomes the user with a brief description of its purpose, along with an introduction to the team behind the project and video instructions to help users understand and navigate the site. New data can be submitted through a downloadable EXCEL template accompanied by an instruction guide. This enables the platform to generate continuously updated maps. Each data contributor can choose a restriction level prior to submitting new records to WoC. This permits that, if a high level of protection (e.g., threatened status of a particular crayfish species or distribution data prior publication) is selected, the exact location (and associated data) is hidden for non-registered users, but those records still contribute to the grid map visualization to ensure the best coverage of a species distribution. A technical review of new datasets is conducted by administrators using an offline preliminary check of the locations' accuracy (and other additional provided information) in accordance with the original sources. The logical workflow is presented in Fig. 1.

Figure 1 here

Database

The database is structured in a single table containing the information, in the same manner of structuring we have provided to potential contributors in the EXCEL template file. The database fields are structured in five sections (Table 1). The first section is dedicated to the source of information, including the Digital Object Identifier (DOI), accompanied by the URL where the article/dataset can be found (if DOI not available) and the citation reference in APA format. The second section consists of location data, coordinates (X - latitude and Y- longitude, decimal degrees), World Geodetic System 1984 (WGS84) projection format, accompanied by accuracy (ensuring that the provided locations are precisely related to the place of a field observation). The third section centralizes the scientific species name (according to the latest taxonomy available in *World Register of Marine Species*, WoRMS, https://www.marinespecies.org/), its status at the locality (native vs. non-native), based on expert assessment in the original source of data records (sensu Soto et al., 2024), and a specific "type locality" mark, if indexing the paper in which a species has been originally described, year of observation and a set of *National Center for Biotechnology Information* (NCBI) GenBank accession codes, if available (COI, 16S, SRA). If there is certain information that a crayfish population has completely disappeared, this section can mark "extinct" which will discard the spot from the time series maps starting with its year of a scientifically documented population extinction record. The fourth section is dedicated to recording details of the crayfish associated pathogens (if any), identified at the specified coordinates of the crayfish host record, alongside pathogen detection and genotyping methods, and eventual genotype and haplotype classification. If detection of the pathogen was confirmed by environmental DNA analysis, then sample coordinates are registered instead of a crayfish host. Finally, the fifth section provides any additional information that might be worth mentioning, including the contributor's name and a confidentiality level that may establish restrictions for data. The confidentiality level will be displayed and downloaded with the exact location for users.

Each record is stored under a unique ID. The EXCEL template has a corresponding table in the *PostgreSQL/PostGIS* database allowing new contributions to be added easily. The corresponding database table has the same attributes as the EXCEL table but also a *PostGIS* specific geometry column so that the location data is easily managed by software. The data from the database is then read by the QGIS Server and served through the WoC platform.

Administrators and Users

The user registration system (upstreamed in the Open-Source code) was developed so that a new user can apply, and receive access approval, based on a specific workflow and requirements setup in the administration side of the platform. New users are reviewed, approved and assigned custom security privileges by the platform administrators who get notified by e-mail of the new sign-up. The platform has an administrator interface that is used to assign granular security privileges for any users: view/edit privileges at project/theme level, layer level, column level or feature level. Feature level permissions are assigned using two kinds of filters: data source level - SQL “WHERE” filters or QGIS Server level - QGIS Expressions. Therefore, the distribution maps’ view is layered with two levels of access: (i) non-registered users (NRU), and (ii) registered users (RU). New users are accepted based on a declaration that can attest to professional interest.

Note to Editors and Reviewers. To facilitate review, we have created a temporary account allowing full access to the platform. The credentials are: username "test", password "forreviewonly".

Display

From the database, the platform will display the information about the selected taxon, projected on an *OpenStreetMap* (https://www.openstreetmap.org/). For NRU, records will be displayed as hexagons with each edge measuring 19 km where the crayfish occurrences per species are aggregated per cell to protect the information on the exact location of the crayfish for conservation purposes. We generated a global hexagonal cell grid using the QGIS platform “Create Grid” algorithm available in the QGIS Processing framework and saved it as a distinct table. To distinguish visually the different occurrences per species, the Jenks natural breaks classification method has been used for grid display. For each species, we correlated the number of occurrences with the opacity value for each cell with a minimum of one occurrence. The opacity scale ranges from 20 (partial opaque cell) to 100 (– fully opaque cell). In contrast, RU, once logged in, may also see a dotted map display with the exact crayfish locations shown on the map according to the coordinates stored in the database. One or multiple taxa can be inspected simultaneously and allocated different colors, either with hexagons or dot shapes displayed. *Aphanomyces astaci* records can be displayed individually, or together with those of crayfish species.

Attribute data

From the WoC database, a set of associated data with the record(s) in the hexagon (for NRU), or dot (for RU), will be displayed. This attribute data lists species names, status (Native/Non-native), number of observations in the selected hexagon (for NRU), years of observations, bibliographic references and the names of the persons who indexed the data in WoC. The bibliographic reference will be linked to a DOI, or similar URL, which will send the user directly to the source paper. Using specific geospatial standards, the attribution of information for each geospatial feature is accessed using a Web Map Service GetFeatureInfo request.

Export

The platform can generate maps and tables to be exported, available for the RU only, listing: GPS coordinates in WGS84 format (if the taxon is not specifically restricted, at the contributor's request), location accuracy on the map, the countries in which it is present, basic statistics of number of records, and the related sourced literature. Also, the platform can be used as an alternative for datasets repository in new publications as it provides unique, identifiable, searchable, and sharable ID (accession code) for each record. The user can access the data through standard geospatial services - OGC (Open Geospatial Consortium) services: WMS (Web Map Service) and WFS (Web Feature Service). Any registered user has access to the data through the WFS endpoint according to its privileges providing the possibilities of download, visualization and embedding into other applications (e.g., QGIS, ArcGIS, Geoserver). For instance, users can access the WMS at: https://map.crayfish.ro/ows/crayfish/?SERVICE=WMS&REQUEST=GetCapabilities.

Data Records

The key features offered by WoC are the compilation of global records into a single accessible platform, enabling users to gain a comprehensive understanding of the distributions of many species of an important freshwater taxonomic group, and the ability to grow by serving as a data repository for newly published studies on freshwater crayfish or the crayfish plague pathogen. Here we present an informative overview of the database at the time of the publication (Fig. 2, and Supplementary Tables 1-3), with 100,750 records indexed belonging to 427 taxa (species, subspecies or species complex; see Supplementary Table 1), from which, a percentage of 75.4% (n = 75,971) is of high geolocation accuracy. In the current dataset, North American continent has the highest diversity (including non-native species) with 390 taxa indexed and 50,979 stored records (50.6%). For a detailed count per country, we refer readers to Supplementary Table 2. The Mississippi River Basin holds the most occurrence records (23,269; 23.1%; Supplementary Table 3). From the total stored data in WoC, 46.8% of the observations (n = 47,201) can be ascribed to non-native species, the most abundant being *P. clarkii* with 39,480 records (39.2 %), covering six continents. The second most reported species outside its native range is *Faxonius limosus* Rafinesque 1817 with 5,879 records (5.8 %). Currently, there are 411 data records associated with *A. astaci,* which are mostly spread over continental Europe.

