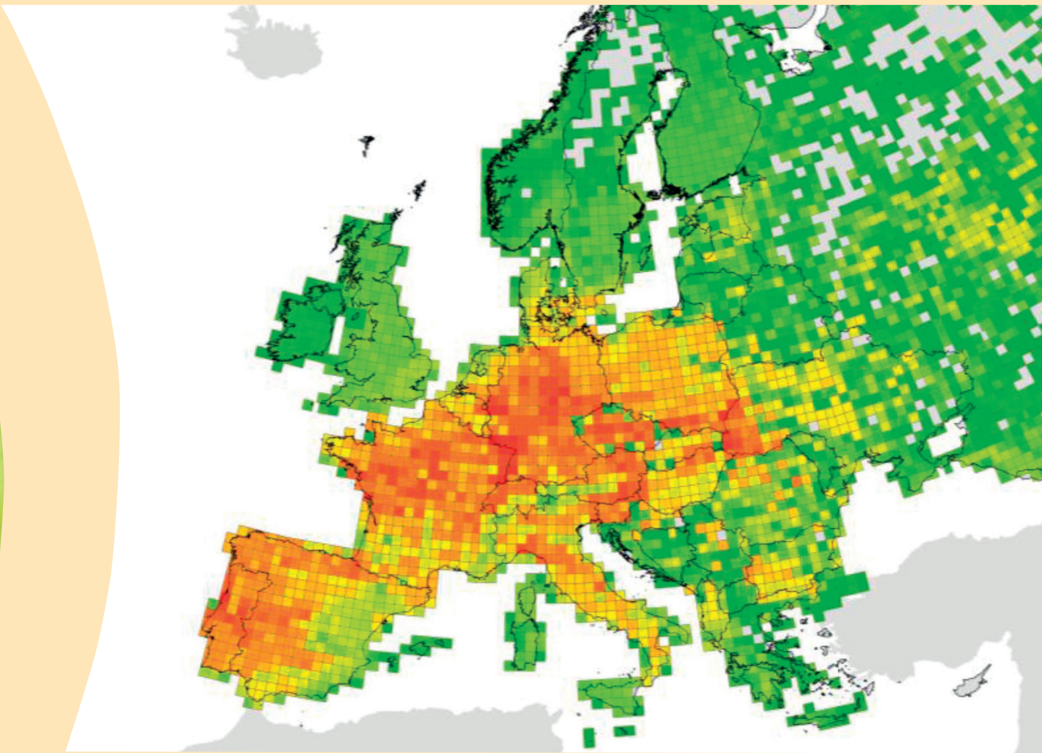
Hotspot analysis of European herpetofauna in the N2000-Emerald network

Wouter Beukema & Ronald Zollinger



RAVON

Hotspot analysis of European herpetofauna in the N2000-Emerald network

Wouter Beukema & Ronald Zollinger

RAVON

Colofon

Status:	Final
Report number:	RAVON 2024.216-1
Date of issue:	10/2024
Title:	Hotspot analysis of European herpetofauna in the N2000-Emerald network
This publication should be cited as follows:	Beukema, W. & Zollinger, R. (2024): Hotspot analysis of European herpetofauna in the N2000-Emerald network. RAVON, Nijmegen.
Compiler's:	Wouter Beukema & Ronald Zollinger
Cover:	Great crested newt (Photo: Jelger Herder), map with number of amphibian species per 50x50km grid recorded in the most recent Europese Atlas (Sillero et al. 2014).
Number of pages incl. attachments:	31
Projectnumber:	2024.216
Projectleader:	Ronald Zollinger
Name and address client:	N.G. Warmelink, Bezuidenhoutseweg 73, 2594 AC Den Haag (n.g.warmelink@minlnv.nl)
Reference client:	EZK_IV_W&I_DV_I / 59383304
Approval for publication:	Jan Kranenbarg
Initials:	

Contents

1 Introduction

1.1 Background

In 2023, Reptile Amphibian Conservation Europe (RACE)/RAVON identified 'hotspots' for herpetofauna during a project for the Bern Convention, using the Natura 2000-Emerald Site network of protected areas as a basis. The focus of this data analysis was not limited to the Netherlands, but considered the entire Natura 2000-Emerald network. During the analysis, several shortcomings and gaps in the Natura 2000-Emerald herpetofauna database were revealed due to which only tentative results were obtained. However, the knowledge gained, the experience accumulated, and the analytical methods developed provided a solid foundation for subsequent analyses by RAVON.

Identifying herpetofauna hotspots both domestically and internationally is crucial to effectively support conservation objectives. Hence, there is an urgent need to compile 'Important Herpetofauna Areas' (IHAs). For birds and butterflies, such 'important areas' were identified many years ago. These areas are crucial on a global and/or European scale for the protection of the respective taxonomic groups. Until recently, distribution data for herpetofauna were insufficient to identify IHAs. However, thanks to recent additions to the Natura 2000-Emerald database and the knowledge and expertise gained by RAVON, it is now possible to initiate this process.

1.2 Renewed analyses

The Dutch Ministry of Agriculture, Fisheries, Food Security and Nature (LVVN) acknowledges the importance of identifying Important Herp Areas. At the request of the Ministry, follow-up analyses were conducted by RAVON in 2024, utilizing recent updates in the data from the Natura 2000-Emerald database. The objective was to provide insights into herpetofauna hotspots and Natura 2000 areas for HR II (and IV) species through mapping, based on the recently revised EEA data. This report presents the mapping materials, along with the methodological steps required to generate the maps.

1.3 Reader’s guide

Chapter 2 describes the steps needed to clean the 'raw data' (metadata) from the Natura 2000-Emerald database so that analyses could be performed and maps could be created. Chapter 3 presents the maps. Chapter 4 provides an overview of possible next steps for identifying definitive IHAs using an approach that takes into account the differences in amphibian and reptile species diversity between countries.

Box 1: Why is the Identification of IHAs Important?

Identifying ‘important areas’ for biodiversity, and specifically for certain species groups such as birds, butterflies, or amphibians and reptiles, has proven to be an effective approach for targeting conservation actions and optimizing protection of areas. This approach also helps to raise awareness about biodiversity. The identification of important areas is generally carried out using specific criteria, such as rarity or endemism of species.

Amphibians and reptiles are a key component of European biodiversity. These species play central roles in ecosystems; they consume numerous invertebrates, including potential pest species, and in turn, are preyed upon by many larger species such as birds and small mammals. Currently, 301 species of amphibians and reptiles are recognized in Europe (Speybroeck *et al.*, 2020). The most recent European Red List showed that 19.4% of reptile species and 22.9% of amphibian species are threatened at the European level (Temple & Cox, 2009b, 2009a). At the national level, these percentages are generally much higher, as many amphibians and reptiles are threatened by habitat loss, climate change, pollution, or invasive diseases.

Furthermore, under the European Nature Restoration Law (NRL), IHAs could play a crucial role in linking conservation goals for herpetofauna species to Natura 2000/Emerald sites and may facilitate the expansion of protected areas or adjustments to existing ones. This information could also be useful when each country submits its pledge to the NRL in autumn 2026.

‘Important areas’ for European reptiles and amphibians have not yet been identified. Although various efforts have been made to identify IHAs (e.g., Stumpel & Edgar, 2004; Zollinger *et al.*, 2019), the available distribution data for amphibians and reptiles in many European countries have been insufficient. However, the recent rapid increase in distribution data from both national databases and citizen science projects offers increasing opportunities to identify an initial set of IHAs. The Netherlands has been a leader in developments related to IHAs due to the experience of organizations like RAVON and RACE in the storage, analysis, and presentation of distribution data.

2 Methods

2.1 Availability of information

Natura 2000 is a network of protected nature areas within the European Union, aimed at the conservation of threatened habitats and species (Figure 1). It consists of areas protected under the Bird- and Habitat Directives. Emerald sites are similar protected areas but fall under the Bern Convention and also include non-EU countries (Figure 2). Both networks are focused on protecting biodiversity across Europe.

