BIOGEOGRAPHIA
The Journal of Integrative Biogeography

*Biogeographia – The Journal of Integrative Biogeography 2025, 40 (2): a050*

*https://doi.org/10.21426/B6.46596*

# An expert-curated dataset on cave-dwelling spider communities in the Western Italian Alps –an open tool for eco-evolutionary research

Giuseppe NICOLOSI[1,2*], Alejandro MARTÍNEZ[1], Elena PIANO[3,4], Marco ISAIA[3,4^], Stefano MAMMOLA[1,4,5^]

*[1] Molecular Ecology Group (MEG), Water Research Institute (IRSA), National Research Council (CNR), Corso Tonolli 50, 28922 Verbania Pallanza, Italy*
*[2] Department of Biological, Geological and Environmental Sciences, University of Catania, Via A. Longo 19, 95125 Catania, Italy*
*[3] Department of Life Sciences and Systems Biology, University of Turin, Via Accademia Albertina 13, 10123, Torino, Italy*
*[4] National Biodiversity Future Center, Piazza Marina 61, 90133 Palermo, Italy*
*[5] Laboratory for Integrative Biodiversity Research (LIBRe), Finnish Museum of Natural History (LUOMUS), University of Helsinki, Pohjoinen Rautatiekatu 13, Helsinki, 00100, Finland*

** corresponding author, email: giuseppe.nicolosi@unict.it*

*^ shared last authorship*

**Keywords**: Arachnida, Araneae, cave, online repository, phylogenesis, subterranean biology.

## SUMMARY

Biodiversity data is essential for eco-evolutionary research. However, data is often scarce for difficult-to-study ecosystems, such as caves and other subterranean environments. Here, we present a taxonomically and geographically consistent database of subterranean spiders from the Italian Western Alps, a coherent biogeographical region with a long history of subterranean fauna diversification. The database (https://doi.org/10.6084/m9.figshare.28524383.v1) comprises 370 geo-referenced subterranean sites (caves, mines, and other artificial subterranean systems). For each site, we provide information on the composition of the spider community (with species richness ranging from 1 to 8 species per site), along with local geomorphological and site features. Collectively, these communities account for 31 unique species and 945 unique geo-referenced occurrence records, which are made available via the Global Biodiversity Information Facility (GBIF: https://www.gbif.org/dataset/72eef995-01bd-44f2-

937a-23dbfe66283d). In addition to the database, we provide a phylogeny for all species based on the cytochrome c oxidase subunit I (COI) gene fragment. This, combined with the interoperability of the European subterranean spider trait database (doi: 10.6084/m9.figshare.16574255.v2), enables the estimation of taxonomic, functional, and genetic diversity within these subterranean communities. We illustrate the utility of this database by estimating and mapping taxonomic, functional, and genetic richness across the Western Italian Alps, providing a comprehensive multi-dimensional view of subterranean spider biodiversity. Although restricted in geographical scope, we envision this database as a promising open resource for eco-evolutionary research and hope the broader scientific community will widely use it. Indeed, the joint availability of distribution data, traits, and phylogenetic information allows quantifying ecologically relevant differences among species, identifying functionally unique taxa, and assessing patterns of adaptation and specialization in subterranean environments, among many other questions.

## INTRODUCTION

Data availability lies at the heart of ecology, enabling researchers to test relationships between living organisms to environmental variables and predict their response to ongoing human-induced global changes (Jetz et al. 2012). In recent years, improvements in storage capabilities, coupled with open data policies, have prompted the publication of extensive biodiversity datasets. This improved data availability allows ecologists to answer a range of previously intractable questions and better inform the conservation and management of biodiversity.

Despite the proliferation of biodiversity data, our understanding of the distribution of life remains uneven across taxa, sites, and regions (Feng et al. 2022). Research efforts tend to prioritize organisms directly beneficial to humans (Wandersee and Schussler, 1999; Mammola et al. 2023) or more visible and charismatic, such as birds, mammals (Clark and May, 2002), butterflies (van Swaay et al. 2008), or dragonflies (Galimberti et al. 2020). Likewise, sites that are more easily accessible to humans tend to be better represented in public datasets, whereas systems that are difficult to map, explore, and sample, such as caves or deep seas, are often poorly covered (Ficetola et al. 2019; Mammola et al. 2021).

Spiders (Arachnida: Araneae) play a special role in biological communities, functioning as generalist predators and displaying various functional adaptations that connect to diverse ecosystem services (Cardoso et al. 2025). Within this group, subterranean-adapted species offer unique study prospects due to their peculiar adaptations to living in permanent darkness (Mammola and Isaia, 2017a; Deharveng and Bedos, 2019). Subterranean spiders have been used to investigate a range of ecological hypotheses, including the effect of global warming (Mammola and Isaia, 2017b; Mammola et al. 2018a; Mammola et al. 2019a; Nicolosi et al. 2023), the potential spread of alien species (Mammola, 2017), the correlation between population genetic structure and speciation mechanisms (Pavlek et al. 2022), and to explore morphological, metabolic, and behavioral adaptations (Hesselberg et al. 2019; Lipovšek et al. 2019; Lunghi et al. 2024).

Yet, our understanding of subterranean spiders, although growing quite rapidly, remains deficient in several areas, including distributional data, phylogenetic relationships, conservation status, and traits diversity. For example, beyond Europe (Mammola et al. 2018b, 2019b, 2024), there is limited information regarding the diversity of subterranean spiders and the macro and micro-scale factors affecting them. Furthermore, the conservation status of most subterranean spiders is unknown, with only a handful of species assessed according to the IUCN criteria (Borges et al., 2016; Cardoso et al. 2017; Mammola et al., 2016a; Mammola, Milano, and Isaia, 2019c; Milano et al. 2022; Isaia et al. 2023).

We here provide a comprehensive database covering over 370 subterranean sites primarily caves) in the Italian Western Alps that were extensively sampled over the past thirteen years in terms of spider fauna. The dataset offers updated data for spider community composition for all these sites offering a robust foundation for ecological analyses. Additionally, in this dataset we provide a phylogeny of the recorded species. Given the interoperability of this data with the existing database focusing on morphological and ecological traits for these species (Mammola et al. 2022), we enable the quantification of functional diversity across communities alongside taxonomic and phylogeny diversity. Taken together, these complementary data allow us to investigate the influence of environmental variables on species distributions, the role of phylogenetic history in shaping community structure, the processes underlying speciation and extinction, and the potential vulnerability of these communities to environmental change, among other topics.

The community database (370 communities) and associated data are available in Figshare (https://doi.org/10.6084/m9.figshare.28524383.v1). Altogether, the database accounts for 31 species and 945 unique geo-referenced occurrence records, made available via the Global Biodiversity Information Facility (GBIF) (doi: 10.15468/pdajjy).

## MATERIALS AND METHODS

### Study area

The Western Alps (*sensu* SOIUSA; Marazzi 2005) form a cohesive biogeographic region within the larger Alpine system. Recognized as a biodiversity hotspot in Europe (e.g., Schmitt 2009), this region is also speleologically rich, with over 2,500 caves in both carbonate and non-carbonate substrates, as well as various artificial subterranean sites, including abandoned mineshafts and Second World War bunkers and blockhouses (Catasto Speleologico Piemontese, 2025). Note that we focused exclusively on the Italian side of the Western Alps (hereafter 'Western Italian Alps'), specifically the Italian regions of Piemonte (Piedmont), Liguria, and Val d'Aosta (Aosta valley).

