



TraitCH: a multi-taxa functional trait dataset for Switzerland and Europe

Yohann Chauvier-Mendes^{1, 2, 3}, Antoine Adde¹, Ariel Bergamini², Gerhard Rambold⁴, Silvia Stofer², Ninetta Graf², Andrin Gross², Stefan Blaser², Stuart P. M. Roberts⁵, Simon G. Potts⁵, Joan Casanelles-Abella^{6, 2}, Marco Moretti², Michael P. Nobis², Jean-Paul Theurillat^{7, 8}, Heike Hofmann⁹, Ann-Michelle Hartwig⁹, François Claude¹⁰, Gauvain Saucy¹¹, Florian Altermatt^{1, 12}

¹ Swiss Federal Institute of Aquatic Science and Technology (EAWAG); 8600 Dübendorf, Switzerland.

² Swiss Federal Institute for Forest, Snow and Landscape Research (WSL); 8903 Birmensdorf, Switzerland.

³ Research Center for Advanced Science and Technology, University of Tokyo, Tokyo, Japan.

10 ⁴ Department of Mycology, University of Bayreuth, Bayreuth 95440, Germany

⁵ Centre for Agri-Environmental Research, School of Agriculture, Policy and Development, University of Reading, RG6 6UR Reading, UK

⁶ Urban Productive Ecosystems, TUM School of Life Sciences, Hans Carl-von-Carlowitz-Platz 2, Feising 85354, Germany

⁷ Centre Alpien de Phytogéographie, Fondation du Jardin botanique Flore-Alpe, 1938 Champex-Lac, Switzerland

15 ⁸ Department of Botany and Plant Biology, University of Geneva, 1292 Chambésy, Switzerland

⁹ Swissbryophytes, Institut für Systematische und Evolutionäre Botanik, Universität Zürich, Zollikerstrasse, 107, 8008 Zürich, Switzerland

¹⁰ info fauna, Avenue Bellevaux 51, 2000 Neuchâtel, Switzerland

¹¹ Dos la Velle 72, 2718 Lajoux, Switzerland

20 ¹² Department of Evolutionary Biology and Environmental Studies, University of Zurich, 8006 Zürich, Switzerland

Correspondence to: Yohann Chauvier-Mendes (yohann.chauvier@wsl.ch), Florian Altermatt (florian.altermatt@eawag.ch)

Abstract. Functional traits of species are becoming increasingly used in ecological research, providing key insights into organisms-environment interactions, ecosystem functions, and responses to environmental changes. In recent years, substantial initiatives have generated major open-access datasets of species' functional traits. However, these resources typically concentrate on a handful of well-studied biological groups—such as plants, birds, and fishes—and less on specific biogeographic regions limiting their applicability in regional biodiversity assessments and conservation planning. Here, we present TraitCH, a comprehensive dataset of functional traits spanning over 71,874 species (≥ 1 functional trait) across 17 major taxonomic groups: Apocrita (2,278), Arachnida (3,728), Coleoptera (8,565), Ephemeroptera/Plecoptera/Trichoptera (1,349), Lepidoptera (3,757), Odonata (234), Orthoptera (1,283), Bryobiotina (2,285), Fungi (12,469), Lichen (2,435), Mollusca (7,493), Pisces (838), Amphibia (151), Aves (1,356), Mammalia (522), Reptilia (298), and Tracheophyta (22,833). Compiled from 43 published and unpublished sources, TraitCH provides a robust representation of total species richness and composition for Switzerland and Europe. For each species, we compiled their taxonomic hierarchy, existing synonymy, geographic origin, conservation status, micro- and macro-habitat types, global range size and available ecological trait values. TraitCH consists of 17 trait tables (one per major taxonomic group), each available in two formats: (1) original and (2) completed versions with missing trait values imputed using a tree-based modelling method. TraitCH was also embedded within a comprehensive checklist of European species from the same groups (~210,000 taxa), encompassing authoritative Swiss and



European checklists, with the exception of Fungi and Lichen, for which only Swiss checklists were available. TraitCH is available on Zenodo: <https://doi.org/10.5281/zenodo.15063844> (Chauvier et al., 2025).

1 Introduction

40 Functional traits are phenotypic characteristics that enable individuals (species) to grow, reproduce and survive, and have therefore a direct link to individual fitness (Violle et al., 2007). They have emerged as a key resource in the fields of ecology and biodiversity sciences, providing critical insights into the functional roles of species within ecosystems and their responses to environmental changes (Gallagher et al., 2021; Green et al., 2022; Massol et al., 2017; Rao et al., 2024). Trait data encompass a diverse range of characteristics – including morphological, physiological, phenological, and behavioural traits – that shape
 45 organisms' interactions with their environment and each other, while increasingly collected in a standardized manner (Moretti et al., 2017). Trait data has offered a novel functional perspective on biodiversity that complements taxonomic and phylogenetic approaches (Devictor et al., 2010), which has allowed ecologists to link individual species' attributes, such as body size, dispersal ability, or feeding strategy, to broader ecosystem processes and patterns (Cote et al., 2022).

Over the last decade, the importance of trait-based approaches has grown substantially, driven by advances in
 50 computational tools, global change research, and the increasing availability of large-scale datasets (e.g., Madin et al., 2016; Moretti et al., 2017; Gallagher et al., 2021; Green et al., 2022; Ho & Altermatt, 2024). Landmark initiatives such as TRY for plants (Kattge et al., 2020), FishBase for fishes (Froese and Pauly, 2000), T-SITA for soil invertebrates (Pey et al., 2014) and VertLife for tetrapods (Moura et al., 2024) have catalysed this growth, providing standardized, openly accessible data for key taxonomic groups. Thanks to this increasing volume of available data, functional traits are now routinely integrated into
 55 biodiversity models, including species distribution models (Vesk et al., 2021), productivity models (He et al., 2023), and ecosystem service assessments (Weiskopf et al., 2022). The integration of trait information in these applications is critical for better understanding how biodiversity contributes to ecosystem resilience and for predicting how species and ecosystems will respond to threats such as climate change, habitat loss, and biological invasions (Aquilué et al., 2020; Funk et al., 2008).