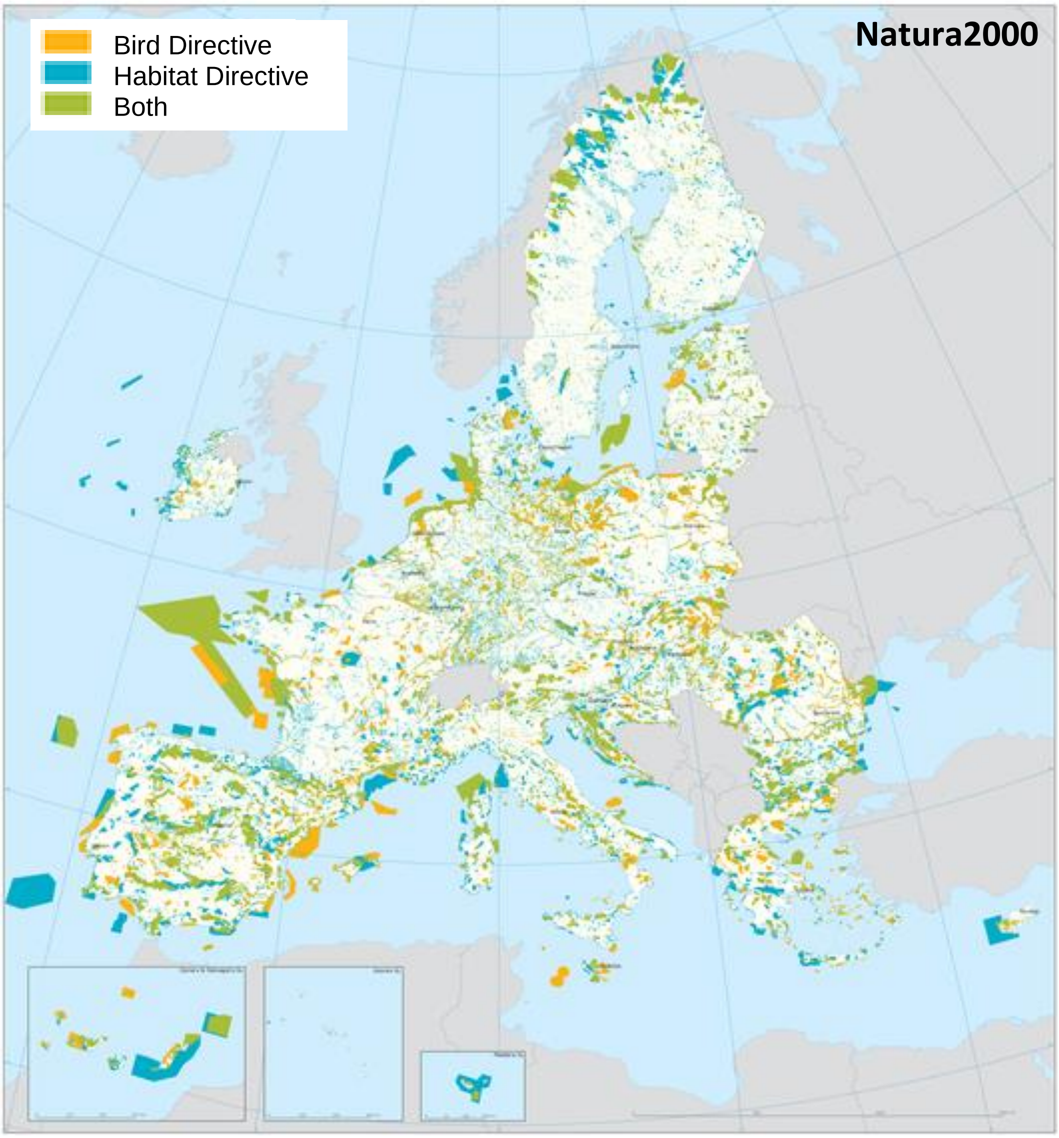


Figure 1: Coverage of Natura 2000 areas within the European Union. Source: European Environment Agency (https://www.eea.europa.eu/data-and-maps/figures/natura-2000-network-terrestrail-and)

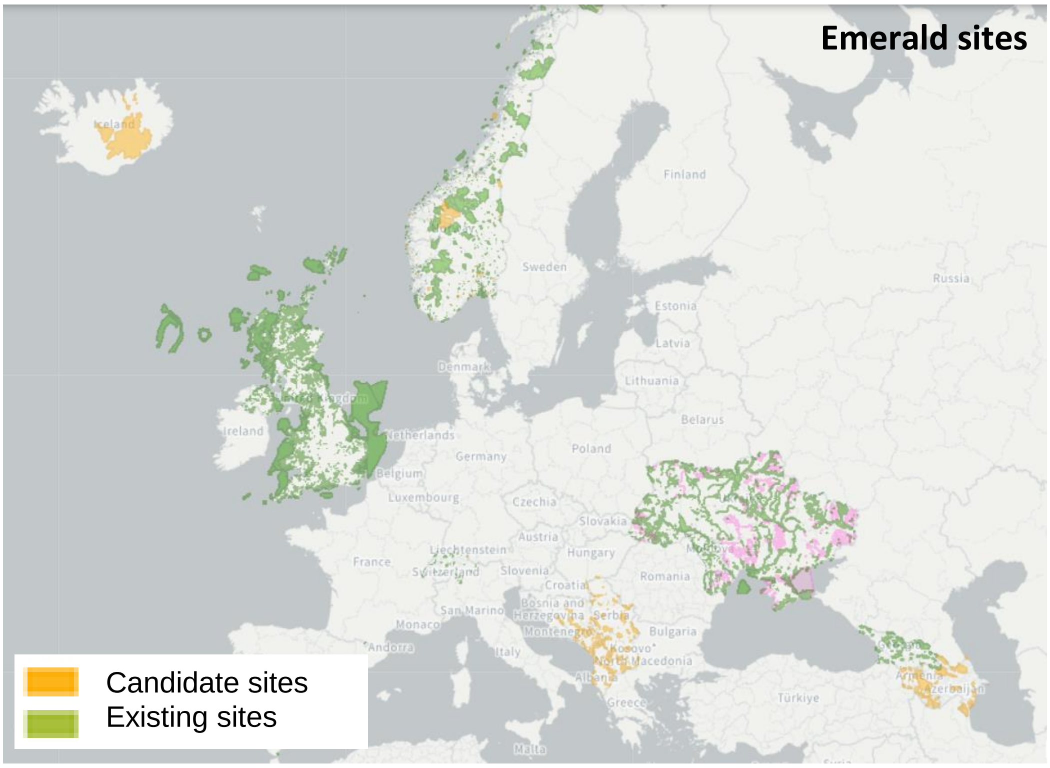


Figure 2: Coverage of Emerald Sites. Source: Council of Europe (http://emerald.eea.europa.eu/).

The spatial data (GIS shape files) for Natura 2000 and Emerald Sites were made available to RAVON by courtesy of Bruno Combal and Frank Vassen of the European Commission, and Marc Roekaerts of the European Environment Agency. The most recent versions of these datasets were provided: the ‘end of 2022 (2023)’ version of Natura 2000 data and the ‘2023’ version of the Emerald site data.

The protected areas, displayed as colored polygons on the map (Figures 1 & 2), contain metadata. These metadata include, for example, the species and habitats for which the protected area was created. However, the metadata is not an exhaustive list of all species present in the area; not all occurring amphibian and reptile species need to be listed when designating a protected area. As initial steps, we therefore:

- Explored which species are present in the available metadata, and
- Investigated the extent to which the distribution of these species within the Natura 2000 - Emerald site network aligns with the actual species distributions as described by Sillero *et al.* (2014).

An initial exploration of the amphibian and reptile species in the metadata indicated that multiple species were represented by different scientific names (Box 2). Specifically, although 185 species and subspecies of amphibians and reptiles are listed in Natura 2000 areas (no reference list has yet been compiled for Emerald sites), there are 477 species and subspecies names present in the Natura 2000 - Emerald metadata. The most recent list of European amphibians and reptiles comprises 301 species (Speybroeck *et al.*, 2020). The surplus of names in the metadata includes outdated scientific names, typographical errors, and incorrectly added species names (Box 2). Therefore, RAVON created a translation key using the R programming language to clean up the majority of the metadata (Appendix 1).

This key is based on the taxonomy of Speybroeck et al. (2020), updates nomenclature in line with current classification and distribution, and corrects typographical errors.

Box 2: Metadata – What is Included, and Why Must It Be Cleaned?

Natura 2000 or Emerald sites are created to ensure the presence of specific protected species or habitats. This means that not all existing biodiversity is documented when a new site is designated. For groups such as reptiles and amphibians, the full list of species present within a Natura 2000 or Emerald site is therefore not always known.