### Literature screening

The starting point for creating the database was the monographic work on subterranean Arachnids of the Western Italian Alps by Isaia et al. (2011). This initial database was subsequently expanded by identifying, downloading, and thoroughly reviewing newly published articles to extract all available records. Further unpublished data were collected by the authors during extensive fieldwork conducted in recent years. Taxonomic identification was conducted based on morphological characteristics, with reference to the established taxonomic literature (World Spider Catalog 2025). For each subterranean site, we extracted the geological information from the regional speleological cadastre of Piemonte and Val d'Aosta (available at https://catastogrotte-piemonte.net/) and Liguria (https://www.catastogrotte.net/liguria/index.php), including the speleological cadastre number, longitude and latitude coordinates of the entrance, elevation, development, and positive, negative, and total drop (calculated as the absolute value of the sum of the positive and negative drops). Furthermore, we indicated whether the subterranean site is located within a protected area and specified the type of protection based on the SAC/SCI - Special Areas of Conservation / Sites of Community Importance raster obtained from the "Geoportale Piemonte" (https://www.geoportale.piemonte.it/geonetwork/srv/ita/catalog.search). We classified the lithology of each subterranean site using the Lithological Map from the "Geoportale Piemonte". Finally, we reported the presence of each recorded subterranean species in each site, along with the respective reference.

## Phylogenetic data

We retrieved available sequences for the target species and their available closest relatives from GenBank using an automated R script. We focused on fragments of the cytochrome c oxidase subunit I (COI) gene, one of the most commonly used markers for spiders, offering good resolution for distinguishing species and above (Coddington et al. 2016; Wheeler et al. 2017). The primary criterion for sequence selection was the longest possible sequence; when available, we further prioritized those from the Western Italian Alps. We selected only one sequence per species, as the purpose of the tree was to calculate phylogenetic distances within spider communities, and we assumed that species are monophyletic. Of the 31 target species, only three—*Cybaeus vignai*, *Leptoneta crypticola*, and *Centromerus pasquini*—lacked COI gene fragments in GenBank. Since the dataset consisted of only one species per each of these genera, we selected the best available sequence for the respective genera from GenBank, i.e. the closest relative of the aforementioned species. The Supplementary Table S1 includes the metadata for each selected sequence, including GenBank ID numbers, references, and raw sequences. We aligned the selected COI using FTT-NS-1 algorithm in the software MAFFT version 7 (Katoh et al. 2013). We then visually inspected the sequences to confirm the absence of stop codons and indels. Then, we explored the phylogenetic signal of the dataset by calculating neighbor-joining and maximum likelihood-based phylogenetic trees. We calculated the neighbor-joining distance-based tree using the functions dist.dna and nj implemented in the R package "ape" version 5.0 (Paradis and Schliep 2019) and the maximum likelihood-based phylogenetic tree using RAxML version 8.2.9 with default parameters (Stamatakis 2014). Both trees were topologically equivalent and only differed on the branch length, thereby providing a virtually identical estimation of the phylogenetic diversity of the data.

## Trait data

The database is fully interoperable with the European subterranean spider trait database (DOI: 10.6084/m9.figshare.16574255.v2), allowing to extract morphological and ecological trait information for each of the species (see Mammola et al. 2022 for a lengthy description of the traits).

## Example analysis with multiple facets of biodiversity

To exemplify a potential analysis based on multiple facets of biodiversity and the interoperable datasets described before, we used functions from the R package BAT (version 2.9.6; Cardoso et al. 2024a) to estimate and map the taxonomic, functional, and genetic richness of these communities. Specifically, we expressed taxonomic richness as the number of species in each community (i.e. site) and we estimated genetic and functional richness using neighbor-joining tree-based functions (Cardoso et al. 2024b). For genetic richness, we used the phylogenetic tree (see section "Phylogenetic analyses"). For functional richness, we processed the trait matrix following the pipeline in Mammola et al. (2022), calculated a functional tree, and used it to estimate functional richness. Finally, we mapped the three components using the function BAT:raster.alpha() and made the resulting rasters available in Figshare for future use (https://doi.org/10.6084/m9.figshare.28524383.v1) (Fig. 5).

# RESULTS

## Data description

The dataset consists of a single table (saved as a tab-delimited file [csv format]) of 46 columns and 370 rows, each row representing a distinct subterranean site. The distribution of examined sites spans three regions (Piemonte, Valle d'Aosta, and Liguria) and 9 provinces (Alessandria, Aosta, Biella, Cuneo, Imperia, Torino, Verbano-Cusio-Ossola, Vercelli, Novara), with elevations ranging from 105 to 2563 meters above sea level (Fig. 1).

The first 15 columns (Table 1) contain information on the characteristics of the subterranean sites included in the database. The following 31 columns represent each spider species recorded in these subterranean sites (Table 2).