However, availability of trait data via harmonized and centralized databases is generally biased toward "charismatic"
 60 or well-studied taxa, such as tetrapods, plants, and fishes, which have long received attention due to their visibility and cultural significance (Troudet et al., 2017). Trait data for other groups – such as invertebrates and fungi – remain significantly underrepresented or scattered in the literature, despite their critical ecological functions and intrinsic importance as biodiversity features (Green et al., 2022; Schneider et al., 2019). The reasons for this imbalance may include the difficulty of accessing or studying these taxa, the lack of standardized trait definitions, and the dispersed or grey literature nature of existing trait data,
 65 which makes data extraction very time consuming; but see for novel approaches using large language models (Keck et al., 2025). Additionally, inconsistencies in taxonomy and unresolved synonymy issues are significant challenges limiting the regional utility of these datasets for ecological research and conservation applications (Feng et al., 2022; Grenié et al., 2023; Pyle et al., 2021).



To address these gaps, we present TraitCH, a multi-taxa functional trait dataset covering 71,874 European species (Fig. 1a, 2) across 17 major taxonomic groups, including neglected taxa such as fungi, lichen, different families of insects and molluscs, alongside better-represented groups, such as plants, tetrapods, and freshwater fishes. TraitCH encompasses data from 43 published and unpublished sources and was embedded within a comprehensive checklist of European species from the same groups (~210,000 taxa), encompassing authoritative Swiss and European checklists. By additionally harmonizing taxonomy and highlighting potential synonymies using the taxonomic backbone of the Global Biodiversity Information Facility (GBIF), this dataset improves trait data accuracy, usability and integration. Finally, TraitCH includes two versions of the trait table: (1) an original version with published trait values and (2) a completed version with imputed missing traits and quality-assessed values, enabling trait extrapolation within organismal groups.

2 Methods

2.1 Species checklist

For all target taxa (Fig. 1a), we first generated a comprehensive checklist of all species scientific names reported in the Swiss Species Information Centre (InfoSpecies, www.infospecies.ch), the Federal Office for the Environment (FOEN; www.bafu.admin.ch), the Swiss Ornithological Institute (www.vogelwarte.ch), the National Data and Information Centre on the Swiss Flora (www.infoflora.ch), Fauna (www.infofauna.ch), Bryophytes (www.swissbryophytes.ch), Lichen (www.swisslichens.ch) and Fungi (www.swissfungi.ch). Excluding the Fungi and Lichen group, for which only Swiss checklists were available, we extended our checklist to a comprehensive European dimension employing authoritative sources. For all remaining target taxa, we added species names from the Flora Alpina (Aeschimann et al., 2004), augmented Euro+Med Plantbase (Dengler et al., 2023), European vascular plant Red List (Lončarević et al., 2024), European Environmental Agency (EEA) Red List (European Red Lists of species, 2009-2022, 2025) and FaunaEuropeae (de Jong et al., 2014). After removing duplicates, incomplete entries, and unknown names, with automated and manual checks (see the `to_GenusSpecies` R function in the Supplementary Material), our final EUR checklist contained a total of 211,123 unique species names.

2.2 Taxonomy and conservation status

For each species names, we reported their scientific name, synonymy status, accepted name, taxonomic hierarchy (Genus, Family, Order, Class, Phylum ranks), and their IUCN (International Union for Conservation of Nature), European and Swiss Red List status. Names, status and hierarchy were retrieved using the `get_status` function of the *gbif.range* R package (Chauvier-Mendes et al., 2025) which relies on the GBIF backbone taxonomy. While retrieving all scientific names and their synonymy for each species of the checklist allowed potential synonymy to be uncovered, this information and the retrieved taxonomic hierarchy also allowed extra co-evolutionary and -adaptation information to be available for trait imputation. IUCN Red List statuses were retrieved from the same function, European ones from the EEA Red List last release (European Red

Lists of species, 2009–2022, 2025) and European vascular plant Red List (Lončarević et al., 2024), and Swiss ones from the
 100 FOEN (Red Lists: Threatened species in Switzerland, 2024).