For the species that are registered, scientific nomenclature in the metadata is not updated after initial registration. However, scientific names change over time due to advancing knowledge and research; for example, the smooth newt *Lissotriton vulgaris* was previously known as *Triturus vulgaris*, and the pool frog *Pelophylax lessonae* was formerly classified as *Rana lessonae*. These updates occur less frequently in Europe nowadays, as the taxonomy of amphibians and reptiles is becoming more stable, largely due to extensive research over the past 20 years.

The fact that Natura 2000 or Emerald site metadata is not updated means that multiple names may exist for the same species in the Natura 2000 or Emerald site database. Species recorded in protected areas designated in the past were registered under outdated names, while those recorded in newly designated areas are registered under current names. In some cases, where a species was recently split into multiple species, species names may also encompass multiple distinct species. This is the case, for example, with the European tree frog *Hyla arborea*, which was divided into four different species over the past decade.

In addition, species that were incorrectly added (e.g., species not present in the respective region or country) and typographical errors in species names have not been corrected. In some cases, up to eight different names for a single species appear in various metadata versions. Before analyses can proceed, metadata cleaning is therefore essential. This process requires both taxonomic and technical expertise.

After cleaning the metadata, 229 species and subspecies names remained in the database. Not all data conflicts could be resolved; for some erroneous genus-species combinations, it was unclear which species was actually meant.

The presence of the remaining 229 amphibian and reptile species and subspecies was then tallied for each species group (i.e., amphibians and reptiles separately) within each Natura 2000 or Emerald site. The result provides a comprehensive overview of the total number of amphibian or reptile species recorded in each area (Figure 3).

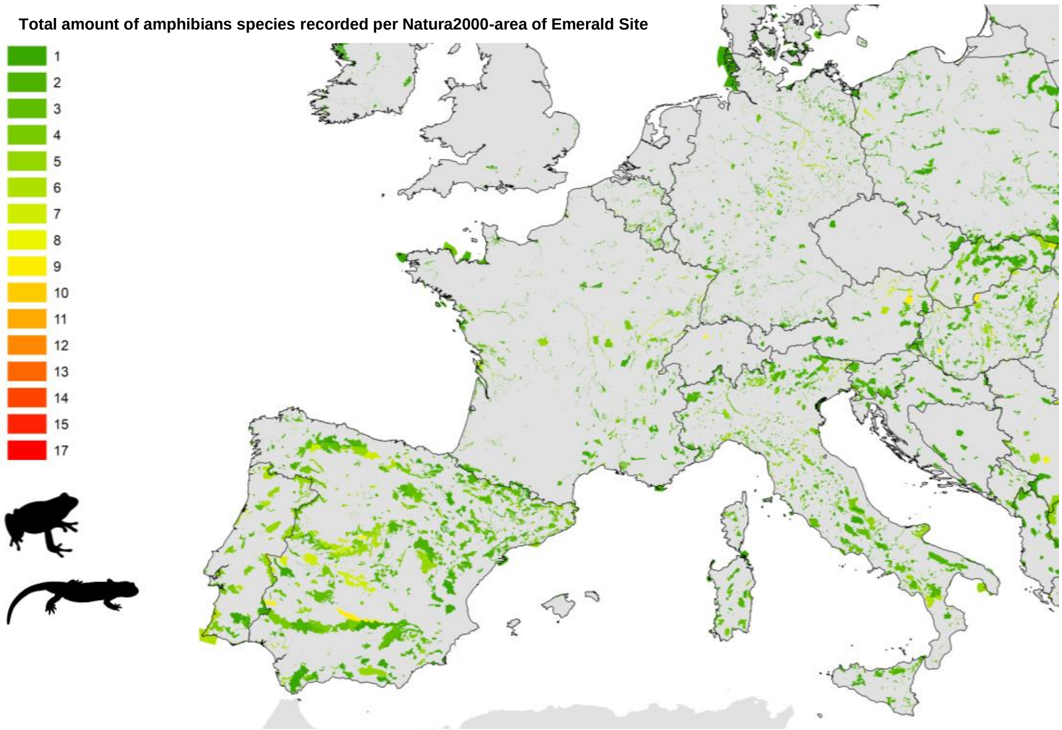


Figure 3: Example overview of the total amount of amphibian species recorded in Natura2000- and Emerald Sites acros Western- and Central Europa, according to the metadata of these sites.

To assess the extent to which the distribution of amphibians and reptiles within the Natura 2000 – Emerald site network aligns with the actual (known) species distributions, the cleaned metadata was compared with t he most recent European atlas by Sillero et al. (2014). The distribution data in this atlas is presented on a 50x50 km grid. To make the data from both sources comparable, the cleaned metadata was converted to the same 50x50 km grid. This final step resulted in mapping that provides insights into herpetofauna hotspots and Natura 2000 areas for HR II (and IV) species, based on the recently revised EEA data.

3 Results

The maps below are presented on a 50x50 kilometer grid to enable comparisons with the full (known) distribution of species (i.e., including areas outside the Natura 2000 – Emerald network). This grid is the same as that used in the most recent European atlas of amphibians and reptiles (Sillero et al., 2014).

3.1 Amphibians

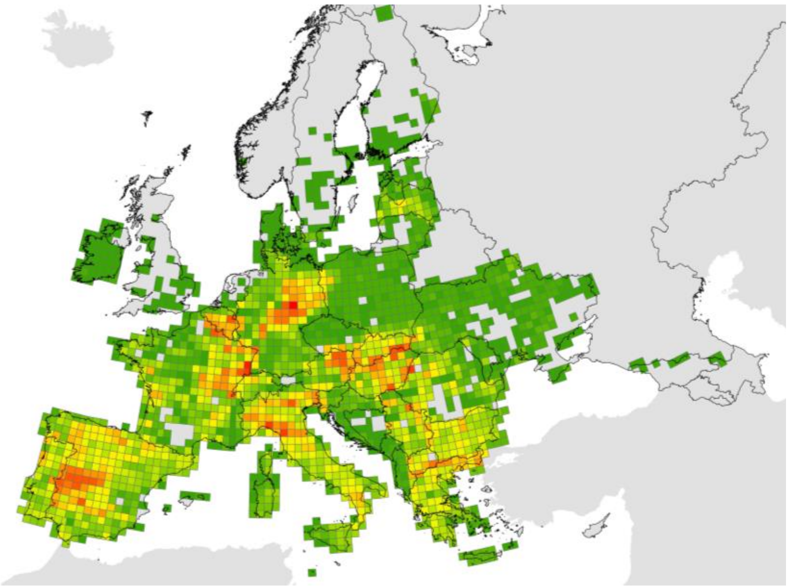


Figure 4: Number of amphibian species per 50x50km grid recorded in Natura 2000 and Emerald site metadata. Warmer colors indicate higher numbers of amphibian species. The maximum number in a single gridcel is 18 species.

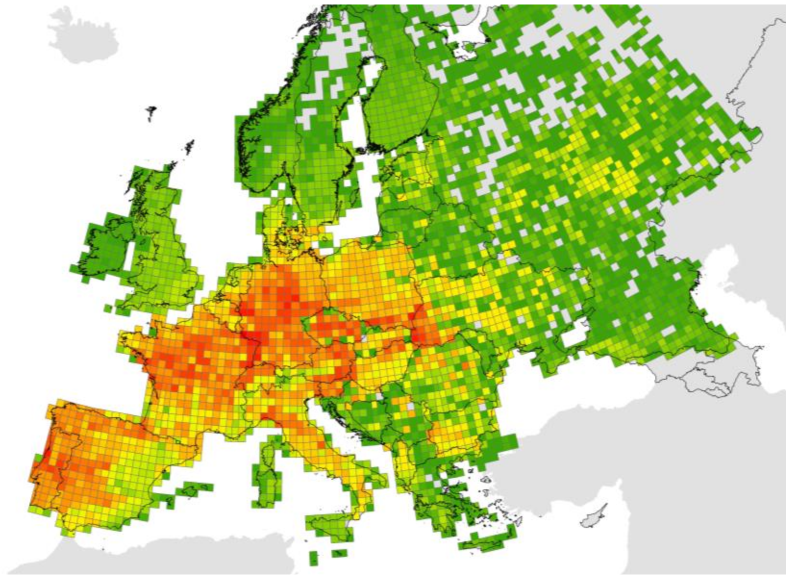


Figure 5: Number of amphibian species per 50x50km grid recorded in the most recent Europese Atlas (Sillero et al. 2014). Warmer colors indicate higher numbers of amphibian species. The maximum number in a single gridcel is 18 species.

