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Biodiversity knowledge through web design: the World of Crayfish platform

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Abstract

Biodiversity databases have expanded rapidly over the past two decades, transforming scattered observations into massive digital repositories of species occurrence records. Yet increased data availability has not necessarily translated into improved accessibility of ecological knowledge. Most biodiversity platforms remain primarily data archives, requiring substantial analytical effort before meaningful biological insights can be extracted. Bridging this gap between stored data and usable knowledge represents a central challenge for biodiversity informatics. Here we present the design philosophy and functionality of the World of Crayfish® platform (https://world.crayfish.ro), a web-based system built around the user experience of transforming species occurrence data into accessible biodiversity knowledge. Through interactive spatial visualization, automated narrative synthesis, structured bibliographic outputs, and standardized data export tools, the platform enables users to move directly from species selection to interpretable biogeographic insight, without requiring specialized analytical expertise. Using freshwater crayfish as a model group, the platform illustrates how web design can function as a critical interface between complex biodiversity infrastructures and diverse user communities, including researchers, conservation practitioners, and decision makers. By prioritizing clarity, transparency, and reproducibility in how biodiversity information is presented, the World of Crayfish® platform demonstrates how user-centred web design can lower the barrier between complex biodiversity infrastructures and the diverse communities who need to use them.

Highlights

- The gap between biodiversity data availability and knowledge accessibility represents a fundamental challenge in biodiversity informatics that web design can directly address.
- The World of Crayfish® platform transforms raw occurrence records into species-level biogeographic knowledge through interactive maps, automated narrative summaries, and standardized export tools.
- Basin-level spatial aggregation using HydroSHEDS units and IUCN-compliant AOO and EOO metrics provide ecologically meaningful and reproducible distributional outputs.
- Local extinction events are incorporated as explicit informative data points, enabling dynamic and reality-aware biodiversity mapping beyond static range depictions.
- The platform's design principles, including modular architecture, narrative synthesis, and export-ready outputs, offer a scalable model for knowledge-oriented biodiversity platforms across taxonomic groups.

Keywords: biodiversity informatics, freshwater crayfish, species distribution, knowledge interface, biogeographic visualization, web platform

Introduction

The digitization of biodiversity data has fundamentally reshaped ecological research. Global initiatives such as the Global Biodiversity Information Facility (Heberling *et al.*, 2021) have aggregated hundreds of millions of species occurrence records into increasingly accessible repositories, enabling unprecedented synthesis across spatial and temporal scales and supporting advances in biogeography, conservation planning, and species distribution modelling.

Despite this rapid growth in data availability, a persistent gap remains between data accessibility and knowledge accessibility. Occurrence databases provide valuable raw information about where species have been recorded, yet extracting ecological meaning from these datasets often requires substantial technical expertise. Researchers must typically download large datasets, perform spatial analyses, calculate distribution metrics, and interpret results before meaningful insights can be obtained. For many users, including conservation practitioners, environmental managers, and students, this process represents a significant barrier, increasingly drowning in data but thirsty for the synthesis of knowledge into understanding (Hui *et al.*, 2024).

Meeting the standards of Findability, Accessibility, Interoperability, and Reusability (FAIR) (Wilkinson *et al.*, 2016) requires more than open data pipelines. It also requires that data be presented in forms that diverse communities can actually use. In practice, biodiversity knowledge is therefore frequently mediated not only by the existence of data but also by the interfaces through which those data are accessed (Gadelha *et al.*, 2021). The design of web platforms plays a critical role in determining how effectively users can explore, interpret, and reuse biodiversity information. Yet the importance of web design in biodiversity informatics has received comparatively little attention. Many platforms focus primarily on data storage and retrieval, while the transformation of data into readily interpretable knowledge is left largely to downstream analytical workflows.

Freshwater crayfish (Decapoda: Astacidea) provide a particularly suitable model system for exploring this issue. With approximately 590 described species globally (Richman *et al.*, 2015), crayfish occupy keystone and ecological engineering roles in freshwater ecosystems across six continents. Invasive crayfish species rank among the most destructive agents of freshwater biodiversity loss worldwide, second only to habitat destruction among causes of biodiversity decline in freshwater systems (Oficialdegui, Sánchez & Clavero, 2020; O'Hea Miller, Davis & Wong, 2024), and approximately 32% of all crayfish species are currently assessed as threatened with extinction (Richman *et al.*, 2015). Accurate IUCN Red

List assessments for many European species remain hindered by fragmented distribution data and unresolved taxonomy (Pârvulescu, 2025), a challenge illustrated by recent phylogeographic work demonstrating that major lineage boundaries and ancestral biogeographic connections within European crayfish genera remain subjects of active revision (Pârvulescu *et al.*, 2025b). Despite this conservation importance, knowledge of crayfish distributions remains fragmented across disparate databases, grey literature, and peer-reviewed sources in multiple languages. Integrating this information into an accessible and coherent knowledge system represents an important challenge.