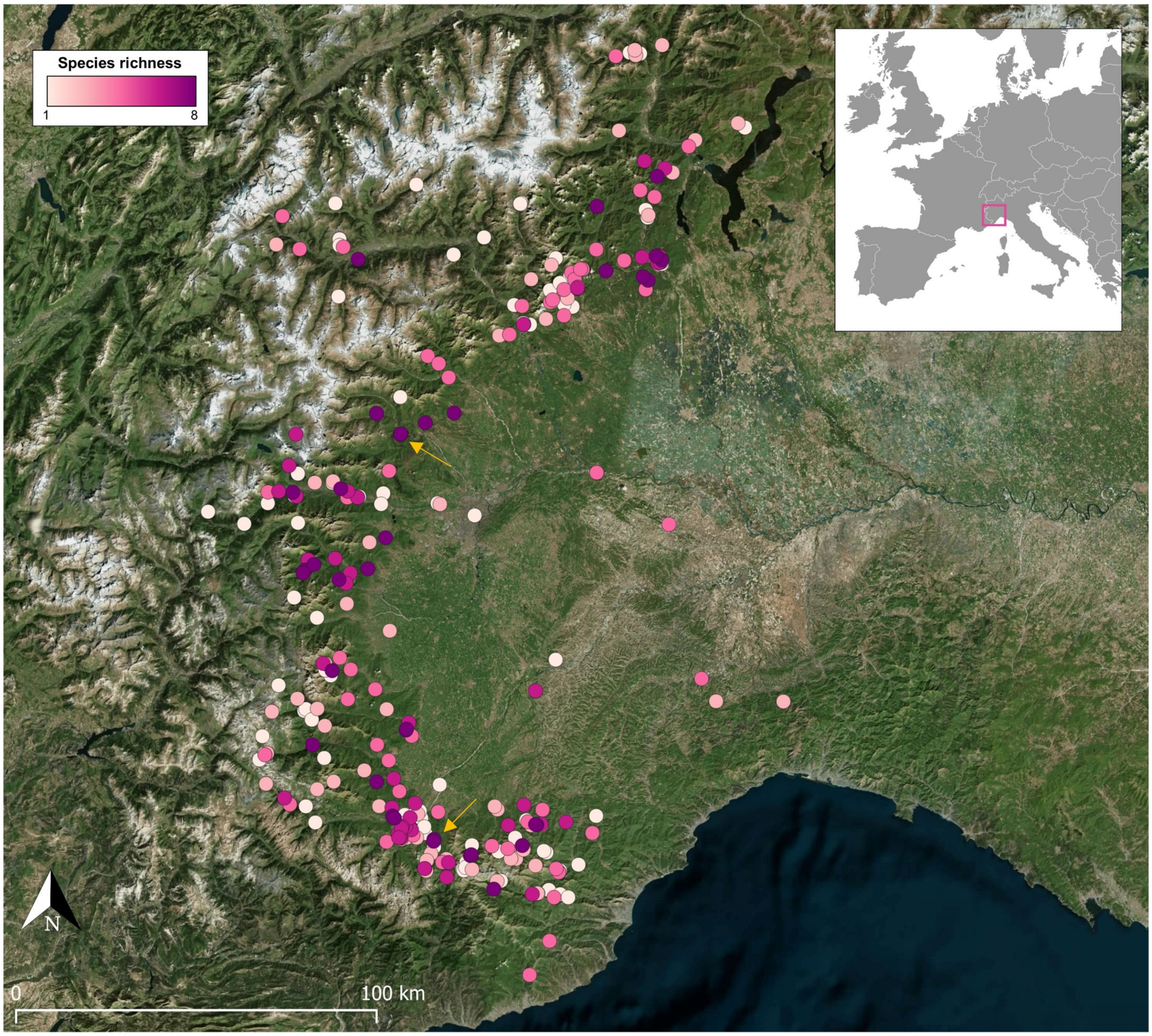


Figure 1. Map of the study area (Western Italian Alps) showing the 370 sites recorded in the database. Bullet points represent species richness per site as recorded by the 31 spider species included in the analysis. Lighter shades indicate lower richness and darker shades indicate higher richness (ranging from 1 to 8 species per site). Sites with the maximum richness (8 species) are highlighted with yellow arrows.

Table 1. Description of the dataset with specific information relative to definitions for each of the first 13 columns of the data set, according to Darwin Core Standards.

| Column label | Column description |
|---|---|
| Cadastre Number | The unique identification number assigned to each subterranean site in the regional cadastre system. |
| Province | The administrative division within the region. |
| Region | The administrative region. |
| Name | The name of the subterranean site registered in the regional cadastre system. |
| Longitude | The geographic longitude (in decimal degrees) of the geographic center of a site. |
| Latitude | The geographic latitude (in decimal degrees) of the geographic center of a site. |
| Elevation | Altitude a.s.l. of the subterranean site's main entrance in metres (m). |
| Development | The subterranean total planimetric development of the site in metres (m). |
| PositiveDrop | The difference in altitude from point 0 to the highest point of the cave in metres (m) |
| NegativeDrop | The difference in altitude from point 0 to the lowest point of the cave in metres (m). |
| TotalDrop | The sum of the negative and positive drops in metres (m). |
| Lithology | The predominant rock type or material constituting the geological formations within the subterranean site |
| ProtectedArea | Binary variable. Indicates whether the subterranean site is situated within a protected area (yes) or not (no). We here refer to protected areas identified by the Italian legislation. |
| Natura2000Code | A unique code indicating the Natura 2000 site in which the subterranean site falls (if applicable). |

Table 2. List of the subterranean species included in the analysis.

| Family | Species |
|---|---|
| Agelenidae | *Tegenaria silvestris* |
| Cybaeidae | *Cybaeus vignai* |
| Leptonetidae | *Leptoneta crypticola* |
| Linyphiidae | *Centromerus pasquinii*, *Palliduphantes pallidus*, *Porrhomma convexum*, *Troglohyphantes bolognai*, *Troglohyphantes bornensis*, *Troglohyphantes delphinicus*, *Troglohyphantes giachinoi*, *Troglohyphantes iulianae*, *Troglohyphantes konradi*, *Troglohyphantes lanai*, *Troglohyphantes lucifer*, *Troglohyphantes lucifuga*, *Troglohyphantes nigraerosae*, *Troglohyphantes pedemontanus*, *Troglohyphantes pluto*, *Troglohyphantes vignai*, *Turinyphia clairi* |
| Nesticidae | *Kryptonesticus eremita*, *Nesticus cellulanus*, *Typhlonesticus angelicus*, *Typhlonesticus morisii* |
| Pimoidae | *Pimoa delphinica*, *Pimoa graphitica*, *Pimoa rupicola* |
| Tetragnathidae | *Meta bourneti*, *Meta menardi*, *Metellina merianae* |

## Summary statistics

Most subterranean sites in the database are limestone caves (133 out of 370, i.e. 36%) associated with the lithology of "Dolomites and limestones" (Fig. 2A). This is followed by "Fine-grained gneisses", which is recorded in 76 sites (20%), "Limestone deposits" found in 33 sites (9%), "Alluvial deposits" found in 29 sites (8%), and "Granites" found in 26 sites (7%). Other lithological substrates are represented in less than 20 sites, cumulatively covering around 20% of considered subterranean sites. Most caves' entrances are found at an elevation between 701 and 1000 meters (92 out of 370, 25%), followed by those between 401 and 700 meters (21%) and 1001 to 1300 meters (20%) (Fig. 2B). The development of most sites ranges between 11 and 50 meters (136 out of 370 sites, 37%), followed by sites with a development of 0–10 meters (14%) (Fig. 2C). The total drop of subterranean sites ranges from 0 to 470 meters, with the majority having a depth of 50 meters or less (257 out of 293, 87%). This is followed by caves with depths between 51 and 100 meters (18, 6.1%) and 101–200 meters (9, 3%) (Fig. 2D).

Approximately 34% of the subterranean sites (127 out of 370) are located within the boundaries of protected areas.

Regarding the spider fauna, the dataset comprises 945 records representing 31 spider species. Species richness in each site ranges from 1 to 8. The family with the highest number of species is Linyphiidae, encompassing 18 out of 31 species (58%) mostly belonging to the genus Troglohyphantes, followed by Nesticidae, which includes 4 species (13%). The species with the highest number of records is *Meta menardi*, totaling 203 records (21%), followed by *Metellina merianae* with 159 records (17%), *Kryptonesticus eremita* with 118 records (12%), and *Tegenaria silvestris* with 101 records (11%) (Fig. 3A). Species richness exhibits a skewed distribution, with most sites showing low species richness (e.g., richness value of 1 in 113 sites and of value 2 in 88 sites). Richness values of 8 and 7 species were recorded in only two sites each: 'Grotta del Pugnetto' and 'Sotterranei del forte (A) di Vernante, Opera 11 Tetto Ruinas' for 8 species, and 'Grotta dei Partigiani di Rossana' and 'Grotta superiore del Pugnetto' for 7 species (Fig. 3B).

## Phylogenetic analyses

We provide a phylogeny for all species (Fig. 4; available in Figshare [https://doi.org/10.6084/m9.figshare.28524383.v1] as a .tre file). The phylogenetic tree includes the 28 target species with available COI sequences and 3 closest relatives, all retrieved from GenBank (Fig. 4). Specifically, for three recorded species —*Cybaeus vignai*, *Leptoneta crypticola*, and *Centromerus pasquini*— COI data were unavailable. However, the use of closely related species (*Cybaeus gotoensis*, *Leptoneta taeguensis* and *Centromerus trilobus*) ensured that their phylogenetic placement remained consistent with expected evolutionary relationships. All congeneric species form clearly delimited monophyletic clades, in line with current taxonomic classifications. For instance, *Troglohyphantes* species cluster tightly together and are well separated from other Linyphiidae such as *Lepthyphantes* and *Centromerus*. Similarly, *Pimoa* species form a distinct and coherent clade, reflecting their phylogenetic distinctiveness within Pimoidae. The phylogenetic positions of the substituted species from GenBank (e.g., *Cybaeus* sp., *Centromerus* sp.) are consistent with the expected placement of the missing taxa.