When the occurrence of European amphibians in the Natura 2000 and Emerald metadata (Figure 4) is compared with the European atlas data (Figure 5), it becomes clear that occurrences are underrepresented in almost all of Western Europe within the Natura 2000 and Emerald metadata. This also applies to parts of Eastern and Northeastern Europe. In Southeastern Europe, the presence of amphibians is better documented in some countries and regions, such as Greece, Bulgaria, Albania, and Slovenia, than in the European atlas data.

3.2 Reptiles

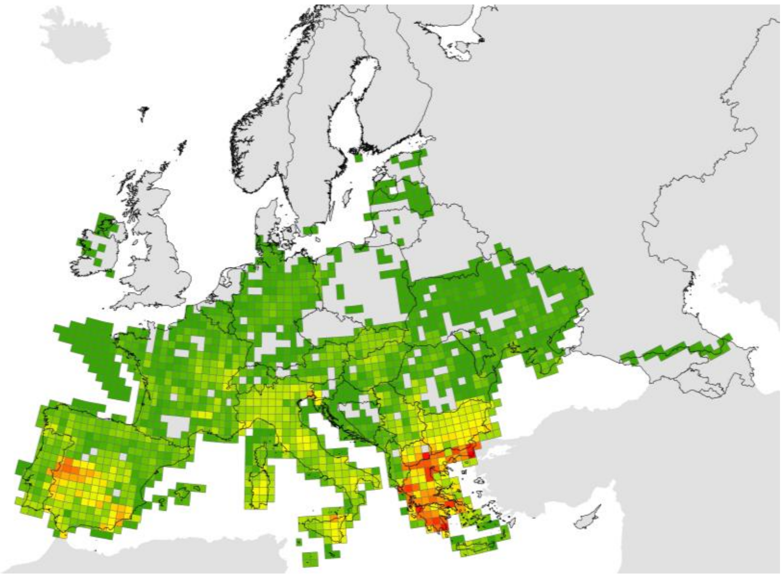


Figure 6: Number of reptile species per 50x50km grid recorded in Natura 2000 and Emerald site metadata. Warmer colors indicate higher numbers of reptile species. The maximum number in a single gridcel is 33 species.

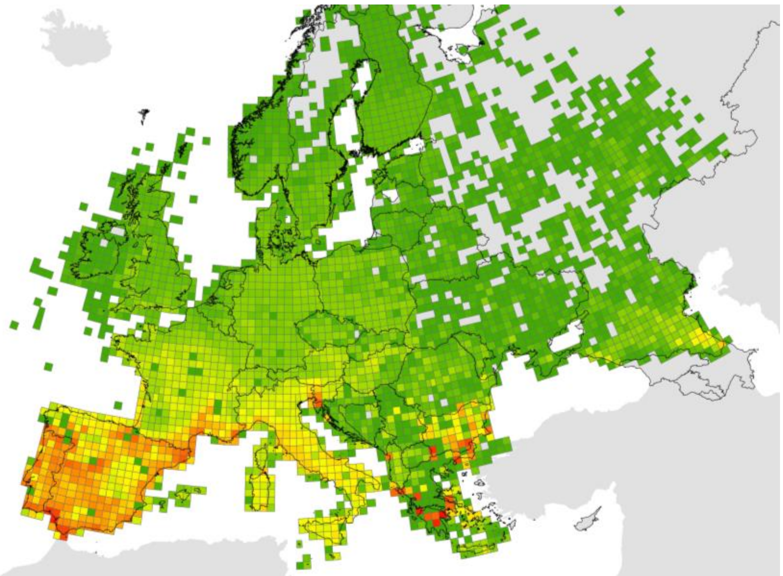


Figure 7: Number of reptile species per 50x50km grid recorded in the most recent Europese Atlas (Sillero et al. 2014). Warmer colors indicate higher numbers of reptile species. The maximum number in a single gridcel is 33 species.

When the occurrence of European reptiles in the Natura 2000 and Emerald metadata (Figure 6) is compared with the European atlas data (Figure 7), it becomes clear that occurrences are underrepresented in large parts of Western, Central, Northern, and Eastern Europe within the Natura 2000 and Emerald metadata (especially in Portugal, Spain, southern France, and Italy). The presence of reptiles in Southeastern Europe is better documented in some countries and regions, such as Bulgaria, North Macedonia, and Greece, than in the European atlas data.

4 Conclusions and next steps

Our analyses indicate that, for various reasons, the presence of European amphibians and reptiles in Natura 2000 and Emerald sites is underrepresented or underestimated. Identifying Important Herp Areas (IHAs) for all of Europe based on the current versions of these datasets would yield an incomplete picture. However, we emphasize that the Natura 2000 and Emerald networks remain by far the most suitable foundation for the future identification of IHAs.

Therefore, further steps are needed to supplement the existing data and move toward an initial selection of IHAs. This is not necessarily a top-down process occurring on a European scale. Ideally, the identification of IHAs is even a bottom-up exercise conducted at the national level. This way, all relevant information available at the national level can be taken into account, and the various sets of IHAs can then be assembled into a comprehensive European network. Endemism of reptiles and amphibians is highest in Southern Europe, where reptile diversity is also the greatest, but this does not mean that IHAs should necessarily be located only in Southern Europe. Such a result might arise from a top-down approach, where data are considered solely from a European perspective. Identifying IHAs per country and combining these sets into a ‘weighted average’ based on appropriate criteria would thus also help ensure the importance of protected areas in, for example, Northwestern Europe.

Nevertheless, action is also needed at the European level to make Natura 2000 and Emerald data suitable for further analysis. We propose the following step at the European level:

- Thoroughly cleaning existing Natura 2000 and Emerald metadata to make this data usable for analyses. Not all data conflicts could be resolved during the analyses for this report. It is noteworthy that Natura 2000 and Emerald metadata has never been revised. To make this data useful for a variety of applications, including biodiversity conservation, it is essential that the data be stored and managed in a consistent and high-quality manner. RAVON can offer technical and taxonomic support in this regard.

At the national level, we propose the following steps:

- Applying the Key Biodiversity Area (KBA) approach to begin identifying an initial set of IHAs on a national scale. The globally recognized KBA approach was created to identify critical areas for biodiversity based on standardized criteria. This approach focuses on areas that are crucial for the conservation of threatened or endemic species or are part of unique ecosystems. Sites are evaluated not only for individual species but also for the presence of hotspots/clusters of multiple species. A variant of the KBA approach has been developed in the United Kingdom, allowing IHAs to be defined on a national scale, taking into account species’ Red List status, occurrence, and other criteria. UK stakeholders are willing to assist other countries in applying this approach.

- Utilizing other data sources, such as species observations collected by citizen scientists, to supplement existing Natura 2000 and Emerald data. Appendix 2 outlines an example to demonstrate the usefulness of this type of opportunistic observations. The use of additional data sources aligns with the KBA approach.

5 References

Sillero, N., *et al*. (2014). Updated distribution and biogeography of amphibians and reptiles of Europe. *Amphibia-Reptilia*, *35*, 1-31.

Speybroeck, J., *et al*. (2020). Species list of the European herpetofauna–2020 update by the Taxonomic Committee of the Societas Europaea Herpetologica. *Amphibia-Reptilia*, *41*(2), 139-189.

Stumpel, A., Edgar, P. (2004). *Important Herpetofaunal Areas in Europe*. Alterra/Herpetological Conservation Trust, Wageningen/Bournemouth.

Temple, H.J., Cox, N. (2009a). *European red list of amphibians*. Office for Official Publications of the European Communities, Luxemburg.

Temple, H.J., Cox, N. (2009b). *European red list of reptiles*. Office for Official Publications of the European Communities, Luxemburg.