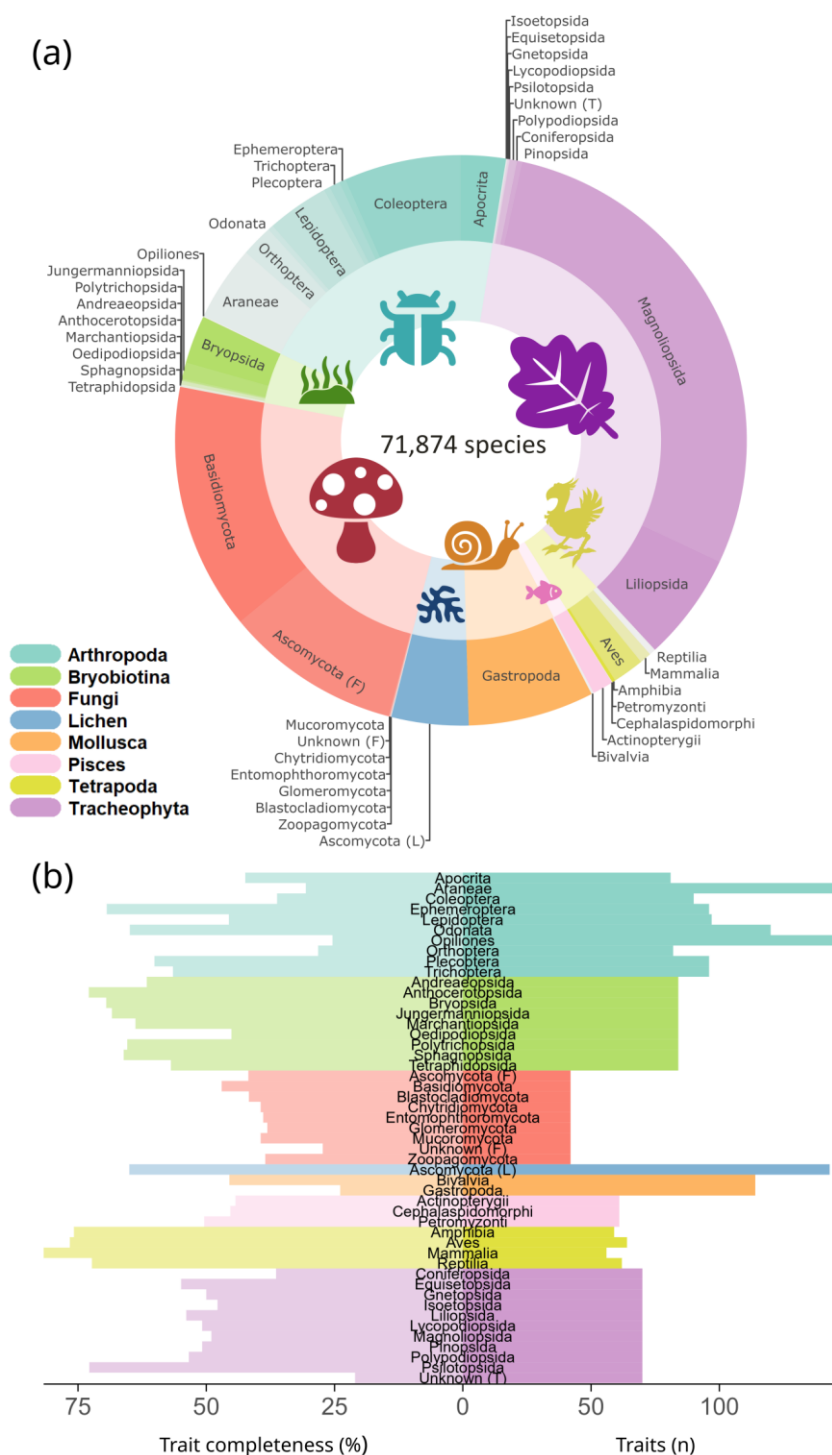


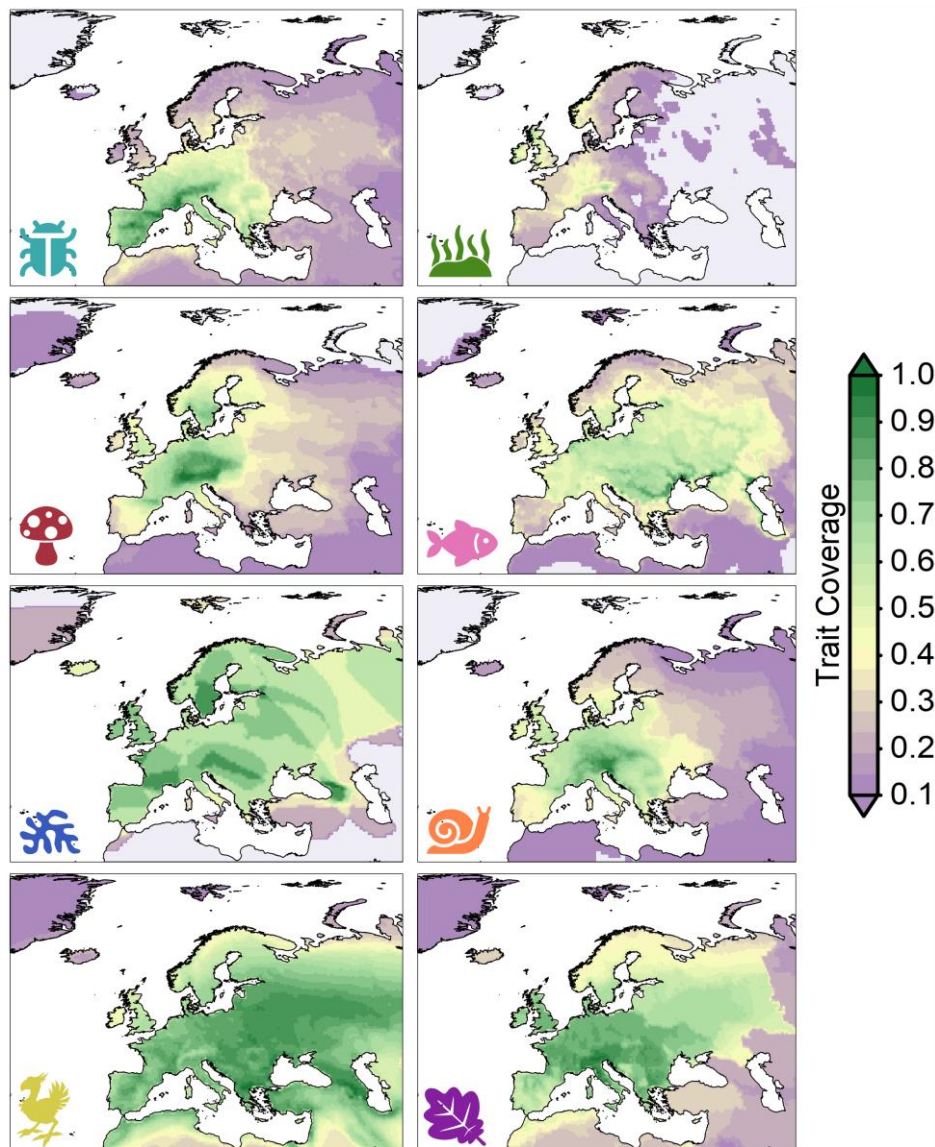


Figure 1: Taxonomic and trait coverage of TraitCH. Panel (a) summarizes taxonomic coverage. Panel (b) summarizes the overall percentage (%) of non-missing trait values and the number of available traits for each taxonomic group. Taxonomic coverage for major taxonomic ranks distributes as such: Arthropoda (n = 21,194), Bryobiotina (n = 2,285), Fungi (n = 12,469), Lichen (n = 2,435), Mollusca (n = 7,493), Pisces (n = 838), Tetrapoda (n = 2,327), Tracheophyta (n = 22,833). This summary only applies for species with ≥ 1 functional trait. Silhouettes from the Noun Project.

In addition, we included information on 16 different habitats using 26 Swiss habitat guilds (Delarze et al., 2015; Rutishauser et al., 2023) and our collected traits (see *Swiss_guilds* and *All* tab sections in the Supplementary Material metadata file), as well as their Swiss (www.infospecies.ch) or European geographic origin (European Red Lists of species, 2009-2022, 2025). Finally, we included information on the global range area (km²) of each species, calculated with the *terra* R package (Hijmans, 2024) based on expert range maps available from IUCN and Birdlife (<https://www.iucnredlist.org/resources/spatial-data-download>, data access: 2025.20.08). For this, we first discarded species distributions labelled as ‘Presence uncertain’, ‘Expected Additional Range’ (i.e., future range expectations), ‘Introduced’, ‘Vagrant’, ‘Origin uncertain’ and ‘Assisted Colonisation’, to keep the strict native distribution of each species, known to strongly correlate with species traits related to dispersal such as body mass or plant height (Alzate and Onstein, 2022).

2.3 Traits compilation

Representing 17 major taxonomic groups, trait data was extracted from 43 sources that we harmonized, cleaned and employed to construct the TraitCH dataset (Table 1). We mainly focused our extraction on traits describing the morphology, life-history, ecological behaviour, environmental niche and habitat of each species. These sources ($n = 43$) included: $n = 11$ for Apocrita, Arachnida, Coleoptera, Ephemeroptera/Plecoptera/Trichoptera, Lepidoptera, Odonata and Orthoptera (Casanelles-Abella et al., 2023; Gossner et al., 2015; Hagge et al., 2021; Klaiber et al., 2017; Logghe