The World of Crayfish® (WoC®) platform (https://world.crayfish.ro) was developed as a response to this challenge (Ion *et al.*, 2024). Rather than functioning solely as a repository of occurrence records, the platform is designed as a web-based environment that facilitates the transformation of biodiversity data into accessible ecological knowledge. Through interactive maps, automated narrative summaries, and structured data outputs, the platform enables users to move directly from species selection to a comprehensive overview of distributional patterns, supporting evidence, and associated metadata.

This article presents the design principles and core functionality of the WoC® platform. Rather than focusing on the analytical engines that generate underlying spatial products, described in separate methodological contributions (Pârvulescu *et al.*, 2025a; Bâcu *et al.*, 2026), we focus here on the web design architecture that enables those products to be translated into usable biodiversity knowledge. In this perspective we argue that web platform design itself can represent a critical layer in biodiversity knowledge production, mediating the transformation of complex biodiversity datasets into interpretable ecological understanding.

Implementation

The WoC® platform is implemented as a web application accessible at https://world.crayfish.ro. The platform draws on a curated global occurrence database compiled from museum collections, published literature, monitoring programmes, and citizen science contribution. At the time of writing, the database encompasses 115,486 raw occurrence records distributed across 465 species in 24 genera, spanning endemic, regional, and cosmopolitan range categories (Figure 1C), with both indigenous and non-indigenous populations documented (Figure 1D), and geospatial ecological trait data available for 275 species (Figure 1E), covering the global indigenous and non-indigenous ranges of freshwater crayfish.

Occurrence data are processed through the che*CkOVER* framework (Pârvulescu *et al.*, 2025a), a generalizable pipeline for transforming raw species occurrence records into standardized knowledge products. Species distribution data are then spatially aggregated to standardized hydrographic basin units derived from the HydroSHEDS framework (Lehner, Verdin & Jarvis, 2008), providing an ecologically meaningful spatial context for distributional analysis. Area of Occupancy (AOO) estimates are calculated at 2 × 2 km resolution following IUCN Red List assessment guidelines (IUCN Standards and Petitions Committee, 2024), and Extent of Occurrence (EOO) is computed as a minimum convex polygon across verified occurrence localities. All spatial artefacts, bibliographic data, and summary statistics are available for download in standardized formats (GeoJSON, CSV, BibTeX) from individual species profile pages.

Precise geographic coordinates of occurrence records are withheld from public display in accordance with widely recognized conservation data-sharing guidelines (Gadelha *et al.*, 2021), and are replaced by aggregated spatial representations in all platform outputs.

Platform architecture and user interaction

The WoC® platform is structured around a simple guiding principle: biodiversity information should be accessible through an intuitive web interface that allows users to explore species knowledge without requiring specialized analytical tools (Bâcu *et al.*, 2026). The platform therefore emphasizes clarity of navigation, modular organization of information, and immediate visual access to spatial data.

Upon entering the platform, users encounter a streamlined interface organized into several primary modules, each representing a different dimension of species knowledge. These modules include species profiles, bibliographic resources, and additional informational components designed to guide exploration of the database. The modular structure allows users to navigate the platform according to their interests while maintaining a coherent overall architecture.

The core of the platform is the species profile interface, which provides a comprehensive overview of each species contained in the database. Species selection is facilitated through a hierarchical search mechanism that allows users to first choose a genus and then select among the species belonging to that genus. This two-step structure simplifies navigation in taxonomically rich groups and reduces visual clutter within the selection interface (Figure 1A).

Once a species is selected, the platform generates a dynamic profile page integrating taxonomic information, spatial distribution data, and contextual ecological knowledge. Taxonomic details are displayed at the top of the page, including the full classification hierarchy and relevant nomenclatural information, linked where possible to external authoritative resources. This design reflects a broader philosophy: the platform does not attempt to replace existing biodiversity infrastructures but instead acts as a knowledge interface, connecting users with multiple sources of biodiversity information within a unified environment for interpretation (Bâcu *et al.*, 2026).