Figure 2 here

With the severe decline of native crayfish populations and the rapid spread of non-native crayfish (Richman et al., 2015), WoC is expected to be the go-to access point for the rapid and reliable interpretation of spatial and temporal dynamics of crayfish species globally. The easy access to contributing references is helpful not only for new studies, but also for making data of existing scientific publications available to a broader audience. Moreover, the contribution of international collaborators allows WoC to reach crayfish gray literature, often written in local languages and concerning local context (Hannah et al., 2024). This issue, although often neglected, holds paramount importance in nature conservation (Amano et al., 2021, 2023). The platform offers the possibility to revise one or multiple indexed locations to list a population as extinct, 126 of such situations being already indexed. This function allows for time series interruptions if new data suggest that populations from a previously published resource have disappeared, indicating a potential focal point for various ecological pressures (for example, habitat degradation or destruction). In contrast, once a regular location point is entered, it remains "forever" visible in the time series from the date of the original observation stored in the database.

By their very nature, global-scale analyses require large datasets, but distributional data are of limited value if not associated with geospatial ecological variables specifically designed to describe the hydrographic networks (Domisch, Amatulli & Jetz, 2015; Pârvulescu et al., 2016; Şandric et al., 2019). State-of-the-art modeling approaches offer a means to explore and uncover previously unrecognized ecological relationships, thereby reducing uncertainty and validating the significance of outputs (Shen et al., 2023). The WoC platform has been designed to address these challenges by storing locations based on the accuracy of each data point, ensuring high-quality representation of the water bodies where the crayfish reside. This enables us to filter data appropriately for different modeling purposes. Therefore, it could provide opportunities to assess habitat selection patterns and post-glacial migration routes taken by crayfish species and identify the glacial refugia these crayfish may have used during the last Ice Age; which can be useful for understanding modern day distributions and predicting future changes in distributions in relation to climate change and other environmental variables (Guiasu, Barr & Dunham, 1996; Guiaşu & Labib, 2021). We advocate for the use geospatial data designed to describe dendritic river networks instead of landscape-based approaches, as they provide a more ecologically relevant representation of crayfish habitats (Fetzner & Crandall, 2003). The next level in the development of the WoC platform is to add this feature, whereby registered users will be able to download customizable datasets to support their modeling procedures.

Technical Validation

The ability to visualize geographic ranges of multiple species and their environmental conditions is a critical resource for ecological and conservation research aiming to assess an organism's responses to change (Villero et al., 2017). Centralized resources will improve capacity for spatially explicit management and policy decision-making regarding endemic, threatened, and non-native crayfish (Taylor et al., 2019). It is important to ensure that such data are based on rigorous investigations to avoid potential errors and inaccuracies. The distinctions and boundaries between native and non-native ranges, particularly in areas where these ranges are adjacent to each other and not separated by any obvious environmental barriers, can often be difficult to establish and decisions on the native or non-native status of species can be subjective (Pereyra & Guiaşu, 2020). Comprehensive, regularly updated, and professionally collected and managed datasets on the distributions of species hold the promise of more accurate diagnoses regarding the status of these species and the evolution of their ranges over time. Raw data, such as those obtained from citizen science online databases are generally useful, at least to some extent, but need expert validations as they may be prone to errors resulting from taxonomic confusion, species misidentification, and mistakes in recording locations, among others (Clare et al., 2019). In the particular case of crayfish, expert-validated data are more likely to be accurate and reliable since they are typically subjected to rigorous taxonomic scrutiny, which is essential for accurate species identification (Jiménez-Valverde, Lobo & Hortal, 2008). In some cases, molecular analyses are additionally used to confirm taxonomic identifications, further increasing the accuracy of the data (Bystriakova et al., 2012). Nevertheless, there are also some disadvantages associated with data from published sources as, for example, the lag time between data being obtained and published may be slow, limiting its usefulness for time-sensitive research. Data from published sources can also be difficult to centralize due to the diverse publication access policies of different journals and the heterogeneity of databasing formats (Reichman, Jones & Schildhauer, 2011).

WoC's maps provide an advantage over drawing from the literature by eliminating the time-consuming, and often repeated, effort for every new study. Our indexed data are delivered in a unitary format, with special emphasis on the projection system of geographic locations and validated accuracy, which greatly eases and streamlines the processes required for modeling input data. The known level of accuracy allows data filtering, saving time, and enabling quality datasets. It is important to note that, when visualizing large-scale distribution maps, accuracy is not always prioritized; hence, our map will display all levels of data accuracy. We provide a confidence rating through the accuracy attribute in our downloadable datasets, this allows modelers to make informed decisions on the preciseness of the data they use. When developing models, the presence of redundancy and imbalances in sampling can impact the overall quality of the model. Therefore, we recommend that researchers consider spatial re-sampling to ensure uniform geographical coverage in their selected areas (Guisan & Zimmermann, 2000). Species-associated data issues can also be related not only to taxonomic errors (Meier & Dikow, 2004) but also to inaccurate or incomplete spatial and temporal information (Meyer, Weigelt & Kreft, 2016). While misidentification should be a lesser issue for data from peer-reviewed articles, spatial errors can occur and need clarification (Graham et al., 2008; Führding-Potschkat, Kreft & Ickert-Bond, 2022). One of the most frequent issues observed while indexing papers for WoC was the insufficient standardization of spatial data formatting and overall dataset heterogeneity. When coordinates of locations were supplied in publications (usually as supplementary material) and not just maps, these were sometimes lacking important information like the type of geographic coordinates used or Universal Transverse Mercator - UTM grid derived systems. These situations generate confusion for most users without GIS training, even when mentioned, geodetic datum (for geographic coordinates) or zone (for UTM coordinates). A lack of more detailed and precise information on the coordinate reference systems may lead to significant positional errors with a shift from the original position between zero and more than 5000 meters (Wieczorek, Guo & Hijmans, 2004; Guralnick et al., 2006). Even though a high correlation between models derived from the *Global Biodiversity Information Facility* (GBIF) and those from expert data is often found (Führding-Potschkat, Kreft & Ickert-Bond, 2022), expert data did not require processing. While this might be true for some taxa, assembling several expert datasets for crayfish still requires some degree of homogenization and a comprehensive review for completeness.

Finally, a concerning trend of declining interest in faunistic studies appears, at least at the level of high-impact scientific journals (Ejsmont-Karabin, 2019). Data of this type may be of more interest to some governmental organizations, which only target certain species, such as those listed in legislation either because they may be vulnerable or endangered or because they may be regarded as invasive. This leaves a large gap in scientific knowledge and the conservation of biodiversity at a global level, since most other species are largely ignored (Valdecasas & Camacho, 2003; Rodríguez et al., 2015). Data curation with the aid of automated information retrieval from published literature is a promising avenue for near real-time databasing (Kopperud, Lidgard & Liow, 2022). Screening tools and automatic data collection from the scientific literature based on natural language processing to extract the locations of crayfish species with text-mined occurrences, and solving language barriers by machine linguistic translation, are essential for sourcing large scale biodiversity data (Amano et al., 2023; Hannah et al., 2024). In addition, features for automated population genetics and phylogenetic analyses are plausible, based on freely accessible data from public genetic databases and popular open-source packages implemented using the R programming language (R Core Team, 2024). All these features may represent future opportunities to improve the WoC platform and reinvigorate the interest for faunistic studies not only on crayfish, but also on a variety of other animal groups. In this context, WoC provides 98.5% of data sourced from scientific papers, data reports, and museum databases, while 1,444 are currently unpublished data. For the latter data category, WoC offers a repository function for further publication. The database also provides, where available, the specific *GenBank* accession codes for the most common DNA sequences from genetic studies on crayfish, with 2,065 for CO1, 1,375 for 16S, and 15 SRA records already being available in WoC. It also has a function to filter if the status attribute of a species record is listed as "type locality", 16 being already indexed for a convenient way users can quickly access hard-to-find information, such as original formal descriptions from the scientific literature linked to visualization on a map. Particularly, the exact geographic location of a species is available for RU, whereas to protect sensitive species information, for non-registered users the platform displays hexagon shapes where records are available.