et al., 2025; Mammola et al., 2022; Middleton-Welling et al., 2020; Pekár et al., 2021; Roberts, 2017; Shirey et al., 2022; Waller et al., 2019), $n = 2$ for Bryobiotina (Hofmann et al., 2011; van Zuijlen et al., 2023), $n = 3$ for Pisces (Brosse et al., 2021; Frimpong and Angermeier, 2009; Schmidt-Kloiber and Hering, 2015), $n = 2$ for Fungi (Gross et al., 2020; Zanne et al., 2020), $n = 3$ for Lichen (Rambold et al., 2016; Stofer et al., 2019; LIAS light – A Database for Rapid Identification of Lichens – Subset Switzerland p. pte.), $n = 3$ for Mollusca (Saucy et al., 2024; Schmidt-Kloiber and Hering, 2015; Tachet et al., 2010), $n = 11$ for Amphibia, Aves, Mammalia and Reptilia (Cox et al., 2021; Genoud et al., 2018; Huang et al., 2023; Jetz et al., 2008; Meiri, 2018; Moura et al., 2024; Oliveira et al., 2017; Oskyrko et al., 2024; Soria et al., 2021; Tobias et al., 2022; Wilman et al., 2014) and $n = 8$ for Tracheophyta (Aeschmann et al., 2004; Chauvier-Mendes et al., 2024; Chauvier et al., 2021, 2022; Dengler et al., 2023; Díaz et al., 2022; Landolt et al., 2010; Lososová et al., 2023). All sourced datasets were either distributed under a Creative Commons license (CC), or, when access was restricted, their use within TraitCH permitted by the authors and editors.



135 **Figure 2: European coverage of TraitCH.** Each summary map was calculated by summing the IUCN-Birdlife expert range maps
 that matched our final EUR species checklist (Arthropoda: 1,820 species; Bryobiotina: 201; Fungi: 85; Pisces: 493; Lichen: 9;
 140 Mollusca: 2,596; Tetrapoda: 1,242; Tracheophyta: 2,238; for icon names, see Fig. 1). To represent effective ranges, species
 distributions labelled as ‘Possibly Extinct’, ‘Extinct’, ‘Presence Uncertain’ and ‘Expected Additional Range’ were discarded
 beforehand. Summed values were normalized from 0.1 to 1.0. Note that the number of IUCN represented species is much lower than
 that of TraitCH, therefore this visual representation shall only give the relative distribution of trait coverage. Silhouettes from the
 Noun Project.

For each dataset, we applied the same cleaning and harmonizing process. First, if any, pre-imputed traits (i.e., traits that were
 artificially imputed from a previous data filling procedure) were assigned to NA to avoid carrying potential error estimates.