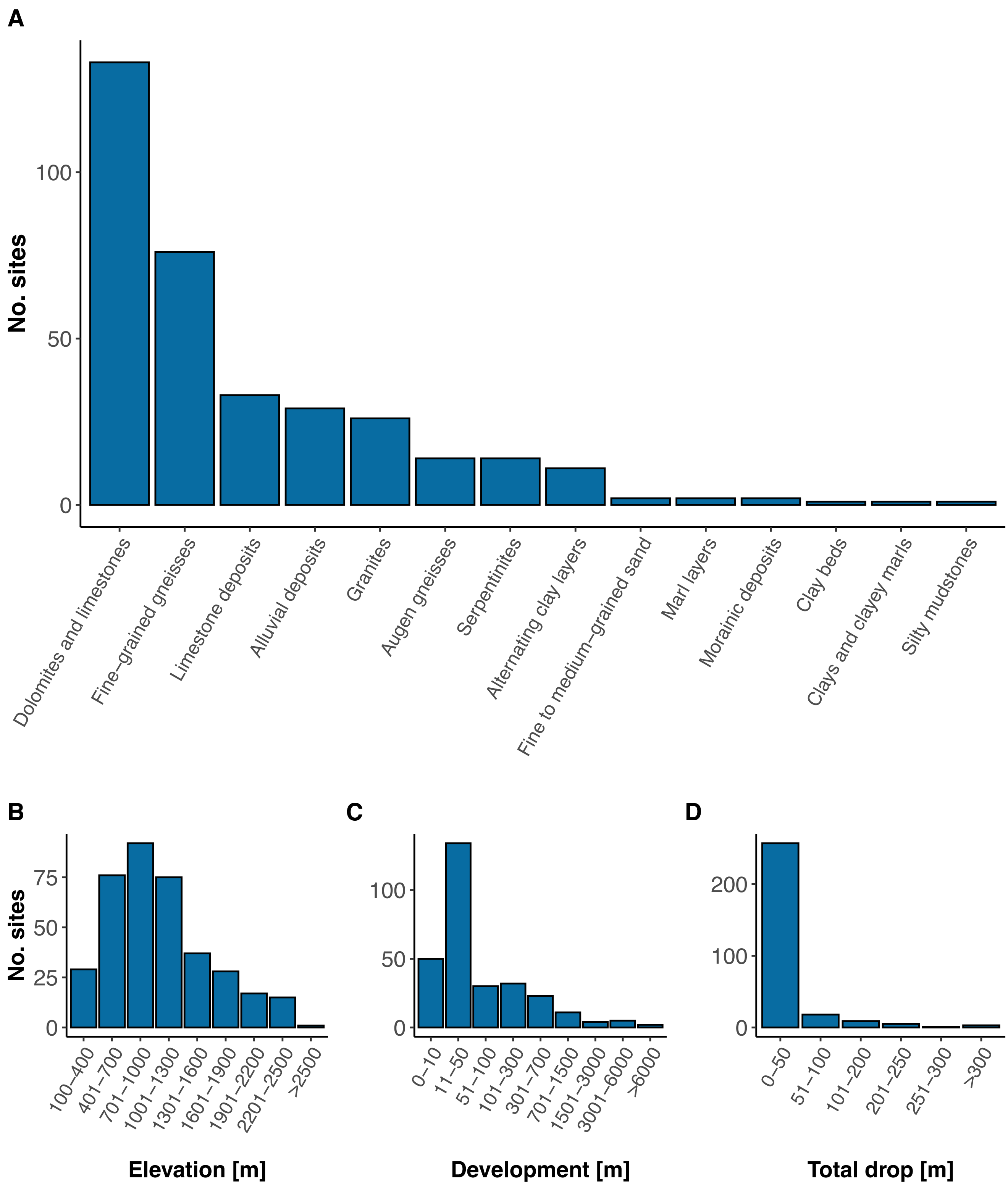


Figure 2. The number of sites included in the dataset for each lithology type (note that, for artificial subterranean sites, the natural substrate of occurrence is reported) (**A**), class of elevation (**B**), class of development (**C**), and class of total drop (**D**).

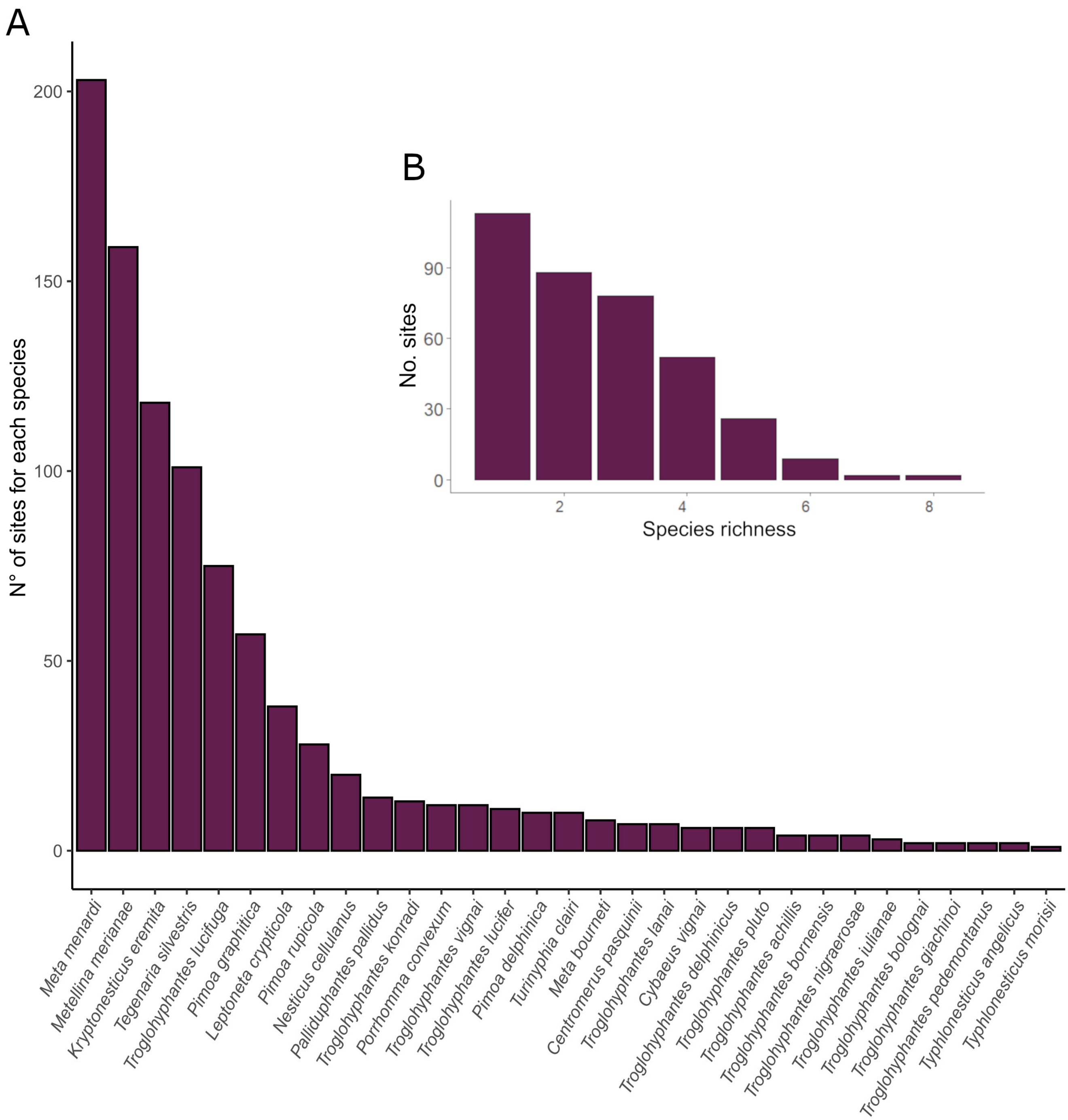


Figure 3. Number of sites for each species included in the database (**A**). Number of subterranean sites by species richness (**B**).