Usage Notes

World of Crayfish itself is a repository database. In addition to the repository files, these data are also available via the interactive web platform (https://world.crayfish.ro/). Access is free, with restricted viewing to the exact location for crayfish species for rational reasons of sensitive species to commercial exploitation purposes. The data are curated to meet the FAIR principles, ensuring that every dataset is findable, accessible, interoperable, and reusable, stored and distributed by WoC platform. The WoC is a word and figurative trademark, pending registration under No. M2024/00394 of 18.01.2024 at the Romanian National Office for Intellectual Property. The request for trademark award is done under Class 42 of the Nice Classification (World Intellectual Property Organization, 2022). The award of the national trademark certification will be followed with a request for international protection at the World Intellectual Property Office in accordance with the Madrid System. However, we encourage citation of those sources associated to any record in WoC, and WoC platform to be cited as the tool for delivering multi-source compilations and various outputs.

Code Availability

All the platform code is Open-Source for gaining fast adaptability of the platform for future development, but also to provide built-in security, using g3w-suite framework (https://github.com/g3w-suite/), a Django based QGIS platform and PostgreSQL database (https://www.postgresql.org/) with PostGIS extension (https://postgis.net/).

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Author contributions

LP conceived the project and write the first draft of the manuscript.
MCI coordinated databasing, and with the help from CCB, CAT, and ȘGK curated the datasets in order to meet the specific criteria for being indexed in WoC.
TIB, AEB, LV, and AL created the platform IT environment.
AM, MN, ADC, AP, and AK provided support in screening the literature
MCI, CCB, FJO, NFS, BWW, KS, MC, FG, MC, TB, ZJL, JJ, TJR, CC, SG, BK, ZMB, JEH, MH, KK, BL, SG, JWF, TC, AW, JB, TT, MT, MB, BG, ONP, AA-A, GD'E, KŚ, AA, HC, JS, NW, KZ, PH, IS, DJB, PJH, PJT, DȘ, PV, CK, SWJ, J-YK, XV, MB, RG, MMH, JD, IK, DB, PB, HM, PRC, JJ, TV, DVB, SMR, JP, DAS, AST, FS, TA, MH, SA, SK, IAG, RM, MVA, ÖA, DMH, TK, ET, ATC, CAT, LP contributed with datasets.
All the authors participated in the writing of the manuscript and approved the final version for publication.

Competing interests

Nothing to declare.

Figure Legends

Figure 1. Schematic representation of the logical workflow in and around the WoC ecosystem.

Figure 2. Overview of the collected data in WoC platform, and various centralisation. A-B display records of natives versus non-native crayfish species records at continental level (type locality and *Aphanomyces astaci* highlighted). C-D display country level record counts (native versus non-native), D-E represents major hydrographic basins record counts (native versus non-native). The lower panel integrates data for the species most well represented.

Tables

Table 1. The World of Crayfish database fields' structure, also available as a template for contributors.

Section	Title	Brief description	Available for	
			NRU	RU
Source information	DOI	Digital object identifier, a mandatory field (if available).	Yes	Yes
	URL	Uniform Resource Locator, the address of a given resource on the Web.	Yes	Yes
	Citation	Full reference for the source (for articles), APA format. For unpublished data, the contributors may ask for unique WoC database identifier.	Yes	Yes
Geolocation	X	Latitude, decimal degree, WGS 84 projection format.	No*	Yes
	Y	Longitude, decimal degree, WGS 84 projection format.	No*	Yes
	Accuracy	Specifies how precise the provided coordinates are related to the place of field observation. High: data sourced from field records, maps at hydrographic level, toponymy with good details. Low: data sourced from continental or national grid systems, estimated locations based on toponymy with low details.	No	Yes
Crayfish	Crayfish scientific name	A mandatory field for the scientific name of the observed crayfish species. Exceptionally empty, when a record of *Aphanomyces astaci* without host (i.e., by eDNA detection) is stored.	Yes	Yes
	Status	Native*: a crayfish species that naturally occurs in a specific region due to natural evolution over time. Non-native*: a crayfish species (or associated pathogen) that has arrived facilitated by non-natural actions in a region where it does not belong due to natural evolution over time. Type locality: if indexing the paper in which a species has been initially described. *these categories in the table are not value-laden	Yes	Yes
	Year of observation	The year when the observation of the crayfish specie was made.	Yes	Yes
	NCBI COI accession code	The accession code in NCBI`s GenBank for COI sequence if such data is available.	No	Yes

	NCBI 16S accession code	The accession code in NCBI`s GenBank for 16S sequence if such data is available.	No	Yes
	NCBI SRA accession code	The Sequence Read Archive in NCBI`s GenBank if such data is available	No	Yes
	Claim extinction	If certain information that a crayfish population has completely disappeared is available. This kind of record will discard the spot from the time series maps starting with its year of record.	No*	Yes
Associated pathogens	Pathogen present	The scientific name of a crayfish associated pathogen, if present (i.e., *A. astaci*), on a crayfish specimen (data stored in Crayfish section).	Yes	Yes
	Pathogen detection method	Contributor declaration of the method used for detection of the pathogen: Molecular/Microscopic/eDNA/any other.	Yes	Yes
	Pathogen genotyping method	If available: Chitinase sequencing/Microsatellites/mtDNA sequencing/AFLP/RFLP/RAPD/Anonymous nuclear markers	Yes	Yes
	Genotype group	If available: A/B/D/E/Up/other described	Yes	Yes
	Haplotype	If available: d1/d2/other described	Yes	Yes
	Year of observation	The year when the samples was taken.	Yes	Yes
Additional information	Comments	Any optional additional information that might be worth mentioning.	Yes	Yes
	*Confidentiality level	The degree of openness that the contributor has chosen for the data. No restrictions: data will be displayed with the exact location for all users. Regular restrictions: 25 km hexagonal shape displayed for NRU, exact location display for RU. High restrictions: data displayed in a 25 km hexagonal shape for all users.		
	Contributor	The name of the contributor holder to the database for a respective record.	Yes	Yes

Supplementary Table 1. Records count per crayfish taxa integrated in WoC platform.

Supplementary Table 2. Crayfish and *A. astaci* records integrated in WoC platform count per country.

Supplementary Table 3. Crayfish and *A. astaci* records integrated in WoC platform count per major hydrographic basins.