145 Second, we ensured that all species names were unique and complete (to_GenusSpecies R function), and that each taxa
 was only represented by one valid scientific name. In cases duplicated names were found, trait values were aggregated by
 unique species name to maintain consistency. This aggregation was done by mode (most frequent value) for categorical traits,
 and by mean when numerical. Third, accepted names according to the GBIF taxonomy were retrieved for each species name
 using the get_status R function (Chauvier-Mendes et al., 2025). Finally, each final dataset had their columns renamed and
 150 restructured for improved user-interface (see the Comments columns in the Supplementary Material metadata file).

For each of the 17 taxonomic group (Table 1), their harmonized trait datasets were merged by species names. Columns
 containing unique trait information were preserved as they were. For columns with overlapping trait information, missing
 values in one dataset were filled with non-missing values from another. When non-missing values overlapped between datasets,
 precedence was given to values of datasets covering more traits, as specified by the order of references in the Ref_ID column
 155 of the Supplementary Material metadata file. In total, we obtained 17 preliminary compiled trait datasets.

Table 1: Data sources employed to compile TraitCH. For each taxonomic group, the number of compiled traits, as well as the number of covered species (≥ 1 functional trait) for Europe (EUR) and Switzerland (CH) are also given. Silhouettes from the Noun Project.

	Taxonomic group	Common name	Data sources	Traits (n)	EUR species (n)	CH species (n)
	Apocrita	Bees & Wasps	EU-FP6 ALARM project • Casanelles-Abella et al. 2023	81	2,278	667
	Arachnida	Spiders & Harvestmans	World Spider Trait database • Gossner et al. 2015 • Mammola et al. 2022	145	3,728	774
	Coleoptera	Beetles		90	8,565	1,394
	Ephemeroptera Plecoptera Trichoptera	EPT	Fauna Indicativa • Gossner et al. 2015 • Hagge et al. 2021 • Waller et al. 2019 • Middleton-Welling et al. 2020 • LepTraits 1.0 • Logghe et al. 2025	96	1,349	441
	Lepidoptera	Butterflies		97	3,757	893
	Odonata	Dragonflies		120	234	90
	Orthoptera	Grasshoppers		82	1,283	123
	Bryobiotina	Bryophytes	SwissBryophytes • BET	84	2,285	1,452
	Fungi	Mushrooms	SwissFungi • FunFun	42	12,469	12,389
	Lichen	Lichens	SwissLichens • LIAS (Swiss subset)	143	2,435	2,362
	Mollusca	Molluscs	Fauna Indicativa • freshwaterecology	114	7,493	331
	Pisces	Freshwater Fishes	FISHMORPH • Fish Traits • freshwaterecology.info	61	838	92
	Amphibia	Amphibians	TetrapodTraits • EltonTraits 1.0 • Cox et al. 2021 • COMBINE • Genoud et al. 2017 • ReptTraits • Traits of lizards of the world • Huang et al. 2023 • AmphiBIO • AVONET • Jetz et al. 2008	59	151	27
	Aves	Birds		64	1,356	235
	Mammalia	Mammals		56	522	98
	Reptilia	Reptiles		62	298	21
	Tracheophyta	Vascular Plants	Flora Indicativa • Flora Alpina • EIVE 1.0 • Diaz et al. 2022 • Lososová et al. 2023 • Chauvier et al. 2020, 2022, 2024	70	22,833	4,138



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TraitCH was iteratively generated for each of the 17 major taxonomic group based on the same procedure. First, the compiled dataset was merged to our EUR checklist by species names, retaining matches (m_1), and excluding non-matching species. Non-matching species of the compiled dataset were grouped by their GBIF-accepted names, with unique entries retained and duplicates aggregated by mean or mode. The resulting data was then merged with the non-matching species of EUR by GBIF names to incorporate all remaining trait information (m_2). Finally, (m_1) and (m_2) were combined, producing a dataset of trait data linked to unique species names, while also accounting for GBIF-accepted names to address potential synonymies and manually impute, by mean and mode, missing trait data for species sharing the same accepted name. This approach ensured comprehensive trait coverage and resolves discrepancies across trait datasets.

2.4 Traits imputation

The sources used for creating TraitCH showed different levels of trait data completeness across taxonomic groups (Fig. 1b). While removing species with missing trait information is a common practice, such practice is problematic if data is not missing at random, for example with a focus given to well-known, widely distributed and conspicuous species (Johnson et al., 2020; Penone et al., 2014), such that trait tables are biased. As an alternative, imputation techniques to infer missing trait values are generally recommended, especially those employing tree-based methods, which can capture both linear and non-linear relationships in the data (Schwerter et al., 2024; Shah et al., 2014; Stekhoven and Bühlmann, 2012). We therefore applied trait imputation for each of our 17 final trait datasets employing the *missRanger* R package (Mayer, 2024) and all available trait values of each species. GBIF-accepted, Genus, Family, Order, Class and Phylum ranks were also added to improve imputation performances. Including taxonomic hierarchy was justified because of its ability to partly capture evolutionary relationships and shared adaptive history, which have demonstrated to enhance the accuracy and biological relevance of predicted trait values compared to using trait data alone (Joswig et al., 2023; Schrodte et al., 2015; Swenson, 2014).

missRanger is an iterative imputation method that uses the efficient *randomForest* implementation from the *ranger* R package (Wright and Ziegler, 2017) that offers robust and flexible imputation for complex high-dimensional datasets (Casiraghi et al., 2023; Schwerter et al., 2024; Suh and Song, 2023). In short, the *missRanger* algorithm uses random forest models to first predict missing (trait) values based on observed data. This process is iterative, as imputed values from one step are used to retrain models in the next, refining predictions. This method handles both numerical and categorical data, avoiding the pitfalls of simple imputation techniques like mean or mode substitution. We parametrized our imputation (function *missRanger*) and, as recommended in the literature (Galbraith, 2012; Schwerter et al., 2024; Soria et al., 2021; Stekhoven and Bühlmann, 2012), repeated the process 25 times by setting the number of iterations to 20 (*maxiter* = 20), the number of trees to 100 (*num.trees* = 100), and employing the optional ‘predictive mean matching’ (*pmm.k* = 3), which ensured that imputed values match those observed in the original data, avoiding implausible values while preserving variance in trait distribution. Calibration errors (or out-of-bag prediction errors; OBB) were provided by the function as $1 - R^2$ and *classification error* for continuous and categorical traits, respectively and summarized as interquartile ranges for each taxonomic group.