Zollinger, R., Stumpel, A., Gent, T., Foster, J., Cogalniceanu, D., van der Hak, D. (2019). *Towards Important Herpetofaunal Areas (IHA's) in Europe*

Appendix 1: Translation key for herpetofauna nomenclature in Natura 2000- en Emerald site metadata

The following R code was used to standardize species and subspecies names of amphibians and reptiles in the Natura 2000 metadata (version "end 2022 (2023)") and Emerald site metadata (version "2023").

```
emerald_species <- read.delim("C:/User/Spreadsheet data/Emerald_2023_SPECIES.txt", h = T, sep = "\t",
row.names = NULL)

emerald_other <- read.delim("C:/User/Spreadsheet data/Emerald_2023_OTHERSPECIES.txt", h = T, sep =
"\t", row.names = NULL)

natura_species <- read.delim("C:/User/Spreadsheet data/Natura2000_end2022_SPECIES.txt", h = T, sep =
"\t", row.names = NULL)

natura_other <- read.delim("C:/User/Spreadsheet data/Natura2000_end2022_OTHERSPECIES.txt", h = T,
sep = "\t", row.names = NULL)

############################Cleaning emerald_species###########################

# Subset herps;
emerald_species_herps <- subset(emerald_species, SPGROUP == c('Amphibians','Reptiles'))

# Change names;
emerald_species_herps$SPECIESNAME <- gsub('Bufo viridis','Bufotes viridis',
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- gsub('Bombina variegata ','Bombina variegata',
emerald_species_herps$SPECIESNAME) # get rid of space
emerald_species_herps$SPECIESNAME <- gsub('Lacerta clarkorum','Darevskia clarkorum',
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- gsub('Elaphe situla','Zamenis situlus',
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- gsub('Elaphe longissima','Zamenis longissimus',
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- gsub('Emys orbicularis ','Darevskia clarkorum',
emerald_species_herps$SPECIESNAME) # get rid of space
emerald_species_herps$SPECIESNAME <- gsub('Rana latastei ','Rana latastei',
emerald_species_herps$SPECIESNAME) # get rid of space
emerald_species_herps$SPECIESNAME <- gsub('Triturus macedonicus ','Triturus macedonicus',
emerald_species_herps$SPECIESNAME) # get rid of space
emerald_species_herps$SPECIESNAME <- gsub('Triturus carnifex','Triturus macedonicus',
emerald_species_herps$SPECIESNAME) # all records in macedonicus range
emerald_species_herps$SPECIESNAME <- gsub('Triturus montandoni','Lissotriton montandoni',
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- gsub('Coluber najadum','Platyceps najadum',
emerald_species_herps$SPECIESNAME)
```

```
emerald_species_herps$SPECIESNAME <- gsub('Podarcis taurica','Podarcis tauricus',
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- gsub('Triturus cristatus karelinii','Triturus karelinii',
emerald_species_herps$SPECIESNAME) # record is from Georgia
emerald_species_herps$SPECIESNAME <- gsub('Triturus cristatus ','Triturus cristatus',
emerald_species_herps$SPECIESNAME) # get rid of space
emerald_species_herps$SPECIESNAME <- gsub('Triturus macedonicus ','Triturus macedonicus',
emerald_species_herps$SPECIESNAME) # get rid of space

# Remove S. s. aurorae from Montenegro...;
emerald_species_herps <- emerald_species_herps[!emerald_species_herps$SPECIESNAME == "Salamandra
salamandra aurorae", ]

# Rename part of Mauremys caspica into Mauremys rivulata. The following code renames the original name to
rivulata only if the country codes AL, ME is found;
emerald_species_herps$SPECIESNAME <- ifelse(grepl("AL|ME",
emerald_species_herps$COUNTRY_CODE), gsub("Mauremys caspica", "Mauremys rivulata",
emerald_species_herps$SPECIESNAME), emerald_species_herps$SPECIESNAME)

# Rename part of Elaphe quatuorlineata into Elaphe urartica or Elaphe sauromates. The following code
renames the original name to urartica only if the country codes AZ is found;
emerald_species_herps$SPECIESNAME <- ifelse(grepl("AZ", emerald_species_herps$COUNTRY_CODE),
gsub("Elaphe quatuorlineata", "Elaphe urartica", emerald_species_herps$SPECIESNAME),
emerald_species_herps$SPECIESNAME)
# For sauromates;
emerald_species_herps$SPECIESNAME <- ifelse(grepl("MD|UA|RU",
emerald_species_herps$COUNTRY_CODE), gsub("Elaphe quatuorlineata", "Elaphe sauromates",
emerald_species_herps$SPECIESNAME), emerald_species_herps$SPECIESNAME)

# Rename part of Vipera ursinii into different species. The following code renames the original name to different
species;
emerald_species_herps$SPECIESNAME <- ifelse(grepl("AZ", emerald_species_herps$COUNTRY_CODE),
gsub("Vipera ursinii", "Vipera eriwanensis", emerald_species_herps$SPECIESNAME),
emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- ifelse(grepl("RU|UA",
emerald_species_herps$COUNTRY_CODE), gsub("Vipera ursinii", "Vipera renardi",
emerald_species_herps$SPECIESNAME), emerald_species_herps$SPECIESNAME)

# Rename part of Triturus karelinii into Triturus ivanbureschi. The following code renames the original name to
ivanbureschi only if the country codes MK, RS is found;
emerald_species_herps$SPECIESNAME <- ifelse(grepl("MK|RS",
emerald_species_herps$COUNTRY_CODE), gsub("Triturus karelinii", "Triturus ivanbureschi",
emerald_species_herps$SPECIESNAME), emerald_species_herps$SPECIESNAME)

# Rename part of Triturus cristatus into different species. The following code renames the original name to
different species based on SITECODE or COUNTRY_CODE. Splits e.g. based on
https://www.researchgate.net/publication/350670662_The_distribution_of_crested_newts_in_Serbia_An_o
verview_and_update.
```

```
emerald_species_herps$SPECIESNAME <- ifelse(grepl("RS0000016|RS0000021|RS0000029",
emerald_species_herps$SITECODE), gsub("Triturus cristatus", "Triturus dobrogicus",
emerald_species_herps$SPECIESNAME), emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- ifelse(grepl("RS0000006|RS0000030|RS0000036",
emerald_species_herps$SITECODE), gsub("Triturus cristatus", "Triturus macedonicus",
emerald_species_herps$SPECIESNAME), emerald_species_herps$SPECIESNAME)
emerald_species_herps$SPECIESNAME <- ifelse(grepl("AL", emerald_species_herps$COUNTRY_CODE),
gsub("Triturus cristatus", "Triturus macedonicus", emerald_species_herps$SPECIESNAME),
emerald_species_herps$SPECIESNAME)

emerald_species_herps <- emerald_species_herps[emerald_species_herps$SPECIESNAME != "--NULL--", ] #
Get rid of the row which has a species called 'NULL'

unique(emerald_species_herps$SPECIESNAME) # check

# Create a vector with database ID, with the number of rows of the database;
DATASET = c(rep("Emerald_2023_SPECIES", nrow(emerald_species_herps)))
# Add to data frame;
emerald_species_herps$DATASET = DATASET

#############################Cleaning emerald_other############################

# Subset herps;
emerald_other_herps <- subset(emerald_other, SPECIESGROUP == c('Amphibians','Reptiles'))

# Change names;
emerald_other_herps$SPECIESNAME <- gsub('Malpolon monpessulanus','Malpolon insignitus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Mediodactylus kotschyi danilewskii|Mediodactylus
kotschyi','Mediodactylus danilewskii',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Podarcis taurica','Podarcis tauricus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Elaphe longissima','Zamenis longissimus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Vipera lebetina','Macrovipera lebetinus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Triturus alpestris','Ichthyosaura alpestris',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Ophisaurus apodus','Pseudopus apodus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Vipera (Pelias) eriwanensis','Vipera eriwanensis',
                    emerald_other_herps$SPECIESNAME, fixed = TRUE) # "Fixed = TRUE" disables regex
emerald_other_herps$SPECIESNAME <- gsub('Pelabates syriacus ihada','Pelobates syriacus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- ifelse(grepl("MK", emerald_other_herps$COUNTRY_CODE),
gsub("Pelobates syriacus", "Pelobates balcanicus", emerald_other_herps$SPECIESNAME),
emerald_other_herps$SPECIESNAME)
emerald_species_herps <- emerald_species_herps[emerald_species_herps$SPECIESNAME != "Pelias
zenordi", ] # Get rid of the row with Pelias zenordi
```

```
emerald_other_herps$SPECIESNAME <- gsub('Rana ridibunda','Pelophylax ridibundus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Typhlops vermicularis','Xerotyphlops vermicularis',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Natrix tesselata','Natrix tessellata',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Tritutus vulgaris','Lissotriton vulgaris',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Lacerta vivipara','Zootoca vivipara',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Zemenis hohenackeri','Zamenis hohenackeri',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- ifelse(grepl("MD|RS|UA",
emerald_other_herps$COUNTRY_CODE), gsub("Hyla arborea", "Hyla orientalis",
emerald_other_herps$SPECIESNAME), emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Triturus vulgaris','Lissotriton vulgaris',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Rana esculenta','Pelophylax kl. esculentus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Rana lessonae','Pelophylax lessonae',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Bufo calamita','Epidalea calamita',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Triturus helveticus','Lissotriton helveticus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Coluber viridiflavus','Hierophis viridiflavus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Bufo viridis','Bufotes viridis',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Coluber gemonensis','Hierophis gemonensis',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- ifelse(grepl("RS", emerald_other_herps$COUNTRY_CODE),
gsub("Lacerta trilineata", "Lacerta dobrogica", emerald_other_herps$SPECIESNAME),
emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- ifelse(grepl("RS", emerald_other_herps$COUNTRY_CODE),