References

Amano T, Berdejo-Espinola V, Akasaka M, de Andrade Junior MAU, Blaise N, Checco J, Çilingir FG, Citegetse G, Corella Tor M, Drobniak SM, Giakoumi S, Golivets M, Ion MC, Jara-Díaz JP, Katayose R, Lasmana FPS, Lin HY, Lopez E, Mikula P, Morales-Barquero L, Mupepele AC, Narváez-Gómez JP, Nguyen TH, Lisboa SN, Nuñez MA, Pavón-Jordán D, Pottier P, Prescott GW, Samad F, Šćiban M, Seo HM, Shinoda Y, Vajna F, Vozykova S, Walsh JC, Wee AKS, Xiao H, Zamora-Gutierrez V. 2023. The role of non-English-language science in informing national biodiversity assessments. *Nature Sustainability 2023 6:7* 6:845–854. DOI: 10.1038/s41893-023-01087-8.

Amano T, Berdejo-Espinola V, Christie AP, Willott K, Akasaka M, Baldi A, Berthinussen A, Bertolino S, Bladon AJ, Chen M, Choi CY, Kharrat MBD, De Oliveira LG, Farhat P, Golivets M, Aranzamendi NH, Jantke K, Kajzer-Bonk J, Cisel Kemahli Aytekin M, Khorozyan I, Kito K, Konno K, Lin DL, Littlewood N, Liu Y, Liu Y, Loretto MC, Marconi V, Martin PA, Morgan WH, Narvaez-Gomez JP, Negret PJ, Nourani E, Ochoa Quintero JM, Ockendon N, Oh RRY, Petrovan SO, Piovezan-Borges AC, Pollet IL, Ramos DL, Reboredo Segovia AL, Nayelli Rivera-Villanueva A, Rocha R, Rouyer MM, Sainsbury KA, Schuster R, Schwab D, Sekercioglu CH, Seo HM, Shackelford G, Shinoda Y, Smith RK, Tao SD, Tsai MS, Tyler EHM, Vajna F, Valdebenito JO, Vozykova S, Waryszak P, Zamora-Gutierrez V, Zenni RD, Zhou W, Sutherland WJ. 2021. Tapping into non-English-language science for the conservation of global biodiversity. *PLOS Biology* 19:e3001296. DOI: 10.1371/JOURNAL.PBIO.3001296.

Barve N, Barve V, Jiménez-Valverde A, Lira-Noriega A, Maher SP, Peterson AT, Soberón J, Villalobos F. 2011. The crucial role of the accessible area in ecological niche modeling and species distribution modeling. *Ecological Modelling* 222:1810–1819. DOI: 10.1016/J.ECOLMODEL.2011.02.011.

Beck HE, Zimmermann NE, McVicar TR, Vergopolan N, Berg A, Wood EF. 2018. Present and future köppen-geiger climate classification maps at 1-km resolution. *Scientific Data* 5:1–12. DOI: 10.1038/sdata.2018.214.

Boakes EH, McGowan PJK, Fuller RA, Chang-Qing D, Clark NE, O'Connor K, Mace GM. 2010. Distorted Views of Biodiversity: Spatial and Temporal Bias in Species Occurrence Data. *PLOS Biology* 8:e1000385. DOI: 10.1371/JOURNAL.PBIO.1000385.

Brooks TM, Pimm SL, Akçakaya HR, Buchanan GM, Butchart SHM, Foden W, Hilton-Taylor C, Hoffmann M, Jenkins CN, Joppa L, Li B V., Menon V, Ocampo-Peñuela N, Rondinini C. 2019. Measuring Terrestrial Area of Habitat (AOH) and Its Utility for the IUCN Red List. *Trends in Ecology and Evolution* 34:977–986. DOI: 10.1016/j.tree.2019.06.009.

Bystriakova N, Peregrym M, Erkens RHJ, Bezsmertna O, Harald S. 2012. Sampling bias in geographic and environmental space and its effect on the predictive power of species distribution models. *Systematics and Biodiversity* 10:305–315. DOI: 10.1080/14772000.2012.705357.

Callaghan CT, Roberts JD, Poore AGB, Alford RA, Cogger H, Rowley JJL. 2020. Citizen science data accurately predicts expert-derived species richness at a continental scale when sampling thresholds are met. *Biodiversity and Conservation* 29:1323–1337. DOI: 10.1007/S10531-020-01937-3/FIGURES/5.

Chucholl C, Schrimpf A. 2016. The decline of endangered stone crayfish (Austropotamobius torrentium) in southern Germany is related to the spread of invasive alien species and land-use change. *Aquatic Conservation: Marine and Freshwater Ecosystems* 26:44–56. DOI: 10.1002/aqc.2568.

Clare JDJ, Townsend PA, Anhalt-Depies C, Locke C, Stenglein JL, Frett S, Martin KJ, Singh A, Van Deelen TR, Zuckerberg B. 2019. Making inference with messy (citizen science) data: when are data accurate enough and how can they be improved? *Ecological Applications* 29:e01849. DOI: 10.1002/EAP.1849.

Costello MJ. 2009. Motivating online publication of data. *BioScience* 59:418–427. DOI: 10.1525/BIO.2009.59.5.9/2/BIO.2009.59.5.9-F01.JPEG.

Costello MJ, Michener WK, Gahegan M, Zhang ZQ, Bourne PE. 2013. Biodiversity data should be published, cited, and peer reviewed. *Trends in Ecology and Evolution* 28:454–461. DOI: 10.1016/j.tree.2013.05.002.

Costello MJ, Wieczorek J. 2014. Best practice for biodiversity data management and publication. *Biological Conservation* 173:68–73. DOI: 10.1016/J.BIOCON.2013.10.018.

Crandall KA, Buhay JE. 2007. Global diversity of crayfish (Astacidae, Cambaridae, and Parastacidae—Decapoda) in freshwater. *Freshwater Animal Diversity Assessment*:295–301. DOI: 10.1007/978-1-4020-8259-7_32.

Crandall KA, De Grave S. 2017. An updated classification of the freshwater crayfishes (Decapoda: Astacidea) of the world, with a complete species list. *Journal of Crustacean Biology* 37:615–653. DOI: 10.1093/jcbiol/rux070.

Domisch S, Amatulli G, Jetz W. 2015. Near-global freshwater-specific environmental variables for biodiversity analyses in 1 km resolution. *Scientific Data* 2:1–13. DOI: 10.1038/sdata.2015.73.

Ejsmont-Karabin J. 2019. Does the world need faunists? Based on rotifer (Rotifera) occurrence reflections on the role of faunistic research in ecology. *International Review of Hydrobiology* 104:49–56. DOI: 10.1002/IROH.201901991.

Emery-Butcher HE, Beatty SJ, Robson BJ. 2020. The impacts of invasive ecosystem engineers in freshwaters: A review. *Freshwater Biology* 65:999–1015. DOI: 10.1111/FWB.13479.

Fetzner JW, Crandall KA. 2003. LINEAR HABITATS AND THE NESTED CLADE ANALYSIS: AN EMPIRICAL EVALUATION OF GEOGRAPHIC VERSUS RIVER DISTANCES USING AN OZARK CRAYFISH (DECAPODA: CAMBARIDAE). *Evolution* 57:2101–2118. DOI: 10.1111/J.0014-3820.2003.TB00388.X.

Fišer C. 2019. Collaborative Databasing Should Be Encouraged. *Trends in Ecology and Evolution* 34:184–185. DOI: 10.1016/j.tree.2018.12.001.