3 Results

In total, TraitCH covers 71,874 species, and is composed of 34 main trait datasets: 17 raw trait tables, and 17 imputed tables
195 averaged from our 25 imputation runs (see folders *raw_traits* and *missRanger_imputed_traits*, respectively, in Supplementary
Material). Each final taxonomic dataset (raw and imputed) provides a common baseline of information regarding each species:
species name ('Species'), scientific name ('scientificName'), species taxonomic rank ('taxonRank'), GBIF synonymy status
(('GBIF_status'), accepted name according to the GBIF backbone taxonomy ('GBIF_accepted'), Genus, Family, Order, Class,
Phylum, TraitCH taxonomic group ('Group'), checklist source ('Source'), species native to Switzerland ('originCH'), species
200 native to Europe ('originEUR'), Swiss Red List status ('swissRedListCategory'), European Red List Status
(('europeanRegionalRedListCategory'), IUCN Red List Status ('iucnRedListCategory'), terrestrial taxa ('EcoTer'), freshwater
taxa ('EcoFresh'), marine taxa ('EcoMar'), ecological strategy (Fossorial, Terrestrial, Aquatic, Arboreal and Aerial; 'Fos',
'Ter', 'Aqu', 'Arb', 'Aer'), habitat types ($n = 16$), global range size ('RangeSize_km2') and other important trait types (see
Fig. 3). TraitCH is provided as space-separated values table (.txt) format, with all trait columns and their description found in
205 the Supplementary Material metadata file.

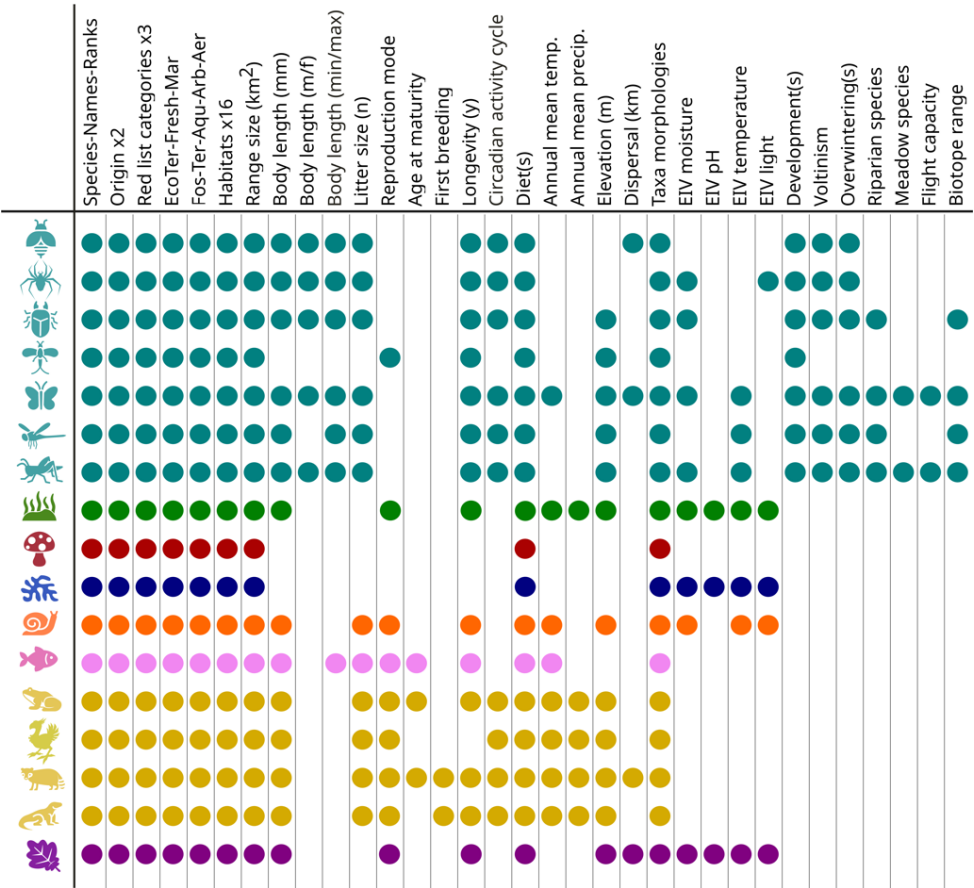




Figure 3: Common baseline of trait species and information in TraitCH. Species-Names-Ranks (seven columns): ‘Species’, ‘scientificName’, ‘taxonRank’, ‘GBIF_status’, ‘GBIF_accepted’, ‘Group’ and ‘Source’. Origin (two columns): ‘originCH’ and ‘originEUR’. Red list categories (three columns): ‘swissRedListCategory’, ‘europeanRedListCategory’, ‘iucnRedListCategory’. EcoTer-Fresh-Mar (3 columns): if terrestrial, freshwater or marine species. Fos-Ter-Aqu-Arb-Aer (five columns): species partial or full adaptation to fossorial, terrestrial, aquatic, arboreal or aerial microhabitats. Habitats (16 columns): water, wetlands, rocks, grassland, forests, deciduous, coniferous, mixed, pioneer, urban, green urban, agricultural, bushes, transitional, heathland and sand. Range size in km² are according to the IUCN. Body length describes plant (m) and seta height (mm) for Tracheophyta and Bryobiotina, respectively. m/f = male/female; y = years. See metadata file for more information. Silhouettes from the Noun Project.