Figure 1 here (two columns)

Figure 1. The World of Crayfish® platform interface illustrated with *Austropotamobius torrentium* (stone crayfish). (A) Interactive species profile showing the hierarchical genus-species selector, distribution map with selectable layers (indigenous basins, non-indigenous basins, type locality, Area of Occupancy, Extent of Occurrence), SVG map export functionality, automated biogeographic narrative summary, and structured export panels (Bibliography, Species Archive; SEB Manifest for AI-readable programmatic access). (B) Ecology knowledge panel displaying statistical summaries of geospatial traits derived from the GeoFRESH framework across Climate, Soil, Land Cover, and Topography variable groups at local catchment and upstream drainage area scales, and the Raw Data Download Engine with stratified indigenous and non-indigenous dataset access. (C) Biogeographic range structure of all 465 platform species (green: endemic; blue: regional; dark red: cosmopolitan). (D) Composition of the validated occurrence records by population origin (amber: indigenous; purple: non-indigenous). (E) Ecological data coverage across species (orange: with geospatial trait data; grey: without).

Interactive biogeographic visualization

Spatial visualization forms the central element of the species profile interface. Each species page contains an interactive distribution map that occupies the majority of the screen and serves as the primary entry point for exploring species biogeography.

The map displays species occurrences aggregated into hydrographic basin units (Lehner *et al.*, 2008), allowing users to quickly identify major patterns in species distribution across river systems. This basin-level representation reduces visual noise compared to point-based occurrence displays while maintaining a meaningful ecological context. To protect sensitive biodiversity data, precise geographic coordinates are not displayed publicly. Instead, spatial information is represented through AOO grid cells at 2 × 2 km resolution, following IUCN Red List guidelines (IUCN Standards and Petitions Committee, 2024), an approach that provides sufficient spatial detail for ecological interpretation while minimizing risks associated with revealing exact localities of vulnerable populations.

A distinctive feature of the platform is its treatment of local extinction information as an explicit component of species distribution. Local extinction events are incorporated into the distributional framework as informative data points rather than gaps, reflecting the principle that biodiversity mapping should be dynamic and reality-aware (Livadariu, Bâcu & Parvulescu, 2026). This approach allows users to explore not only current species ranges but also patterns of historical contraction and documented disappearance from previously occupied localities.

Users can dynamically customize the map display through a series of selectable layers, including representations of indigenous and non-indigenous distributions, type localities, AOO, and EOO (Figure 1A). An additional feature enables users to export customized maps as scalable vector graphics (SVG), generating publication-ready figures that remain fully editable in external software. Species profiles are further contextualized through integration of environmental descriptors derived from the GeoFRESH framework (Domisch *et al.*, 2024), providing catchment-level climate, soil, land cover, and topographic variables at both local and upstream drainage area scales for each occurrence locality (Figure 1B).

Synthesizing biodiversity knowledge through narrative summaries

While spatial visualization provides an intuitive overview of species distributions, understanding biodiversity patterns often requires contextual interpretation. To address this need, the platform integrates automated biogeographic narrative summaries within each species profile (Bâcu *et al.*, 2026). These summaries present concise textual overviews of species distributions, including information about occurrence counts, geographic coverage, and representation across ecological or administrative regions. By translating complex datasets into readable summaries, the platform allows users to quickly grasp the key characteristics of a species' distribution without manually analysing underlying data.

The narrative generation process is grounded in the che*CkOVER* framework (Pârvulescu *et al.*, 2025a), which standardizes the transformation of occurrence records into structured knowledge products. Narrative summaries remain directly linked to the underlying datasets from which they are derived, ensuring transparency and reproducibility, two principles central to FAIR data practice (Wilkinson *et al.*, 2016). Bibliographic information is organized and presented in multiple export formats (JSON, CSV, BibTeX), with references automatically ranked by frequency within the underlying dataset, allowing users to quickly identify the most influential sources contributing to the species knowledge base (Figure 1B).

Web design as a bridge between data and knowledge

The WoC® platform illustrates how thoughtful web design can substantially enhance the accessibility of biodiversity knowledge. This is particularly significant in a landscape where most existing biodiversity platforms prioritize data storage and retrieval over knowledge communication (Bâcu *et al.*, 2026).