Führding-Potschkat P, Kreft H, Ickert-Bond SM. 2022. Influence of different data cleaning solutions of point-occurrence records on downstream macroecological diversity models. *Ecology and Evolution* 12:e9168. DOI: 10.1002/ECE3.9168.

Gonzalez A, Vihervaara P, Balvanera P, Bates AE, Bayraktarov E, Bellingham PJ, Bruder A, Campbell J, Catchen MD, Cavender-Bares J, Chase J, Coops N, Costello MJ, Czúcz B, Delavaud A, Dornelas M, Dubois G, Duffy EJ, Eggermont H, Fernandez M, Fernandez N, Ferrier S, Geller GN, Gill M, Gravel D, Guerra CA, Guralnick R, Harfoot M, Hirsch T, Hoban S, Hughes AC, Hugo W, Hunter ME, Isbell F, Jetz W, Juergens N, Kissling WD, Krug CB, Kullberg P, Le Bras Y, Leung B, Londoño-Murcia MC, Lord JM, Loreau M, Luers A, Ma K, MacDonald AJ, Maes J, McGeoch M, Mihoub JB, Millette KL, Molnar Z, Montes E, Mori AS, Muller-Karger FE, Muraoka H, Nakaoka M, Navarro L, Newbold T, Niamir A, Obura D, O'Connor M, Paganini M, Pelletier D, Pereira H, Poisot T, Pollock LJ, Purvis A, Radulovici A, Rocchini D, Roeoesli C, Schaepman M, Schaepman-Strub G, Schmeller DS, Schmiedel U, Schneider FD, Shakya MM, Skidmore A, Skowno AL, Takeuchi Y, Tuanmu MN, Turak E, Turner W, Urban MC, Urbina-Cardona N, Valbuena R, Van de Putte A, van Havre B, Wingate VR, Wright E, Torrelio CZ. 2023. A global biodiversity observing system to unite monitoring and guide action. *Nature Ecology & Evolution 2023 7:12* 7:1947–1952. DOI: 10.1038/s41559-023-02171-0.

Graham CH, Elith J, Hijmans RJ, Guisan A, Townsend Peterson A, Loiselle BA, Anderson RP, Dudk M, Ferrier S, Huettmann F, Leathwick J, Lehmann A, Li J, Lohmann L, Loiselle B, Manion G, Moritz C, Nakamura M, Nakazawa Y, Overton J, Phillips S, Richardson K, Pereira RS, Schapire R, Soberón J, Williams S, Wisz M, Zimmermann N. 2008. The influence of spatial errors in species occurrence data used in distribution models. *Journal of Applied Ecology* 45:239–247. DOI: 10.1111/J.1365-2664.2007.01408.X.

Guareschi S, Cancellario | T, Oficialdegui | F J, Clavero | M. 2024. Insights from the past: Invasion trajectory and niche trends of a global freshwater invader. *Global Change Biology* 30:e17059. DOI: 10.1111/GCB.17059.

Guiasu RC, Barr DW, Dunham DW. 1996. Distribution and Status of Crayfishes of the Genera Cambarus and Fallicambarus (Decapoda: Cambaridae) in Ontario, Canada. *Journal of Crustacean Biology* 16:373–383. DOI: 10.1163/193724096X00162.

Guiaşu RC, Labib M. 2021. The unreliable concept of native range as applied to the distribution of the rusty crayfish (Faxonius rusticus) in North America. *Hydrobiologia* 848:1177–1205. DOI:

10.1007/S10750-021-04523-Y/TABLES/1.

Guisan A, Zimmermann NE. 2000. Predictive habitat distribution models in ecology. *Ecological Modelling* 135:147–186. DOI: 10.1016/S0304-3800(00)00354-9.

Guralnick RP, Wieczorek J, Beaman R, Hijmans RJ. 2006. BioGeomancer: Automated georeferencing to map the world's biodiversity data. *PLoS Biology* 4:1908–1909. DOI: 10.1371/JOURNAL.PBIO.0040381.

Hannah K, Haddaway NR, Fuller RA, Amano T. 2024. Language inclusion in ecological systematic reviews and maps: Barriers and perspectives. *Research Synthesis Methods*. DOI: 10.1002/JRSM.1699.

Jiménez-Valverde A, Lobo JM, Hortal J. 2008. Not as good as they seem: the importance of concepts in species distribution modelling. *Diversity and Distributions* 14:885–890. DOI: 10.1111/J.1472-4642.2008.00496.X.

Jussila J, Edsman L. 2020. Relaxed attitude towards spreading of alien crayfish species affects protection of native crayfish species: case studies and lessons learnt from a Fennoscandian viewpoint. *Freshwater Crayfish* 25:39–46. DOI: 10.5869/FC.2020.V25-1.039.

Jussila J, Edsman L, Maguire I, Diéguez-Uribeondo J, Theissinger K. 2021. Money Kills Native Ecosystems: European Crayfish as an Example. *Frontiers in Ecology and Evolution* 0:476. DOI: 10.3389/FEVO.2021.648495.

Kaufman D, McKay N, Routson C, Erb M, Davis B, Heiri O, Jaccard S, Tierney J, Dätwyler C, Axford Y, Brussel T, Cartapanis O, Chase B, Dawson A, de Vernal A, Engels S, Jonkers L, Marsicek J, Moffa-Sánchez P, Morrill C, Orsi A, Rehfeld K, Saunders K, Sommer PS, Thomas E, Tonello M, Tóth M, Vachula R, Andreev A, Bertrand S, Biskaborn B, Bringué M, Brooks S, Caniupán M, Chevalier M, Cwynar L, Emile-Geay J, Fegyveresi J, Feurdean A, Finsinger W, Fortin MC, Foster L, Fox M, Gajewski K, Grosjean M, Hausmann S, Heinrichs M, Holmes N, Ilyashuk B, Ilyashuk E, Juggins S, Khider D, Koinig K, Langdon P, Larocque-Tobler I, Li J, Lotter A, Luoto T, Mackay A, Magyari E, Malevich S, Mark B, Massaferro J, Montade V, Nazarova L, Novenko E, Pařil P, Pearson E, Peros M, Pienitz R, Płóciennik M, Porinchu D, Potito A, Rees A, Reinemann S, Roberts S, Rolland N, Salonen S, Self A, Seppä H, Shala S, St-Jacques JM, Stenni B, Syrykh L, Tarrats P, Taylor K, van den Bos V, Velle G, Wahl E, Walker I, Wilmshurst J, Zhang E, Zhilich S. 2020. A global database of Holocene paleotemperature records. *Scientific Data 2020 7:1* 7:1–34. DOI: 10.1038/s41597-020-0445-3.

Kopperud BT, Lidgard S, Liow LH. 2022. Enhancing georeferenced biodiversity inventories: automated information extraction from literature records reveal the gaps. *PeerJ* 10:e13921. DOI: 10.7717/PEERJ.13921/SUPP-2.

Kosmala M, Wiggins A, Swanson A, Simmons B. 2016. Assessing data quality in citizen science. *Frontiers in Ecology and the Environment* 14:551–560. DOI: 10.1002/FEE.1436.