gsub("Pelobates fuscus", "Pelobates vespertinus", emerald_other_herps$SPECIESNAME),
emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Coluber najadum','Platyceps najadum',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Telescopus falax','Telescopus fallax',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Coluber caspius','Dolichophis caspius',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Elaphe situla','Zamenis situlus',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Salamandara salamandara','Salamandra salamandra',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Angius fragilis','Anguis fragilis',
                    emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Ranagraeca','Rana graeca',
```

```
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Malpolon monospessulanus','Malpolon monspessulanus',
emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Rana balcanica','Pelophylax ridibundus',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Bufio bufo','Bufo bufo',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Natrix tessallata','Natrix tessellata',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Lacerta praticola','Darevskia praticola',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Mesotriton alpestris','Ichthyosaura alpestris',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Pelobates fuscus vespertinus','Pelobates vespertinus',
emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Coronella avstriaca','Coronella austriaca',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Lacerta  agilis','Lacerta agilis',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Hierophis caspius','Dolichophis caspius',
                              emerald_other_herps$SPECIESNAME)
emerald_other_herps$SPECIESNAME <- gsub('Pelophylax ridibundus (Pallas, 1771)','Pelophylax ridibundus',
emerald_other_herps$SPECIESNAME, fixed = TRUE) # "Fixed = TRUE" disables regex
emerald_other_herps$SPECIESNAME <- gsub('Tenuidactilus kotschyi','Mediodactylus kotschyi',
                              emerald_other_herps$SPECIESNAME)

# Remove empty record from Ukraine;
emerald_other_herps <- emerald_other_herps[!emerald_other_herps$SPECIESNAME == "--NULL--", ]
unique(emerald_other_herps$SPECIESNAME) # check

# Create a vector with database ID, with the number of rows of the database;
DATASET = c(rep("Emerald_2023_OTHERSPECIES", nrow(emerald_other_herps)))
# Add to data frame;
emerald_other_herps$DATASET = DATASET

#############################Cleaning natura_species###########################

# Subset herps;
natura_species_herps <- subset(natura_species, SPGROUP == c('Amphibians','Reptiles'))

# Change names;
natura_species_herps$SPECIESNAME <- gsub('Triturus montandoni','Lissotriton montandoni',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Mauremys caspica','Mauremys rivulata',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Coluber cypriensis','Hierophis cypriensis',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Elaphe situla','Zamenis situlus',
natura_species_herps$SPECIESNAME)
```

```
natura_species_herps$SPECIESNAME <- gsub('Triturus karelinii','Triturus ivanbureschi',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Bombina pachypus','Bombina variegata pachypus',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Emys trinacris','Emys orbicularis trinacris',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Triturus vulgaris ampelensis','Lissotriton vulgaris ampelensis',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Natrix natrix helvetica','Natrix helvetica',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Discoglossus jeanne','Discoglossus galganoi jeanneae',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Lacerta monticola','Iberolacerta monticola',
natura_species_herps$SPECIESNAME)
natura_species_herps <- natura_species_herps[natura_species_herps$SPECIESNAME != "Buxbaumia
viridis", ]
natura_species_herps$SPECIESNAME <- gsub('Bufo calamita','Epidalea calamita',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Elaphe longissima','Zamenis longissimus',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Podarcis taurica','Podarcis tauricus',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Macrovipera schweizeri','Macrovipera lebetinus schweizeri',
natura_species_herps$SPECIESNAME)
natura_species_herps$SPECIESNAME <- gsub('Bufo viridis','Bufotes viridis',
natura_species_herps$SPECIESNAME)

unique(natura_species_herps$SPECIESNAME) # check

# Create a vector with database ID, with the number of rows of the database;
DATASET = c(rep("Natura2000_SPECIES", nrow(natura_species_herps)))
# Add to data frame;
natura_species_herps$DATASET = DATASET

##########################Cleaning natura_other_herps##########################

# While working on this dataset, I found out that it is rife with typos, outdated taxonomy, there are mammals,
birds, plants present - it is truely very messy. I tried to clean this up as good as I could given the available time;

# Subset herps;
natura_other_herps <- subset(natura_other, SPECIESGROUP == c('Amphibians','Reptiles'))

# Get rid of a French site that includes a Hierviri name with a unicode replacement that affects all other
analyses. Not an ideal method (it also gets rid of other species that inhabit this site), but I don't have another
immediate solution;
natura_other_herps <- natura_other_herps[natura_other_herps$SITECODE != "FR7300909", ]

# Get rid of unnecessary columns;
natura_other_herps <-natura_other_herps[, c("SITECODE", "COUNTRY_CODE", "SPECIESGROUP",
"SPECIESNAME", "SPECIESCODE")]
```

```
# First check (393 taxa, incl. plants, mammals, many typos, what a mess...);
unique(natura_other_herps$SPECIESNAME) # check

# Replace names from 2023 check;
natura_other_herps$SPECIESNAME <- gsub('Rana lessonae','Pelophylax lessonae',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Bufo viridis','Bufotes viridis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Bufo calamita','Epidalea calamita',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana kl. esculenta|Rana esculenta|Rana esculenta
kl.|Pelophylax esculenta|Pelophylax esculentus|Rana kL. esculenta/lessonae|Pelophylax kl. esculentus
comp.|Pelophylax kl. esculentus sp|Pelophylax kl. esculentus kL.|Rana kL. esculenta','Pelophylax kl. esculentus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Triturus vulgaris','Lissotriton vulgaris',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Triturus alpestris','Ichthyosaura alpestris',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta vivipara|Lacerta vivipara vivipara','Zootoca vivipara',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Triturus helveticus','Lissotriton helveticus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Elaphe longissima|Elaphe longissimus','Zamenis longissimus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta muralis','Podarcis muralis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coluber caspius','Dolichophis caspius',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coluber jugularis','Dolichophis jugularis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Cyrtodactylus kotschyi','Mediodactylus orientalis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coluber viridiflavus','Hierophis viridiflavus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Natrix natrix helvetica','Natrix helvetica',
natura_other_herps$SPECIESNAME)
natura_other_herps <- natura_other_herps[natura_other_herps$SPECIESNAME != "Pelophylax spp.", ]
natura_other_herps$SPECIESNAME <- gsub('Hyla arborea Laubfrosch','Hyla arborea',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana arvalis waltersdorfi','Rana arvalis wolterstorffi',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta v. vivipara','Zootoca vivipara',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta viviparia','Zootoca vivipara',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Pelophylax ridibundus s.L.','Pelophylax ridibundus',
natura_other_herps$SPECIESNAME)

# Remove German horvathi and unclear Pelophylax;
```

```
natura_other_herps <- natura_other_herps[!natura_other_herps$SPECIESNAME == "Lacerta horvathi", ]
natura_other_herps <- natura_other_herps[!natura_other_herps$SPECIESNAME == "Pelophylax kl.
esculentus/lessonae", ]

# Rename Rana ridibunda into Pelophylax ridibundus and P. cypriensis. The following code renames the
original name to cypriensis only if the country code CY is found;
natura_other_herps$SPECIESNAME <- ifelse(grepl("CY", natura_other_herps$COUNTRY_CODE),
                                gsub("Rana ridibunda", "Pelophylax cypriensis",
                                    natura_other_herps$SPECIESNAME),
                                natura_other_herps$SPECIESNAME)
# Now convert the rest;
natura_other_herps$SPECIESNAME <- gsub('Rana ridibunda','Pelophylax ridibundus',
natura_other_herps$SPECIESNAME)

# Rename Hyla arborea into different taxa based on country- or sitecode;
natura_other_herps$SPECIESNAME <- ifelse(grepl("ES", natura_other_herps$COUNTRY_CODE),
                                gsub("Hyla arborea", "Hyla molleri",
                                    natura_other_herps$SPECIESNAME),
                                natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- ifelse(grepl("PLH180045", natura_other_herps$SITECODE),
                                gsub("Hyla arborea", "Hyla orientalis",
                                    natura_other_herps$SPECIESNAME),
                                natura_other_herps$SPECIESNAME)

unique(natura_other_herps$SPECIESNAME) # check - 368 taxa, didn't solve a lot...

# A second rough selection can be made by discarding the 700 rows without SPECIESCODE; these include most
of the typos, species from other species groups, etc. Ideally you would sort all of this out of course, but time is