Global occurrence aggregators such as GBIF (Heberling *et al.*, 2021) represent foundational infrastructure for biodiversity science, providing open access to over one billion occurrence records standardized through the Darwin Core framework. AquaMaps has pioneered large-scale species distribution modelling for aquatic organisms, generating predicted range maps that support global analyses (Ready *et al.*, 2010; Reygondeau *et al.*, 2026). Both platforms have been transformative in enabling biodiversity research at scales previously inaccessible to individual researchers. Yet they operate primarily as data retrieval systems or modelling environments: a GBIF query for a crayfish species returns a table of occurrence records requiring downstream processing, while AquaMaps provides modelled probability surfaces rooted in coarse environmental envelopes (Reygondeau *et al.*, 2026) that do not integrate verified occurrence datasets or bibliographic provenance specific to a taxonomic group. Neither platform delivers the species-level synthesis that the WoC® platform provides directly to the user, including occurrence counts, hydrographic basin coverage, narrative biogeographic summaries, ranked bibliographic outputs, and publication-ready maps. This need is particularly acute for European crayfish, where IUCN Red List evaluations continue to reflect evidence gaps rather than biological reality in the absence of harmonized distributional evidence (Pârvulescu, 2025).

The distinction is not that WoC® improves on GBIF or AquaMaps within their own domains. Rather, WoC® occupies a different position in the biodiversity informatics landscape: it is a knowledge interface rather than a data infrastructure or modelling platform. By integrating verified distributional data with automated synthesis and interactive visualization within a purpose-built web environment, the platform delivers outputs that require no post-processing and are immediately interpretable by diverse user communities. The incorporation of local extinction data as explicit map information (Livadariu *et al.*, 2026) further distinguishes the platform by making visible the historical dimension of species ranges alongside their current extent.

Several design principles underpin this approach. Information is organized into modular components that allow users to navigate complex datasets without becoming overwhelmed by detail. Spatial visualization is prioritized as a primary tool for communicating ecological information. Automated narrative summaries provide an accessible entry point for understanding distributional patterns while maintaining direct links to the underlying data. Together, these elements transform the platform from a simple data repository into a knowledge environment where users can move fluidly between raw data, synthesized knowledge, and spatial visualization (Gadelha *et al.*, 2021).

This design philosophy reflects a broader shift in biodiversity informatics toward systems that prioritize usability and interpretability alongside data availability, a shift increasingly recognized as essential for ensuring that the growing volume of biodiversity data reaches and benefits the full range of users who depend on it (Hui *et al.*, 2024).

Outlook

As biodiversity datasets continue to expand and the urgency of freshwater conservation grows (Richman *et al.*, 2015), the challenge of transforming data into usable knowledge becomes increasingly important. Web platforms capable of integrating visualization, interpretation, and data access within a unified environment may play a central role in meeting this challenge. The WoC® platform represents one example of how such systems can be implemented for a specific taxonomic group. While the platform currently focuses on freshwater crayfish, the underlying design principles, namely modular architecture, species-level narrative synthesis, basin-level spatial aggregation, and export-ready outputs grounded in the che*C*k*OVER* standardization framework (Pârvulescu *et al.*, 2025a), are broadly applicable to other biodiversity domains. By emphasizing clarity, transparency, and accessibility in the presentation of ecological information, web-based platforms can help ensure that the growing volume of biodiversity data translates into meaningful scientific and conservation insights. Biodiversity informatics is entering a phase in which the challenge is no longer only data mobilization but also knowledge accessibility (Groom *et al.*, 2023; Feng *et al.*, 2025; Islam *et al.*, 2026), and purpose-built knowledge interfaces may therefore become essential components of future biodiversity infrastructures, alongside the broader computational infrastructure needed to make digitised biodiversity data processable at scale.

Author contributions

L.P.: Conceptualisation, Investigation, Formal analysis, Software, Visualisation, Writing – original draft, Writing – review & editing.

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Data availability statement

The manuscript draws on publicly available artefacts disseminated via World of Crayfish® (https://world.crayfish.ro/).

AI use statement

Claude (Anthropic) artificial intelligence (AI) tools were used to assist with language refinement and manuscript structuring. All scientific content, interpretations, and conclusions were developed and critically evaluated by the author. The author takes full responsibility for the content of the manuscript.

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