Kouba A, Petrusek A, Kozák P. 2014. Continental-wide distribution of crayfish species in Europe: update and maps. *Knowledge and Management of Aquatic Ecosystems* 413:05–31. DOI: 10.1051/kmae/2014007.

Li Y, Bearup D, Liao J. 2020. Habitat loss alters effects of intransitive higher-order competition on biodiversity: a new metapopulation framework. *Proceedings of the Royal Society B: Biological Sciences* 287:20201571. DOI: 10.1098/rspb.2020.1571.

Liang J, Gamarra JGP. 2020. The importance of sharing global forest data in a world of crises. *Scientific Data* 7. DOI: 10.1038/s41597-020-00766-x.

Lidova J, Buric M, Kouba A, Velisek J. 2019. Acute toxicity of two pyrethroid insecticides for five non-indigenous crayfish species in Europe. *Veterinarni Medicina* 64:125–133. DOI: 10.17221/136/2018-VETMED.

Lipták B, Kouba A, Patoka J, Paunović M, Prokop P. 2024. Biological invasions and invasive species in freshwaters: perception of the general public. *Human Dimensions of Wildlife* 29:48–63. DOI: 10.1080/10871209.2023.2177779.

Liu C, Wolter C, Xian W, Jeschke JM. 2020. Species distribution models have limited spatial transferability for invasive species. *Ecology Letters* 23:1682–1692. DOI: 10.1111/ele.13577.

Lodge DM, Deines A, Gherardi F, Yeo DCJ, Arcella T, Baldridge AK, Barnes MA, Lindsay Chadderton W, Feder JL, Gantz CA, Howard GW, Jerde CL, Peters BW, Peters JA, Sargent LW, Turner CR, Wittmann ME, Zeng Y. 2012. Global introductions of crayfishes: Evaluating the impact of species invasions on ecosystem services. *Annual Review of Ecology, Evolution, and Systematics* 43:449–472. DOI: 10.1146/ANNUREV-ECOLSYS-111511-103919/1.

Manfrin C, Souty-Grosset C, Anastácio PM, Reynolds J, Giulianini PG. 2019. Detection and Control of Invasive Freshwater Crayfish: From Traditional to Innovative Methods. *Diversity 2019, Vol. 11, Page 5* 11:5. DOI: 10.3390/D11010005.

Marques V, Milhau T, Albouy C, Dejean T, Manel S, Mouillot D, Juhel J. 2021. GAPeDNA: Assessing and mapping global species gaps in genetic databases for eDNA metabarcoding. *Diversity and Distributions* 00:ddi.13142. DOI: 10.1111/ddi.13142.

Martínez-Ríos M, Martín-Torrijos L, Diéguez-Uribeondo J. 2023. Protocols for studying the crayfish plague pathogen, Aphanomyces astaci, and its host-pathogen interactions. *Journal of Invertebrate Pathology* 201:108018. DOI: 10.1016/J.JIP.2023.108018.

Mcclenachan L, Ferretti F, Baum JK. 2012. From archives to conservation: Why historical data are needed to set baselines for marine animals and ecosystems. *Conservation Letters* 5:349–359. DOI: 10.1111/j.1755-263X.2012.00253.x.

Meier R, Dikow T. 2004. Significance of Specimen Databases from Taxonomic Revisions for Estimating and Mapping the Global Species Diversity of Invertebrates and Repatriating Reliable Specimen Data. *Conservation Biology* 18:478–488. DOI: 10.1111/J.1523-1739.2004.00233.X.

Meyer C, Weigelt P, Kreft H. 2016. Multidimensional biases, gaps and uncertainties in global plant occurrence information. *Ecology Letters* 19:992–1006. DOI: 10.1111/ELE.12624.

Miller AD, Inamine H, Buckling A, Roxburgh SH, Shea K. 2021. How disturbance history alters invasion success: biotic legacies and regime change. *Ecology Letters*:ele.13685. DOI: 10.1111/ele.13685.

Momot WT. 1995. Redefining the role of crayfish in aquatic ecosystems. *Reviews in Fisheries Science* 3:33–63. DOI: 10.1080/10641269509388566.

Oficialdegui FJ, Sánchez MI, Clavero M. 2020. One century away from home: how the red swamp crayfish took over the world. *Reviews in Fish Biology and Fisheries* 30:121–135. DOI: 10.1007/S11160-020-09594-Z/FIGURES/4.

Pârvulescu L, Zaharia C, Groza M-I, Csillik O, Satmari A, Drăguţ L. 2016. Flash-flood potential: a proxy for crayfish habitat stability. *Ecohydrology* 9:1507–1516. DOI: 10.1002/eco.1744.

Pereyra PJ, Guiaşu RC. 2020. Debate over the importance and meaning of native range in invasion biology: reply to Courchamp et al. *Conservation Biology* 34:1044–1046. DOI: 10.1111/COBI.13529.

Pyšek P, Hulme PE, Simberloff D, Bacher S, Blackburn TM, Carlton JT, Dawson W, Essl F, Foxcroft LC, Genovesi P, Jeschke JM, Kühn I, Liebhold AM, Mandrak NE, Meyerson LA, Pauchard A, Pergl J, Roy HE, Seebens H, van Kleunen M, Vilà M, Wingfield MJ, Richardson DM. 2020. Scientists' warning on invasive alien species. *Biological Reviews* 95:1511–1534. DOI: 10.1111/brv.12627.

R Core Team. 2024. R: A Language and Environment for Statistical Computing. *R Core Team*.

Reaser JK, Burgiel SW, Kirkey J, Brantley KA, Veatch SD, Burgos-Rodríguez J. 2019. The early detection of and rapid response (EDRR) to invasive species: a conceptual framework and federal capacities assessment. *Biological Invasions*. DOI: 10.1007/s10530-019-02156-w.

Reaser JK, Frey M, Meyers NM. 2019. Invasive species watch lists: guidance for development, communication, and application. *Biological Invasions*. DOI: 10.1007/s10530-019-02176-6.

Reichman OJ, Jones MB, Schildhauer MP. 2011. Challenges and Opportunities of Open Data in Ecology. *Science* 331:703–705. DOI: 10.1126/SCIENCE.1197962.

Richman NI, Böhm M, Adams SB, Alvarez F, Bergey EA, Bunn JJS, Burnham Q, Cordeiro J, Coughran J, Crandall KA, Dawkins KL, DiStefano RJ, Doran NE, Edsman L, Eversole AG, Füreder L, Furse JM, Gherardi F, Hamr P, Holdich DM, Horwitz P, Johnston K, Jones CM, Jones JPG, Jones RL, Jones TG, Kawai T, Lawler S, López-Mejía M, Miller RM, Pedraza-Lara C, Reynolds JD, Richardson AMM, Schultz MB, Schuster GA, Sibley PJ, Souty-Grosset C, Taylor CA, Thoma RF, Walls J, Walsh TS, Collen B. 2015. Multiple drivers of decline in the global status of freshwater crayfish (Decapoda:

Astacidea). *Philosophical Transactions of the Royal Society B: Biological Sciences* 370:20140060. DOI: 10.1098/rstb.2014.0060.

Robinson OJ, Ruiz-Gutierrez V, Reynolds MD, Golet GH, Strimas-Mackey M, Fink D. 2020. Integrating citizen science data with expert surveys increases accuracy and spatial extent of species distribution models. *Diversity and Distributions* 26:976–986. DOI: 10.1111/DDI.13068.