short. Let's therefore first see how far we get by just focusing on the 22.000 rows incl SPECIESCODE;
natura_other_herps <- natura_other_herps[!(is.na(natura_other_herps$SPECIESCODE) |
natura_other_herps$SPECIESCODE==""), ]

unique(natura_other_herps$SPECIESNAME) # check - 240 taxa, already better

# Get rid of species from other species groups;
natura_other_herps <- natura_other_herps[!(natura_other_herps$SPECIESNAME %in% c("Mustela
erminea", "Lepus timidus hibernicus", "Alburnus alburnus alborella", "Crocidura suaveolens", "Esox lucius",
"Scardinius erythrophthalmus", "Tinca tinca", "Perca fluviatilis", "Glis glis", "Sus scrofa")), ]

# Get rid of undetermined species;
natura_other_herps <- natura_other_herps[!(natura_other_herps$SPECIESNAME %in% c("Natrix sp.")), ]

unique(natura_other_herps$SPECIESNAME) # check - 229 taxa

# Still a lot of outdated taxonomy present; no time to split up species by checking the origin of the records, let's
just correct taxonomy for now, and get rid of subspecies;
natura_other_herps$SPECIESNAME <- gsub('Zootoca vivipara pannonica|Zootoca vivipara
carniolica','Zootoca vivipara', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Zamenis longissima','Zamenis longissimus',
natura_other_herps$SPECIESNAME)
```

```
natura_other_herps$SPECIESNAME <- gsub('Rana ridibunda|Rana ridibunda s.L.','Pelophylax ridibundus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana arvalis wolterstorffi','Rana arvalis', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis taurica','Podarcis tauricus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta praticola','Darevskia praticola', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coluber najadum','Platyceps najadum', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Pelobates syriacus balcanicus','Pelobates balcanicus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Ophisaurus apodus','Pseudopus apodus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Mabuya vittata','Heremites vittatus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Ophisops elegans schlueteri','Ophisops elegans', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta horvathi','Iberolacerta horvathi', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis hispanica','Podarcis hispanicus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta lepida','Timon lepidus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana perezi','Pelophylax perezi', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coluber hippocrepis','Hierophis hippocrepis', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Elaphe scalaris','Zamenis scalaris', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Triturus boscai','Lissotriton boscai', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Vipera latasti','Vipera latastei', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Bufo bufo spinosus','Bufo spinosus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Psammodromus hispanicus edwarsianus','Psammodromus edwarsianus', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Macroprotodon cucullatus brevis','Macroprotodon brevis', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Bufotes balearicus','Bufotes viridis', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Tarentola mauritanica mauritanica','Tarentola mauritanica', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Salamandra salamadra','Salamandra salamandra', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Discoglossus jeanneae','Discoglossus galganoi', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis sicula','Podarcis siculus', natura_other_herps$SPECIESNAME)
```

```
natura_other_herps$SPECIESNAME <- gsub('Epidalea calamitas','Epidalea calamita',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana saharica','Pelophylax saharicus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta tangitana','Timon tangitanus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Alytes variegata','Bombina variegata',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coronella austriaca laurenti','Coronella austriaca',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta agilis linnaeus','Lacerta agilis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana dalmatina bonaparte','Rana dalmatina',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Coronella austriaca austriaca','Coronella austriaca',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta agilis agilis','Lacerta agilis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Epidalea calamita laurenti','Epidalea calamita',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Alytes obstretricans|Alytes obsetricans|Alytes o.
obstreticans','Alytes obstetricans', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis muralis rasquinetti|Potarcis muralis','Podarcis
muralis', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Zamenis longissimus longissima','Zamenis longissimus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Triturus marmaratus','Triturus marmoratus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Pelobates cultripede','Pelobates cultripes',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Anguis fragilis fragilis','Anguis fragilis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis hispanica atrata','Podarcis liolepis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta veridis','Lacerta viridis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Lacerta bedriagae paessleri|Lacerta bedriagae','Archaeolacerta
bedriagae', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Natrix natrix corsa|Natrix natrix sicula|Natrix natrix
cetti','Natrix helvetica', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Hyla arborea sarda','Hyla sarda',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Vipera xanthina','Montivipera xanthina',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Zamenis situla','Zamenis situlus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana epeirotica','Pelophylax epeiroticus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis peloponnesiaca','Podarcis peloponnesiacus',
natura_other_herps$SPECIESNAME)
```

```
natura_other_herps$SPECIESNAME <- gsub('Eirenis modesta','Eirenis modestus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Ablepharus kitaibelii fitzingeri','Ablepharus kitaibelii',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Bufotes viridis complex','Bufotes viridis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Ichthyosaura alpestris apuanus','Ichthyosaura alpestris',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Vipera aspis francisciredi|Vipera aspis hugy|Vipera
hugyi','Vipera aspis', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Chalcides chalcides chalcides','Chalcides chalcides',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Chalcides ocellatus tiligugu','Chalcides ocellatus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis raffonei raffonei|Podarcis raffonei antoninoi','Podarcis
raffonei', natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Discoglossus pictus pictus','Discoglossus pictus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Chamaeleo chamaeleon chamaeleon','Chamaeleo chamaeleon',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Vipera ursinii moldavica','Vipera ursinii',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Dermochelis coriacea','Dermochelys coriacea',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Euproctus asper','Calotriton asper',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Hydromantes italicus','Speleomantes italicus',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Podarcis hispanicus atrata','Podarcis liolepis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Rana temporia','Rana temporaria',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Typhlops vermicularis','Xerotyphlops vermicularis',
natura_other_herps$SPECIESNAME)
natura_other_herps$SPECIESNAME <- gsub('Pelophylax ridibundus s.L.','Pelophylax ridibundus',
natura_other_herps$SPECIESNAME)

# Get rid of "Pelias zenordi";
natura_other_herps <- natura_other_herps[natura_other_herps$SPECIESNAME != "Pelias zenordi", ]

# Get rid of the single hybrid Bombina record;
natura_other_herps <- natura_other_herps[natura_other_herps$SPECIESNAME != "Bombina bombina x
variegata", ]

unique(natura_other_herps$SPECIESNAME) # check - 168 taxa

# Create a vector with database ID, with the number of rows of the database;
DATASET = c(rep("Natura2000_OTHERSPECIES", nrow(natura_other_herps)))
# Add to data frame;
natura_other_herps$DATASET = DATASET
```

```
###################################Merge#####################################

# First, clean up data frames as the amounts of columns don't match. I did not retain 'SPECIESCODE' and
'MOTIVATION' as the former now contains erroneous values due to taxonomy of some records being updated,
and the latter is not included in Emerald Sites.
emerald_other_herps2 <- emerald_other_herps[,c("COUNTRY_CODE","SITECODE", "SPECIESGROUP",
"SPECIESNAME", "DATASET")]
emerald_species_herps2 <- emerald_species_herps[,c("COUNTRY_CODE","SITECODE", "SPGROUP",
"SPECIESNAME", "DATASET")]
names(emerald_species_herps2)[names(emerald_species_herps2) == 'SPGROUP'] <- 'SPECIESGROUP'
natura_other_herps2 <- natura_other_herps[,c("COUNTRY_CODE","SITECODE", "SPECIESGROUP",
"SPECIESNAME", "DATASET")]
natura_species_herps2 <- natura_species_herps[,c("COUNTRY_CODE","SITECODE", "SPGROUP",
"SPECIESNAME", "DATASET")]
names(natura_species_herps2)[names(natura_species_herps2) == 'SPGROUP'] <- 'SPECIESGROUP'

# Combine;
combined_datasets <- rbind(emerald_other_herps2, emerald_species_herps2, natura_other_herps2,
natura_species_herps2)

unique(combined_datasets$SPECIESNAME) # 229 taxa
unique(combined_datasets$COUNTRY_CODE)

# Write to disk;
write.table(combined_datasets, file = "C:/User/combined_datasets.txt", sep = "\t", col.names = TRUE)
```