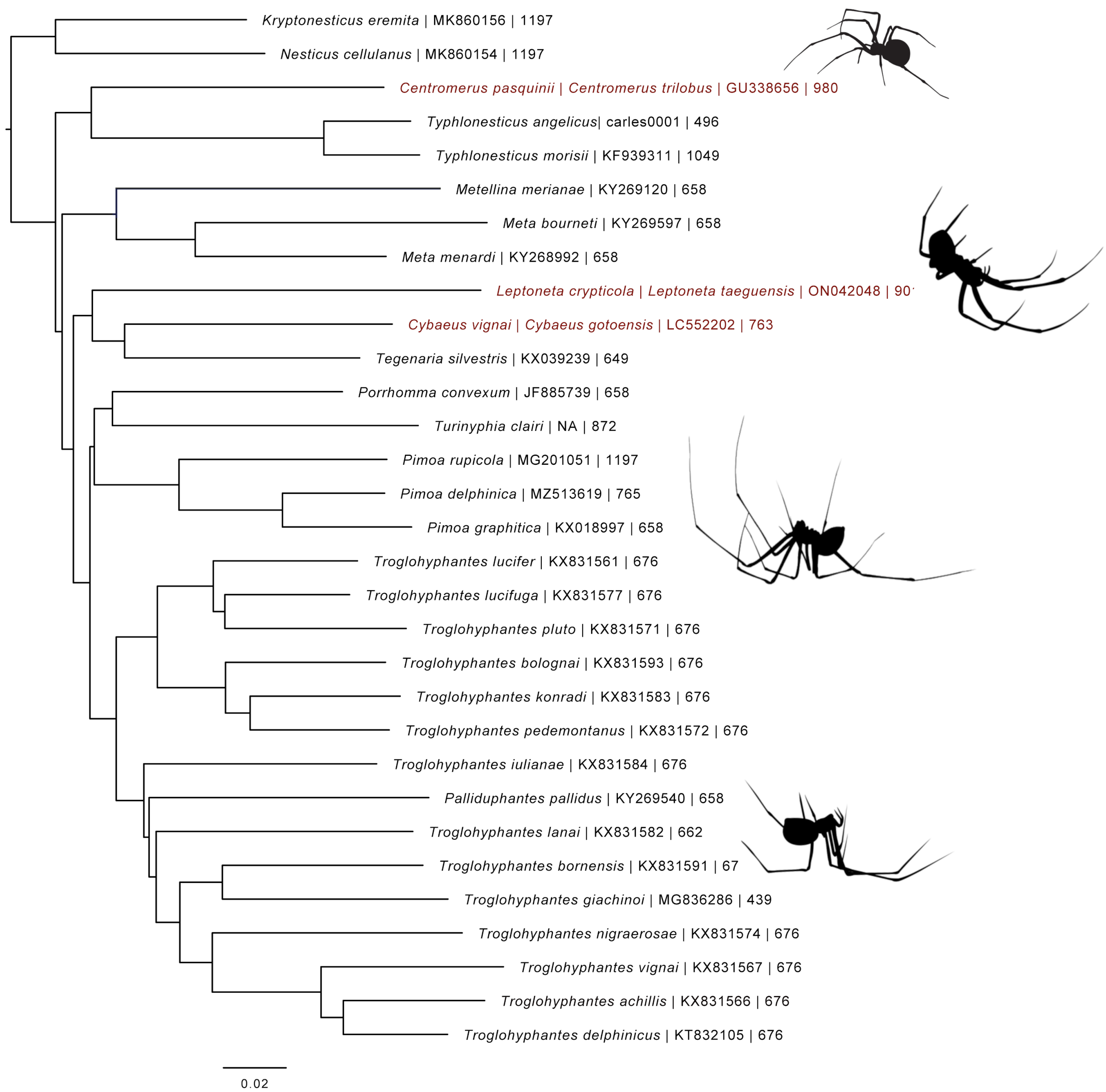


Figure 4. Phylogenetic tree inferred using the maximum likelihood method in RAxML. Each COI sequence is labeled with its GenBank accession number, followed by the sequence length.

## Mapping of multiple facets of biodiversity

Map of the taxonomic, functional, and genetic richness were estimated and the resulting rasters made available in Figshare for future use (https://doi.org/10.6084/m9.figshare.28524383.v1) (Fig. 5). These maps provide a spatially explicit view of community diversity and can inform research on biodiversity patterns, community assembly, and conservation prioritization based on multiple biodiversity dimensions. Spatial patterns show that taxonomic, functional, and genetic richness are not evenly distributed across the Western Italian Alps (Fig. 5). Higher levels of richness are generally concentrated in the southern and central portions of the study area, which may reflect a combination of habitat heterogeneity, historical connectivity among caves, and sampling intensity. These patterns suggest that different drivers may shape taxonomic, functional, and genetic diversity, and that areas of high multidimensional richness may represent key targets for conservation efforts.

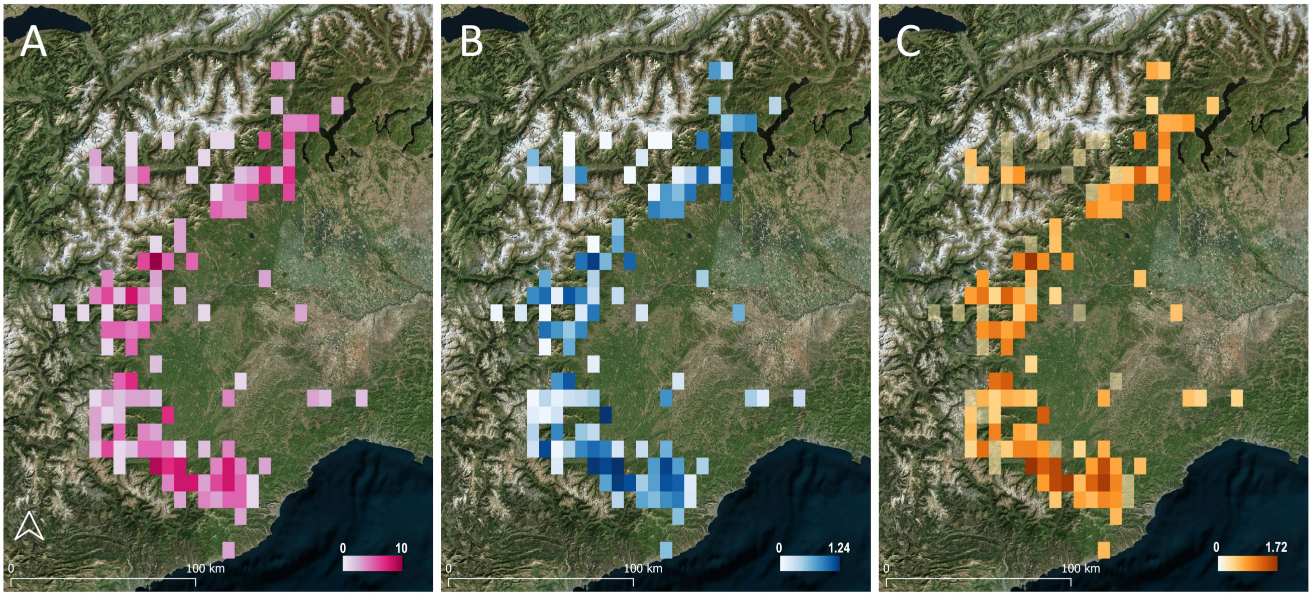


Figure 5. Maps of taxonomic (**A**), functional (**B**), and genetic (**C**) richness of spider communities in the Western Italian Alps. Taxonomic richness is expressed as the number of species per site, while functional and genetic richness are estimated using neighbor-joining tree-based functions.