Rocchini D, Hortal J, Lengyel S, Lobo JM, Jiménez-Valverde A, Ricotta C, Bacaro G, Chiarucci A. 2011. Accounting for uncertainty when mapping species distributions: The need for maps of ignorance. *http://dx.doi.org/10.1177/0309133311399491* 35:211–226. DOI: 10.1177/0309133311399491.

Rodríguez JP, Keith DA, Rodríguez-Clark KM, Murray NJ, Nicholson E, Regan TJ, Miller RM, Barrow EG, Bland LM, Boe K, Brooks TM, Oliveira-Miranda MA, Spalding M, Wit P. 2015. A practical guide to the application of the IUCN Red List of Ecosystems criteria. *Philosophical Transactions of the Royal Society B: Biological Sciences* 370:20140003. DOI: 10.1098/rstb.2014.0003.

Salomaki ED, Eme L, Brown MW, Kolisko M. 2020. Releasing uncurated datasets is essential for reproducible phylogenomics. *Nature Ecology and Evolution* 4:1435–1437. DOI: 10.1038/s41559-020-01296-w.

Şandric I, Satmari A, Zaharia C, Petrovici M, Cîmpean M, Battes K-P, David D-C, Pacioglu O, Weiperth A, Gál B, Pîrvu M, Muntean H, Neagul M, Spătaru A, Toma CG, Pârvulescu L. 2019. Integrating catchment land cover data to remotely assess freshwater quality: a step forward in heterogeneity analysis of river networks. *Aquatic Sciences* 81. DOI: 10.1007/s00027-019-0624-5.

Sax DF, Gaines SD. 2003. Species diversity: From global decreases to local increases. *Trends in Ecology and Evolution* 18:561–566. DOI: 10.1016/S0169-5347(03)00224-6.

Scholtz G, Richter S. 1995. Phylogenetic systematics of the reptantian Decapoda (Crustacea, Malacostraca). *Zoological Journal of the Linnean Society* 113:289–328. DOI: 10.1006/ZJLS.1995.0011.

Shen C, Appling AP, Gentine P, Bandai T, Gupta H, Tartakovsky A, Baity-Jesi M, Fenicia F, Kifer D, Li L, Liu X, Ren W, Zheng Y, Harman CJ, Clark M, Farthing M, Feng D, Kumar P, Aboelyazeed D, Rahmani F, Song Y, Beck HE, Bindas T, Dwivedi D, Fang K, Höge M, Rackauckas C, Mohanty B, Roy T, Xu C, Lawson K. 2023. Differentiable modelling to unify machine learning and physical models for geosciences. *Nature Reviews Earth & Environment 2023 4:8* 4:552–567. DOI: 10.1038/s43017-023-00450-9.

Soto I, Ahmed DA, Beidas A, Oficialdegui FJ, Tricarico E, Angeler DG, Amatulli G, Briski E, Datry T, Dohet A, Domisch S, England J, Feio MJ, Forcellini M, Johnson RK, Jones JI, Larrañaga A, L'Hoste L, Murphy JF, Schäfer RB, Shen LQ, Kouba A, Haubrock PJ. 2023. Long-term trends in crayfish invasions across European rivers. *Science of The Total Environment* 867:161537. DOI: 10.1016/J.SCITOTENV.2023.161537.

Soto I, Balzani P, Carneiro L, Cuthbert RN, Macêdo R, Tarkan AS, Ahmed DA, Bang A, Bacela-Spychalska K, Bailey SA, Baudry T, Ballesteros-Mejia L, Bortolus A, Briski E, Britton JR, Buřič M, Camacho-Cervantes M, Cano-Barbacil C, Copilaş-Ciocianu D, Coughlan NE, Courtois P, Csabai Z, Dalu T, Santis V De, Dickey JWE, Dimarco RD, Falk-Andersson J, Fernandez RD, Florencio M, Franco ACS, García-Berthou E, Giannetto D, Glavendekic MM, Grabowski M, Heringer G, Herrera I, Huang W, Kamelamela KL, Kirichenko NI, Kouba A, Kourantidou M, Kurtul I, Laufer G, Lipták B, Liu C, López-López E, Lozano V, Mammola S, Marchini A, Meshkova V, Milardi M, Musolin DL, Nuñez MA, Oficialdegui FJ, Patoka J, Pattison Z, Pincheira-Donoso D, Piria M, Probert AF, Rasmussen JJ, Renault D, Ribeiro F, Rilov G, Robinson TB, Sanchez AE, Schwindt E, South J, Stoett P, Verreycken H, Vilizzi L, Wang Y-J, Watari Y, Wehi PM, Weiperth A, Wiberg-Larsen P, Yapıcı S, Yoğurtçuoğlu B, Zenni RD, Galil BS, Dick JTA, Russell JC, Ricciardi A, Simberloff D, Bradshaw CJA, Haubrock PJ. 2024. Taming the terminological tempest in invasion science. *Biological Reviews* 17:0–000. DOI: 10.1111/BRV.13071.

Strand DA, Jinnerot T, Aspán A, Viljamaa-Dirks S, Heinikainen S, Rolén E, Vrålstad T. 2023. Molecular detection of Aphanomyces astaci – An improved species specific qPCR assay. *Journal of Invertebrate Pathology* 201:108008. DOI: 10.1016/J.JIP.2023.108008.

Strand DA, Johnsen SI, Rusch JC, Agersnap S, Larsen WB, Knudsen SW, Møller PR, Vrålstad T. 2019.

Monitoring a Norwegian freshwater crayfish tragedy: <scp>eDNA</scp> snapshots of invasion, infection and extinction. *Journal of Applied Ecology* 56:1661–1673. DOI: 10.1111/1365-2664.13404.

Taylor CA, DiStefano RJ, Larson ER, Stoeckel J. 2019. Towards a cohesive strategy for the conservation of the United States' diverse and highly endemic crayfish fauna. *Hydrobiologia 2019 846:1* 846:39–58. DOI: 10.1007/S10750-019-04066-3.

Thessen AE, Cui H, Mozzherin D. 2012. Applications of natural language processing in biodiversity science. *Advances in Bioinformatics* 2012. DOI: 10.1155/2012/391574.

Ungureanu E, Mojžišová M, Tangerman M, Ion MC, Parvulescu L, Petrusek A. 2020. The spatial distribution of Aphanomyces astaci genotypes across Europe: introducing the first data from Ukraine. *Freshwater Crayfish* 25:77–87. DOI: 10.5869/fc.2020.v25-1.077.

Valdecasas AG, Camacho AI. 2003. Conservation to the rescue of taxonomy. *Biodiversity and Conservation* 12:1113–1117. DOI: 10.1023/A:1023082606162/METRICS.

Villero D, Pla M, Camps D, Ruiz-Olmo J, Brotons L. 2017. Integrating species distribution modelling into decision-making to inform conservation actions. *Biodiversity and Conservation* 26:251–271. DOI: 10.1007/S10531-016-1243-2/METRICS.

Wieczorek J, Guo Q, Hijmans RJ. 2004. The point-radius method for georeferencing locality descriptions and calculating associated uncertainty. *International Journal of Geographical Information Science* 18:745–767. DOI: 10.1080/13658810412331280211.