While Mammalia, Aves, Amphibia, Reptilia and Lichen were the groups with the highest average trait data completeness (Fig. 1b; 81.7, 76.6, 75.8, 72.3 and 65 %, respectively), Bryobiotina, Amphibia, Pisces, Reptilia, Aves and Odonata were the groups with the highest EUR (96.3, 96.2, 94.3, 93.7, 91.1 and 90.7 %, respectively) and CH checklist coverages (96, 100, 91.1, 95.5, 99.6 and 100 %, respectively; Fig. 4a). Regarding trait imputation uncertainties, Amphibia, Fungi, Bryobiotina, Pisces, Orthoptera and Tracheophyta demonstrated the largest interquartile range (IQR) of imputation error estimates across their traits (Q_1 – Q_3 = 0.0005–0.22, 0.007–0.21, 0.015–0.2, 0.0–0.15, 0.01–0.14 and 0.007–0.13, respectively; Fig. 4b). See folder *missRanger_evaluations* in Supplementary Material for detailed imputation errors on individual traits per taxa.

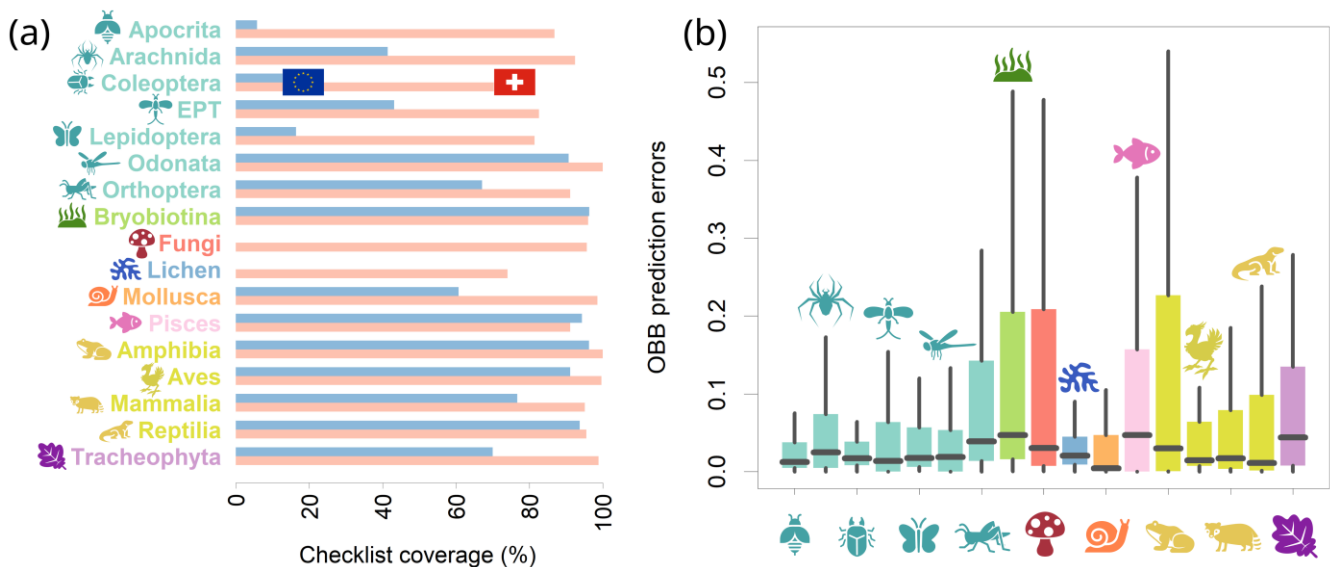


Figure 4: Species checklist coverage and imputation error estimates of TraitCH. Panel (a) summarizes per taxonomic group the overlap between the TraitCH species (having ≥ 1 trait) and the Switzerland (CH, red) and European checklists (EUR, blue). Missing EUR coverages for Fungi and Lichen are explained by the absence of existing European checklists. Panel (b) shows per taxonomic group the error range of imputations applied to all ecological traits. Error estimate is integrated within the *missRanger* imputation function and highlights the uncertainty of the random forest fit. Note: Arachnida only accounts for spiders and harvestmen. Silhouettes from the Noun Project.



235 It is important to note that each table includes a ‘MISSING_ALL_TRAITS’ column that provides information on trait
 availability for each species. Species officially included in TraitCH ($n = 71,874$ with ≥ 1 trait) are designated as ‘NO,’ while
 ‘YES’ highlights species from the EUR checklist that did not match any trait databases ($n = 139,249$). These species were kept
 in the imputation process, but their imputed values relied solely on available taxonomic hierarchy (GBIF-accepted, Genus,
 Family, Order, Class and Phylum). Although only subject to phylogenetic approximations, retaining this part of the imputed
 240 information still provides valuable resource to explore ecological questions where trait differentiation by taxonomic rank may
 contribute to broader analyses.

4 Discussion

TraitCH represents a significant advancement in functional trait research, providing a multi-taxa dataset spanning over 70,000
 European species across 17 taxonomic groups (Fig. 2). By integrating ecological traits, taxonomic classifications, and
 245 conservation statuses, this resource addresses critical gaps in regional biodiversity research, particularly for understudied
 groups such as invertebrates and fungi. However, several limitations highlight the need for cautious interpretation and future
 refinement.