**Community dataset (Figshare)**

*Object name*: Subterranean spiders (Arachnida: Araneae) from the Western Italian Alps.

*Character encoding*: UTF_8

*Format name*: csv, comma-separated values.

*Format version*: 1.0

*Description*: A dataset with all the referenced distribution points of the species considered in the subterranean sites included in the P.R.I.N. 2022 project "DEEPCHANGE" (2022MJSYF8), funded by the Ministry of Universities and Research (Italy).

*Distribution*: the data set is available as supplementary material to this paper (as a comma-separated csv file), and is uploaded to Figshare (https://doi.org/10.6084/m9.figshare.28524383.v1).

*Date of creation*: 15 January 2024

*Date of last revision*: 26 February 2025

*Date of publication*: 06 March 2025

*Update policy*: None foreseen. However, potential updates based on published literature and ongoing surveys may be released in the future.

*Language*: English

*License of use*: if used by researchers, administrators, managers, amateurs, general public, and others, the access is free from the eScholarship webpage of Biogeographia (https://escholarship.org/uc/biogeographia) and from Figshare (https://doi.org/10.6084/m9.figshare.28524383.v1). This dataset [A dataset on cave-dwelling spiders (Arachnida: Araneae) from the Western Italian Alps] is made available under the Creative Commons Attribution License (CC-BY) 4.0: http://www.creativecommons.org/licenses/by/4.0/legalcode

*Metadata language*: English

*Metadata providers*: Giuseppe Nicolosi (giuseppe.nicolosi@unict.it), Stefano Mammola (stefano.mammola@cnr.it), Marco Isaia (marco.isaia@unito.it).

*Resource Citation*: Nicolosi, Giuseppe; Martínez, Alejandro; Piano, Elena; Isaia, Marco; Mammola, Stefano (2025). Subterranean spiders (Arachnida: Araneae) from the Western Italian Alps. figshare. Dataset. https://doi.org/10.6084/m9.figshare.28524383.v1.

**Occurrence dataset (GBIF)**

*Object name*: Subterranean spiders (Arachnida: Araneae) from the Western Italian Alps.

*Character encoding*: UTF_8

*Format name*: csv, comma-separated values.

*Format version*: 1.0

*Description*: A dataset with all the referenced distribution points of the species considered in the subterranean sites included in the P.R.I.N. 2022 project "DEEPCHANGE" (2022MJSYF8), funded by the Ministry of Universities and Research (Italy). This biodiversity dataset is constructed following the Darwin Core standard.

*Distribution*: the dataset (as a csv file) is uploaded to GBIF (doi: 10.15468/pdajjy).

*Date of creation*: 03 February 2025

*Date of last revision*: 01 March 2025

*Date of publication*: 05 March 2025

*Update policy*: None foreseen. However, potential updates based on published literature and ongoing surveys may be released in the future.

*Language*: English

*License of use*: if used by researchers, administrators, managers, amateurs, general public, and others, the access is free from GBIF (doi: 10.15468/pdajjy). This data set [Subterranean-dwelling spiders (Arachnida: Araneae) from the Western Italian Alps] is made available under the Creative Commons Attribution License (CC-BY) 4.0: http://www.creativecommons.org/licenses/by/4.0/legalcode

*Metadata language*: English

*Metadata providers*: Giuseppe Nicolosi (giuseppe.nicolosi@unict.it), Stefano Mammola (stefano.mammola@cnr.it), Marco Isaia (marco.isaia@unito.it).

*Resource Citation*: Nicolosi G, Martínez A, Piano E, Isaia M, Mammola S (2025). Subterranean-dwelling spiders (Arachnida: Araneae) from the Western Italian Alps. Version 1.1. Consiglio Nazionale delle Ricerche - Istituto di Ricerca sulle Acque. Occurrence dataset https://doi.org/10.15468/pdajjy accessed via GBIF.org on 2025-03-05.

**Management details**

*Project title*: Biodiversity conservation goes DEEP: integrating subterranean ecosystems into climate CHANGE agendas and biodiversity targets [P.R.I.N. 2022: 2022MJSYF8]

*Database manager*: Giuseppe Nicolosi, Stefano Mammola, Marco Isaia

*Temporal coverage*: the present data set ranges from 1854 to 2024.

*Record basis*: Literature records and sampling activities.

*Sampling methods*: The dataset was created by systematically reviewing existing literature documenting the presence of subterranean spiders in the Western Italian Alps. Relevant articles were identified, downloaded, and thoroughly reviewed to extract all available records. For each subterranean site, we extracted the geological information from the regional speleological cadastre of Piemonte and Val d'Aosta (available at https://catastogrotte-piemonte.net/) and Liguria (https://www.catastogrotte.net/liguria/index.php), including the speleological cadastre number, longitude and latitude coordinates of the entrance, elevation, development, and positive, negative, and total drop (calculated as the absolute value of the sum of the positive and negative drops). Furthermore, we indicated whether the subterranean site is located within a protected area and specified the type based on the SAC/SCI - Special Areas of Conservation / Sites of Community Importance raster obtained from the "Geoportale Piemonte" (https://www.geoportale.piemonte.it/geonetwork/srv/ita/catalog.search). We classified the lithology of each subterranean site using the Lithological Map from the "Geoportale Piemonte". Finally, we reported the presence of each recorded subterranean species in each site, along with the respective reference.

Further data were enhanced by conducting field activities carried out during recent years with species identified morphologically following standard taxonomic references (World Spider Catalog 2025).

*Funding grants*: European Union - Next Generation EU. Bandi PRIN 2022 MUR

*Publishing organization*: Molecular Ecology Group (dark-MEG), Water Research Institute (IRSA), National Research Council (CNR); University of Turin, Department of Life Sciences and System Biology.

## Geographic coverage

*Study area*: Western Italian Alps

*Bounding box*: Subterranean sites including between 43.9138716 – 46.2169319 Latitude and 6.7338506 – 8.759438 Longitude.

*Sampling design*: The dataset was created including all the available publications on cave-dwelling spiders recorded in subterranean sites through the literature search and unpublished records based on recent sampling activities.

*Site type*: Subterranean sites including natural and artificial caves.

*Geographic region*: Italian Western Alps (Piedmont, Liguria, Val d'Aosta).

*Country*: Italy.

*Lithology unit*: Alluvial deposits, Alternating clay layers, Augen gneisses, Clay beds, Clays and clayey marls, Dolomites and limestones, Fine to medium-grained sand, Fine-grained gneisses, Granites, Limestone deposits, Marl layers, Morainic deposits, Serpentinites, Silty mudstones.

*Quality control for geographic data*: Quality control was performed using Google maps/QGIS identification of sites, and latitude and longitude coordinates provided by data providers.

*General description*: We first based our dataset on the records of the most recent review by Isaia et al. 2011. We then searched for additional papers about spiders in the Western Italian Alps.

*Literature search method*: Online bibliography research tools (i.e. Google Scholar, Scopus, and Clarivate Web of Science)

*Literature list*: We gathered information on subterranean sites in which the presence of cave-dwelling spiders is recorded based on 12 publications (Isaia et al. 2011, 2023; Mammola, 2012; Mammola et al. 2015, 2016a, 2016b, 2017a, 2017b, 2020a; Mammola and Isaia, 2018; Lana et al. 2021; Milano et al. 2022).

## Taxonomic coverage

*General description*: The dataset covers all records of the spiders (Arachnida: Araneae) found in caves and other subterranean sites in the Western Italian Alps.