World Intellectual Property Organization. 2022. Nice Agreement Concerning the International Classification of Goods and Services for the Purposes of the Registration of Marks. :11th edition.

Figure 1

Figure 1

Schematic representation of the logical workflow in and around the WoC ecosystem

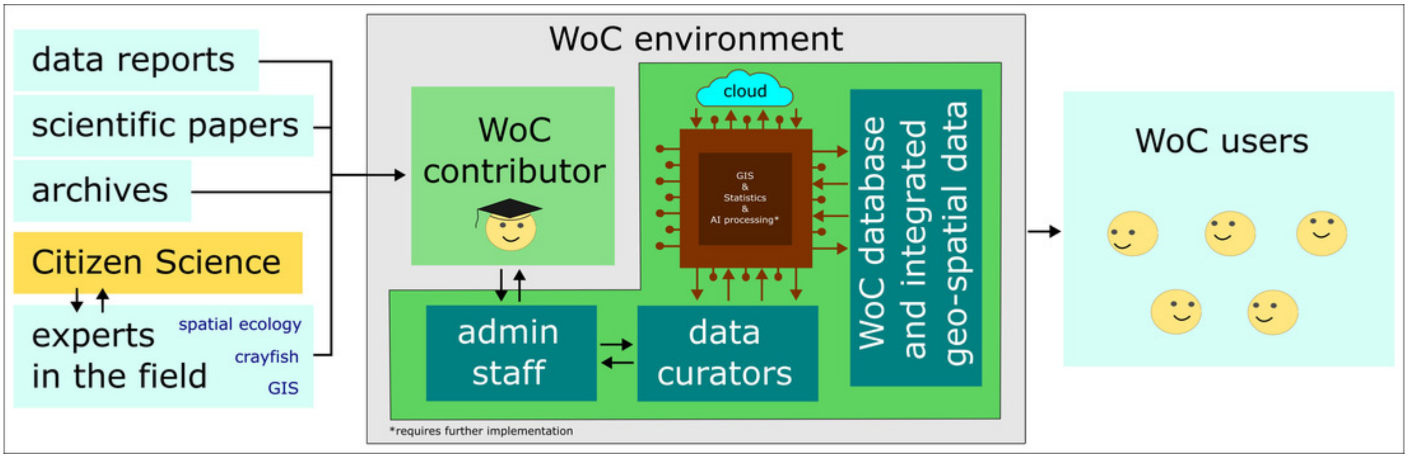
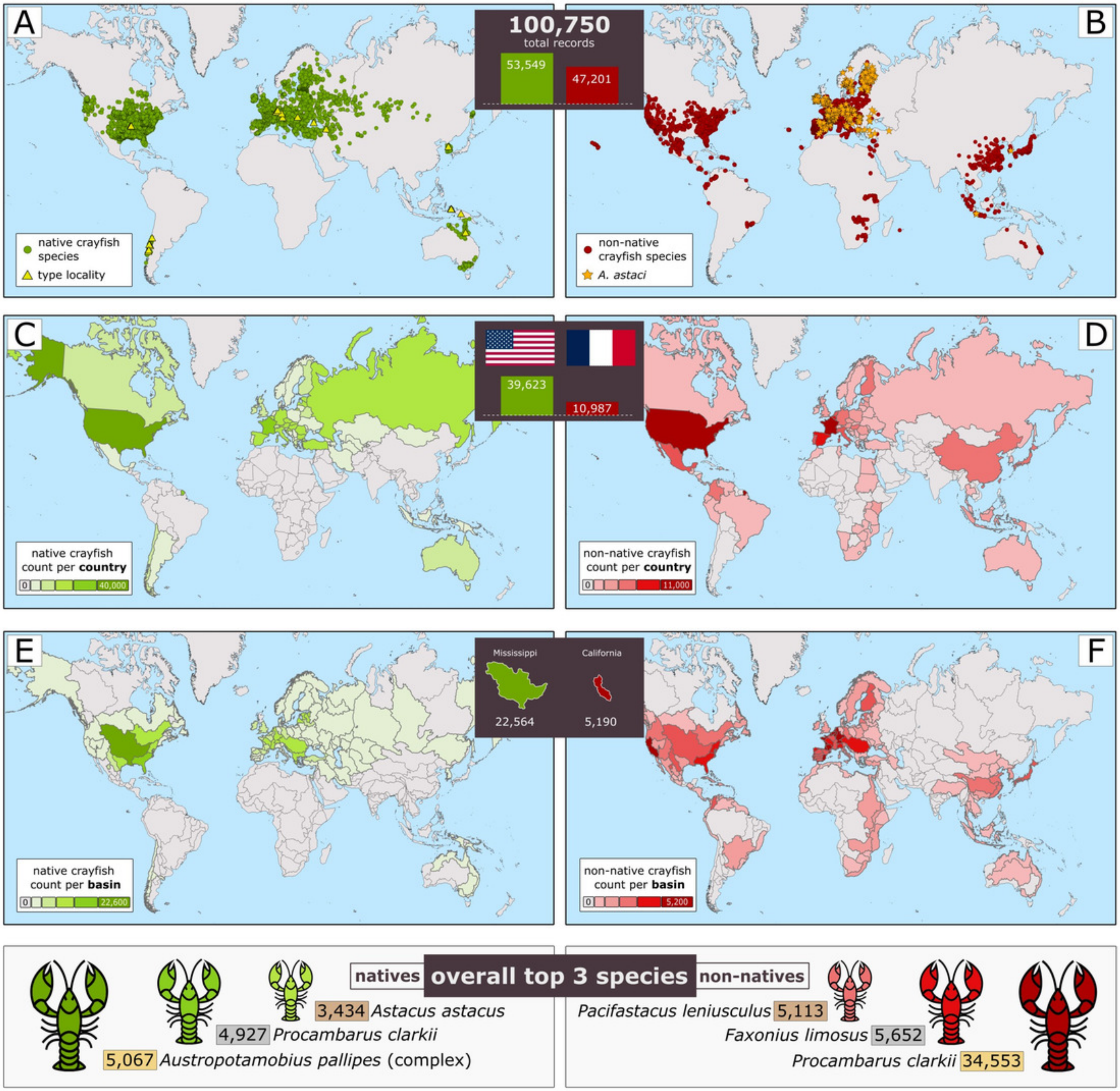


Figure 2

Figure 2

Overview of the collected data in WoC platform, and various centralisation. A-B display records of natives versus non-native crayfish species records at continental level (type locality and *Aphanomyces astaci* highlighted). C-D display country level record counts (native versus non-native), D-E represents major hydrographic basins record counts (native versus non-native). The lower panel integrates data for the species most well represented.


A
B
100,750
total records
53,549
47,201
native crayfish species
type locality
non-native crayfish species
A. astaci
C
D
39,623
10,987
native crayfish count per country
0
40,000
non-native crayfish count per country
0
11,000
E
F
Mississippi
California
22,564
5,190
native crayfish count per basin
0
22,600
non-native crayfish count per basin
0
5,200
natives
overall top 3 species
non-natives
3,434 Astacus astacus
4,927 Procambarus clarkii
5,067 Austropotamobius pallipes (complex)
Pacifastacus leniusculus 5,113
Faxonius limosus 5,652
Procambarus clarkii 34,553