While TraitCH encompasses species from Switzerland and broader Europe (Fig. 2), its coverage is uneven. For
 example, Apocrita, Coleoptera and Lepidoptera are under-represented (Fig. 4a), and hyper diverse insect orders like Diptera
 250 and Hymenoptera (excluding Apocrita) – which comprise thousands of species in central Europe (de Jong et al., 2014) – are
 entirely excluded. Recent DNA barcoding studies estimate that Germany alone harbours 1,800–2,200 undiscovered Diptera
 species, underscoring the scale of missing data in these "dark taxa" (Chimeno et al., 2022). This highlights the need for future
 efforts to expand the dataset to include these and other underrepresented taxa, which are essential for a holistic understanding
 of biodiversity and its functions. Moreover, the dataset's assumption of static trait values (one value per species) may
 255 oversimplify the complexity of trait variability. Many traits are plastic and can vary significantly across space and time, as
 well as within species (Altermatt, 2010; Bolnick et al., 2011; Violle et al., 2012). This intraspecific variability is particularly
 relevant in the context of climate change and evolutionary processes, where traits such as voltinism or trophic levels can exhibit
 substantial changes (Altermatt, 2010; Altermatt and Pearse, 2011; Pearse and Altermatt, 2013). Therefore, while TraitCH
 offers a valuable starting point, future research should focus on capturing and understanding this intraspecific trait variability.

260 The robustness of our trait imputation within the dataset is also a critical consideration (Fig. 4b). While the imputation
 provided good prediction estimates overall, with all median OBB prediction errors < 0.1 , validation metrics varied across
 taxonomic groups. Large groups such as Lichen and Aves exhibited both high trait data completeness and low imputation
 errors, indicating that comprehensive data led to more accurate imputations. In contrast, groups of varied size and trait
 completeness – Amphibia, Fungi, Bryobiotina, Pisces, Orthoptera and Tracheophyta – demonstrated more imputation
 265 uncertainties, suggesting that traits within some of these groups have more gaps and may be less correlated, making accurate



imputation more challenging. Users should consider these differences when interpreting TraitCH outputs, particularly for groups with more variable data structures. To support informed usage, detailed imputation error metrics per taxa and trait are available in the folder *missRanger_evaluations* in the Supplementary Material.

270 Despite these challenges, TraitCH offers a valuable resource for advancing functional trait-based research and
fostering a deeper understanding of ecosystem functioning and biodiversity responses to environmental changes. The dataset's
publicly accessible format encourages collaboration and further development, paving the way for novel IA approaches in
ecological data collection and analysis (Keck et al., 2025). As we continue to gather more trait data, the importance of naturalist
observations and innovative methodologies will become increasingly apparent, driving forward our ability to address the
complex challenges facing biodiversity in the 21st century.

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Data and code availability

The TraitCH data and code are available on GitHub at <https://github.com/8Ginette8/TraitCH>, and published versions of TraitCH are released to Zenodo: <https://doi.org/10.5281/zenodo.15063844> (Chauvier et al., 2025). Due to copyright reasons and given the unpublished nature of some of the trait sources, part of the data compilation of TraitCH ('Tch0' R script) cannot
 280 be run (commented-out code), as well as the whole IUCN diversity maps generation ('Tch3' R script).

Author contribution

YCM, AA and FA conceived the study. YCM processed the dataset, performed the analyses and wrote the first draft of the manuscript. Further versions were revised by YCM, AA, GR, AG, MM and FA. All authors were involved in unpublished data acquisition, curation and coordination, edit and approved the final version of the submitted manuscript.

285 Competing interests

The authors declare that they have no conflict of interest.

Acknowledgments

We would like to particularly thank the many unnamed scientists, taxonomists and natural history experts who collected all the trait data. We would like to also thank all various contributors and compilers for openly sharing their trait datasets that
 290 made possible the large taxonomic extent of this study: Rafael Achury, Paul L. Angermeier, Nico Blüthgen, Katrin Böhning-Gaese, Dries Bonte, Sébastien Brosse, Philipp Brun, Louise Boulangeat, Pedro Cardoso, Gabriel C. Costa, Daniel T. C. Cox, Jürgen Dengler, Lukas Drag, Weiguo Du, Emmanuel A. Frimpong, Florian Jansen, Michel Genoud, François Gillet, Martin M. Gossner, Maya Guéguen, Jonas Hagge, Nico Heer, Walter Jetz, Sébastien Lavergne, Garben Logghe, Zdeňka Lososová, Stefano Mammola, Robert D. Martin, Shai Meiri, Mario R. Moura, Brunno F. Oliveira, Oleksandra Oskyrko, Julien Renaud,
 295 Ira Richling, Leslie Ries, Carlos Rondinini, Jörg Rüetschi, Matthias Schleuning, Stefan Seifert, Tim Shreeve, Nadja Simons, Carmen D. Soria, Michael Staab, Erik I. Svensson, Wilfried Thuiller, Joseph A. Tobias, Dragmar Triebel, Sébastien Villéger, Wolfgang W. Weisser, Weivei Zhou, Niklaus E. Zimmermann and Kristel van Zuijlen. Without their vast and often unnamed efforts, such data would never come together. This study is part of the SPEED2ZERO Joint Initiative, which received support from the ETH-Board under the Joint Initiatives scheme. The Swiss Species Information Center InfoSpecies
 300 (www.infospecies.ch) supplied Swiss-level species occurrence data and expertise on species' ecology, and we acknowledge their support regarding the database. Further funding is from the Swiss National Science Foundation to YCM (Postdoc.Mobility grant P500PB_225432), FA (grant 310030_197410) and JCA (Postdoc.Mobility grant P500PN_217754).



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