*Taxonomic ranks*: Species level.

*Taxon specialists*: Marco Isaia.

*Quality control for taxonomic data*: Taxonomic data were checked and updated to include revision of names through a comparison with the Catalog of Italian spiders "Araneae.it" (Pantini and Isaia 2019).

## Conclusions

This data paper presents a comprehensive dataset documenting the distribution of subterranean spiders across 370 sites in the Western Italian Alps. Encompassing 31 species, the dataset provides detailed insights into local geomorphological and sites characteristics. Despite its regional focus, its open-access nature enhances its potential for broad applications in eco-evolutionary research. By integrating species composition with environmental data and including a phylogeny for all species, this dataset serves as a valuable resource for studying the ecological dynamics of subterranean spider communities. Furthermore, its interoperability with functional trait data opens new avenues for exploring key questions in subterranean ecology. The authors are already analyzing this dataset in this context, but we strongly encourage other researchers to explore its potential in addressing a wide range of scientific questions.


**Acknowledgments**

Special thanks to Diego Fontaneto, Martina Pavlek, Diego Patiño Sauma, Ilaria Vaccarelli, and Luisa Dainelli for accompanying us in different surveys in the field.

**Funding**

This research was funded by the P.R.I.N. 2022 projects "DEEPCHANGE" (2022MJSYF8) and "ANCHIALOS" (2022LLNF3N), funded by the Ministry of Universities and Research (Italy), by project "FRAGGLE" (PID2021-124640NB-I00), funded by MCIN/AEI/10.13039/501100011033 and by "ERDF A way of making Europe". Additional support is provided by Biodiversa+, the European Biodiversity Partnership under the 2021–2022 BiodivProtect joint call for research proposals, co-funded by the European Commission (GA N°101052342) and with the funding organisations Ministry of Universities and Research (Italy), Agencia Estatal de Investigación – Fundación Biodiversidad (Spain), Fundo Regional para a Ciência e Tecnologia (Azores, Portugal), Suomen Akatemia – Ministry of the Environment (Finland), Belgian Science Policy Office (Belgium), Agence Nationale de la Recherche (France), Deutsche Forschungsgemeinschaft e.V. (Germany), Schweizerischer Nationalfonds (Grant N° 31BD30_209583, Switzerland), Fonds zur Förderung der Wissenschaftlichen Forschung (Austria), Ministry of Higher Education, Science and Innovation (Slovenia), and the Executive Agency for Higher Education, Research, Development and Innovation Funding (Romania). EP, MI, and SM acknowledge additional support of the "National Biodiversity Future Center - NBFC" funded under the National Recovery and Resilience Plan (NRRP), Mission 4 Component 2 Investment 1.4 - Call for tender No. 3138 of 16 December 2021, rectified by Decree n.3175 of 18 December 2021 of Italian Ministry of University and Research funded by the European Union – NextGenerationEU (Project code CN_00000033, Concession Decree No. 1034 of 17 June 2022 adopted by the Italian Ministry of University and Research, CUP D13C22001350001 and CUP B83C22002930006).


## REFERENCES


Borges, P., Crespo, L., Cardoso, P. (2016). Species conservation profile of the cave spider *Turinyphia cavernicola* (Araneae, Linyphiidae) from Terceira Island, Azores, Portugal. Biodiversity Data Journal, 4, e10274. DOI: 10.3897/BDJ.4.e10274

Cardoso, P., Crespo, L., Silva, I., Borges, P., Boieiro, M. (2017). Species conservation profiles of endemic spiders (Araneae) from Madeira and Selvagens archipelagos, Portugal. Biodiversity Data Journal, 5, e20810. DOI: 10.3897/BDJ.5.e20810

Cardoso, P., Pekar, S., Birkhofer, K., Chuang, A., Fukushima, C. S., Hebets, E. A. et al. (2025). Ecosystem services provided by spiders. Biological Review, in press. DOI: 10.1111/brv.70044

Cardoso, P., Mammola, S., Rigal, F., Carvalho, J. (2024a). BAT: Biodiversity Assessment Tools. R package version 2.9.6, <https://CRAN.R-project.org/package=BAT>.

Cardoso, P., Guillerme, T., Mammola, S., Matthews, T. J., Rigal, F., Graco-Roza, C., Graco-Roza, C., Carlos Carvalho, J. (2024b). Calculating functional diversity metrics using neighbor-joining trees. Ecography, 2024(7), e07156. DOI: 10.1111/ecog.07156

Clark, J. A., May, R. M. (2002). Taxonomic bias in conservation research. Science, 297(5579), 191–192. DOI: 10.1126/science.297.5579.191b

Coddington, J. A., Agnarsson, I., Cheng, R. C., et al. (2016). DNA barcode data accurately assign higher spider taxa. PeerJ, 4, e2201. DOI: 10.7717/peerj.2201

Deharveng, L., Bedos, A. (2019). Biodiversity in the tropics. In Encyclopedia of caves (pp. 146-162). Academic Press.

Feng, X., Enquist, B. J., Park, D. S., et al. (2022). A review of the heterogeneous landscape of biodiversity databases: Opportunities and challenges for a synthesized biodiversity knowledge base. Global Ecology and Biogeography, 31(7), 1242-1260. DOI: 10.1111/geb.13497

Ficetola, G. F., Canedoli, C., Stoch, F. (2019). The Racovitzan impediment and the hidden biodiversity of unexplored environments. Conservation Biology, 33(1), 214-216. DOI: 10.1111/cobi.13179

Galimberti, A., Assandri, G., Maggioni, D., Ramazzotti, F., Baroni, D., Bazzi, G., et al. (2020). Italian odonates in the Pandora's box: A comprehensive DNA barcoding inventory shows taxonomic warnings at the Holarctic scale. Molecular Ecology Resources, 21, 183–200. DOI: 10.1101/2020.04.23.056911

Hesselberg, T., Simonsen, D., Juan, C. (2019). Do cave orb spiders show unique behavioural adaptations to subterranean life? A review of the evidence. Behaviour, 156(10), 969–996. DOI: 10.1163/1568539X-00003564

Isaia, M., Paschetta, M., Lana, E., Pantini, P., Schönhofer, A. L., Christian, E., Badino, G. (2011). Subterranean Arachnids of the Western Italian Alps (Arachnida: Araneae, Opiliones, Palpigradi, Pseudoscorpiones). Monografie XLVII. Museo Regionale di Scienze Naturali: Torino, Italy.

Isaia, M., Nicolosi, G., Infuso, A., Ribera, C. (2023). Two new subterranean *Typhlonesticus* (Araneae: Nesticidae) from the Alps with notes on their ecology, distribution and conservation. Arthropod Systematics and Phylogeny, 81, 801-818. DOI: 10.3897/asp.81.e106948

Jetz, W., McPherson, J. M., Guralnick, R. P. (2012). Integrating biodiversity distribution knowledge: Toward a global map of life. Trends in Ecology and Evolution, 27(3), 151-159. DOI: 10.1016/j.tree.2011.09.007

Katoh, K., Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution, 30(4), 772-780. DOI: 10.1093/molbev/mst010

Lana, E., Giachino, P. M., Casale, A. (2021). Fauna Hypogaea Pedemontana. Grotte e ambienti sotterranei del Piemonte e della Valle d'Aosta. WBA Monographs, 6.