Appendix 2: Use of citizen scientist observations during identification of Important Herp Areas

This report demonstrates that, for various reasons, the Natura 2000 and Emerald databases do not adequately represent the distribution of European amphibians and reptiles, often underestimating the coverage of many species. For instance, species may not be recorded in certain areas because they are not listed in the Habitats Directive or are not target species for the relevant Natura 2000 site. However, information on the presence of all amphibian and reptile species within Natura 2000 and Emerald sites is essential for identifying Important Herp Areas (IHAs). Citizen science data, particularly observations collected by citizen scientists, can contribute to building a more comprehensive picture.

Various international citizen science databases collect species observations, such as Observation (observation.org) and iNaturalist (inaturalist.org). A significant portion of this data is freely available for scientific purposes. These databases hold vast amounts of data; for example, iNaturalist contains over 500,000 records of European reptiles and amphibians, and a similar volume is available on Observation.

In the example below, we illustrate how validated citizen science data can be utilized to refine the identification of IHAs based on the Natura 2000 and Emerald networks. For this purpose, we use iNaturalist data on the great crested newt Triturus cristatus (Figure 8), a species listed in Annexes II and IV of the Habitats Directive.

Figure 8: Great crested newt, Triturus cristatus. *photo: Jelger Herder.*

At the time of writing, approximately 2,600 validated observations of the great crested newt (*Triturus cristatus*) are available on iNaturalist, providing a good representation of the species' global distribution (Figure 9). We retrieved all publicly available validated observations and combined them with cartographic data (GIS polygons) of the Natura 2000 and Emerald sites.

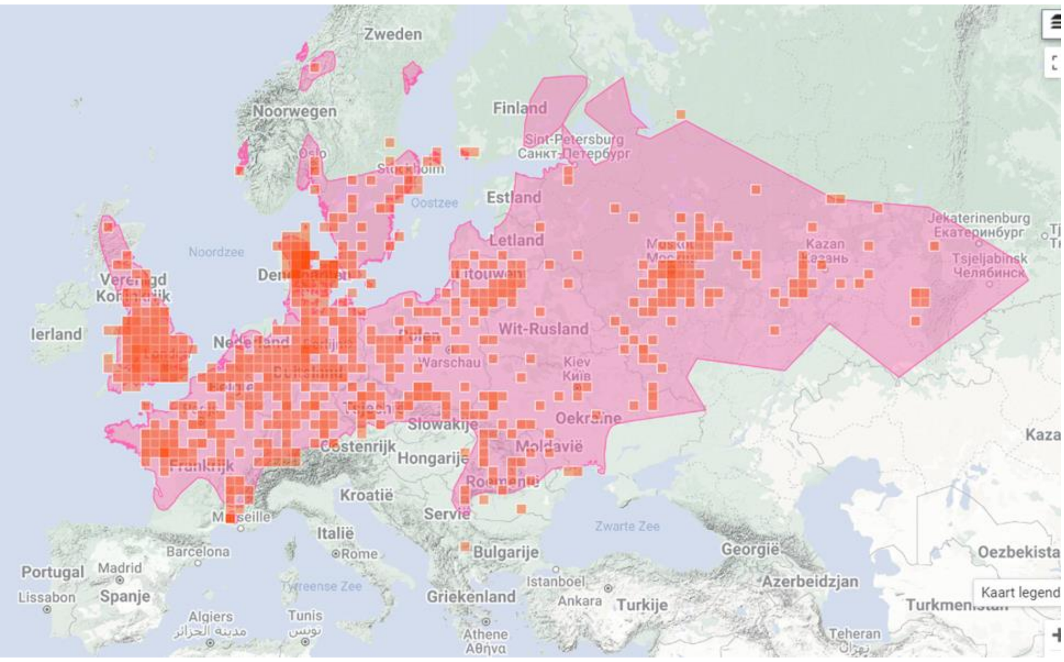


Figure 9: Validated observations of Great Crested Newt Triturus cristatus from www.inaturalist.org, *collected by citizen scientists*

During this exercise, we first identified protected areas where the great crested newt is recorded. This resulted in a total of 851 sites. However, citizen science data also frequently pinpoint the presence of the species in protected areas where it is not officially recorded or may have been overlooked. This was the case in 146 protected areas. Figure 10 summarizes the results on the map.

Our data analysis reveals that the great crested newt occurs in at least 17% more existing Natura 2000 and Emerald sites than currently documented. This highlights the significant complementary role citizen science data can play in enhancing the existing records in the Natura 2000 and Emerald databases. Similar exercises for other species can be relatively easily programmed and automated, thereby simplifying and accelerating the identification of IHAs in the short term.

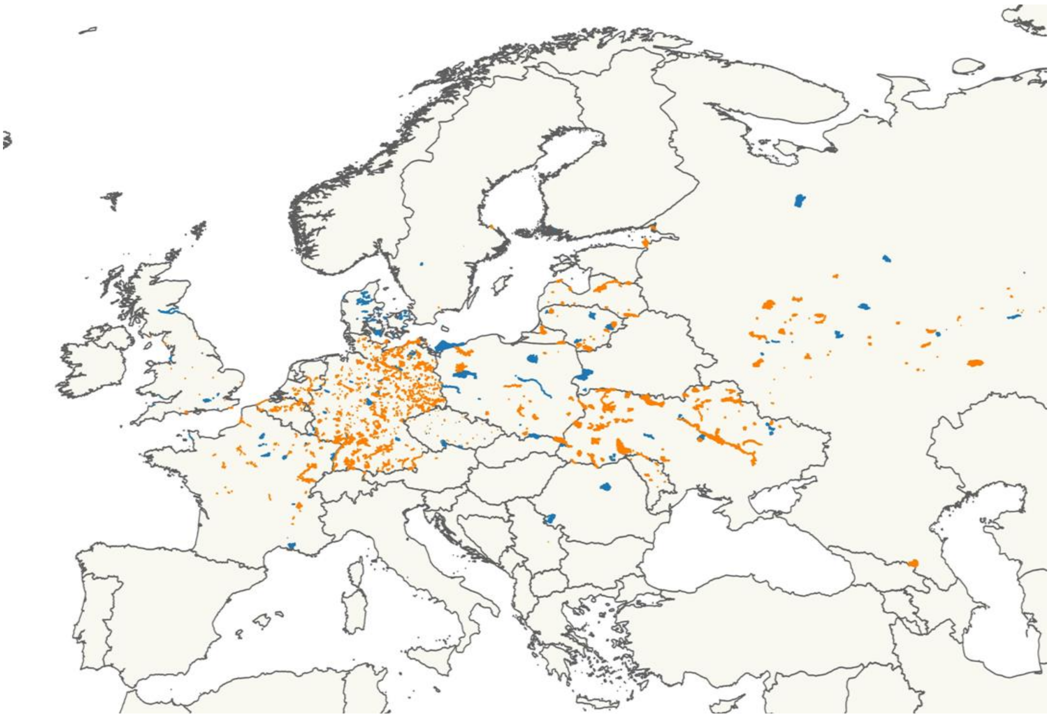


Figure 10: Occurrence of Great Crested Newt Triturus cristatus *in Natura2000- en Emerald sites. Occurrence in the orange sites is recorded in Natura2000- and Emerald Site metadata. Occurrence in blue sites was unknown, and was identified using our data analyses approach that leverages citizen scientist observations.*

RAVON
Reptielen Amfibieën Vissen Onderzoek Nederland

Natuurplaza
Toernooiveld 1 - 6525 ED Nijmegen
Postbus 1413 - 6501 BK Nijmegen

T: 024 - 7 410 600 (alg.)
www.ravon.nl