Lipovšek, S., Leitinger, G., Janžekovič, F., et al. (2019). Towards understanding partial adaptation to the subterranean habitat in the European cave spider, *Meta menardi*: An ecocytological approach. Scientific Reports, 9(1), 9121. DOI: 10.1038/s41598-019-45291-z

Lunghi, E., Mammola, S., Martínez, A., Hesselberg, T. (2024). Behavioural adjustments enable the colonization of subterranean environments. Zoological Journal of the Linnean Society, 201(2), 549-559. DOI: 10.1093/zoolinnean/zlad133

Mammola, S. (2012). Ecologia e life history di *Meta menardi* (Latreille, 1804) e *M. bourneti* Simon, 1922 (Araneae, Tetragnathidae). Tesi Magistrale, Università degli Studi di Torino.

Mammola, S., Isaia, M., Arnedo, M. A. (2015). Alpine endemic spiders shed light on the origin and evolution of subterranean species. PeerJ, 3, e1384. DOI: 10.7717/peerj.1384

Mammola, S., Hormiga, G., Arnedo, M. A., Isaia, M. (2016a). Unexpected diversity in the relictual European spiders of the genus *Pimoa* (Araneae: Pimoidae). Invertebrate Systematics, 30(6), 566-587. DOI: 10.1071/IS16017

Mammola, S., Piano, E., Isaia, M. (2016b). Step back! Niche dynamics in cave-dwelling predators. Acta Oecologica, 75, 35–42. DOI: 10.1016/j.actao.2016.06.011

Mammola, S., Isaia, M. (2017a). Spiders in caves. Proceedings of the Royal Society B: Biological Sciences, 284, 20170193. DOI: 10.1098/rspb.2017.0193

Mammola, S., Isaia, M. (2017b). Rapid poleward distributional shifts in the European cave-dwelling *Meta* spiders under the influence of competition dynamics. Journal of Biogeography, 44(12), 2789–2797. DOI: 10.1111/jbi.13087

Mammola, S., Isaia, M. (2018). Day–night and seasonal variations of a subterranean invertebrate community in the twilight zone. Subterranean Biology, 27, 31-51. DOI: 10.3897/subtbiol.27.28909

Mammola, S., Goodacre, S. L., Isaia, M. (2018a). Climate change may drive cave spiders to extinction. Ecography, 41(1), 233-243. DOI: 10.1111/ecog.02902

Mammola, S., Cardoso, P., Ribera, C., Pavlek, M., Isaia, M. (2018b). A synthesis on cave-dwelling spiders in Europe. Journal of Zoological Systematics and Evolutionary Research, 56(3), 301-316. DOI: 10.1111/jzs.12201

Mammola, S., Piano, E., Cardoso, P., Vernon, P., Domínguez-Villar, D., Culver, D. C., Pipan, T., Isaia, M. (2019a). Climate change going deep: The effects of global climatic alterations on cave ecosystems. The Anthropocene Review, 6(1-2), 98-116. DOI: 10.1177/2053019619851594

Mammola, S., Cardoso, P., Angyal, D., et al. (2019b). Local-versus broad-scale environmental drivers of continental β-diversity patterns in subterranean spider communities across Europe. Proceedings of the Royal Society B, 286(1914), 20191579. DOI: 10.1098/rspb.2019.1579

Mammola, S., Milano, F., Isaia, M. (2019c). Taxonomy, ecology and conservation of the cave-dwelling spider *Histopona palaeolithica*, with the description of *H. petrovi* sp. nov. (Araneae: Agelenidae). Journal of Arachnology, 47, 317-325. DOI: 10.1636/0161-8202-47.3.317

Mammola, S., Chiappetta, N., Giachino, P. M., Antić, D. Ž., Zapparoli, M., Isaia, M. (2020a). Exploring the homogeneity of terrestrial subterranean communities at a local spatial scale. Ecological Entomology, 45(5), 1053-1062. DOI: 10.1111/een.12883

Mammola, S., Lunghi, E., Bilandžija, H., Cardoso, P., Grimm, V., Schmidt, S. I., Hesselberg, T., Martínez, A. (2021). Collecting eco-evolutionary data in the dark: Impediments to subterranean research and how to overcome them. Ecology and Evolution, 11(11), 5911-5926. DOI: 10.1002/ece3.7556

Mammola, S., Pavlek, M., Huber, B. A., et al. (2022). A trait database and updated checklist for European subterranean spiders. Scientific Data, 9(1), 236. DOI: 10.1038/s41597-022-01316-3

Mammola, S., Adamo, M., Antić, D., et al. (2023). Drivers of species knowledge across the Tree of Life. Elife, 12, RP88251. DOI: 10.7554/eLife.88251.3.sa0

Mammola, S., Graco-Roza, C., Ballarin, F., et al. (2024). Functional convergence underground? The scale-dependency of community assembly processes in European cave spiders. Global Ecology and Biogeography, 33(6), e13840. DOI: 10.1111/geb.13840

Marazzi, S. (2005). Atlante orografico delle Alpi: SOIUSA: suddivisione orografica internazionale unificata del sistema alpino. Priuli and Verlucca.

Milano, F., Borio, L., Komposch, C., Mammola, S., Pantini, P., Pavlek, M., Isaia, M. (2022). Species conservation profiles of the endemic spiders *Troglohyphantes* (Araneae, Linyphiidae) from the Alps and the north-western Dinarides. Biodiversity Data Journal, 10, e87261. DOI: 10.3897/BDJ.10.e87261

Nicolosi, G., Piano, E., De Beni, E., Isaia, M. (2023). Double dare: Climate change and volcanic activity threatens local populations of *Meta menardi* (Araneae, Tetragnathidae) in Sicily. Global Ecology and Conservation, 48, e02699. DOI: 10.1016/j.gecco.2023.e02699

Pantini, P., Isaia, M. (2019). Araneae.it: The online catalog of Italian spiders, with addenda on other arachnid orders occurring in Italy (Arachnida: Araneae, Opiliones, Palpigradi, Pseudoscorpionida, Scorpiones, Solifugae). Fragmenta Entomologica, 51(2), 127-152. DOI: 10.13133/2284-4880/374

Paradis, E., Schliep, K. (2019). ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. Bioinformatics, 35, 526-528. DOI: 10.1093/bioinformatics/bty633

Pavlek, M., Gauthier, J., Tonzo, V., et al. (2022). Life-history traits drive spatial genetic structuring in Dinaric cave spiders. Frontiers in Ecology and Evolution, 10, 910084. DOI: 10.3389/fevo.2022.910084

Schmitt, T. (2009). Biogeographical and evolutionary importance of the European high mountain systems. Frontiers in Zoology, 6, 1-10. DOI: 10.1186/1742-9994-6-9

Stamatakis, A. (2014). RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics, 30(9), 1312-1313. DOI: 10.1093/bioinformatics/btu033

Van Swaay, C., Nowicki, P., Settele, J., van Strien, A. J. (2008). Butterfly monitoring in Europe: Methods, applications and perspectives. Biodiversity and Conservation, 17, 3455-3469. DOI: 10.1007/s10531-008-9491-4

Wandersee, J. H., Schussler, E. E. (1999). Preventing plant blindness. American Biology Teacher, 61, 82-86. DOI: 10.2307/4450624.

Wheeler, W. C., Coddington, J. A., Crowley, et al. (2017). The spider tree of life: phylogeny of Araneae based on target-gene analyses from an extensive taxon sampling. Cladistics, 33(6), 574-616. DOI: 10.1111/cla.12182

World Spider Catalog (2025). World Spider Catalog. Version 26. Natural History Museum Bern, online at http://wsc.nmbe.ch, accessed on 28 February 2025. DOI: 10.24436/2

*Submitted: 10 March 2025*

*First decision: 2 June 2025*

*Accepted: 2 July 2025*

*Published online: 16 July 2025*

*Edited by Emiliano Mori*