

Can we identify European snakes by color patterns?

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Abstract. We investigated to what extent European snakes can be identified by using their color, pattern and location. We coded these criteria for all 84 snake species of Europe, including European Russia, Ukraine, and Turkey as their eastern border. Brown and blotched snakes are most common, followed by dark (brown, black) and uniformly colored species. Some highly variable species can have a dozen or more color patterns. However, in 96% of localities (grid cells) these three criteria are sufficient to narrow down the number of possible species to no more than 10, and in most cases proper identification is possible with a few photos for comparison. Given that about two dozen European vipers (and a few other species) are venomous, accurately identifying snakes is also of medical importance. In addition to identifying snakes, we provide color and pattern data for future phylogenetic and for future phylogenetic and ecological studies.

Key words. Squamata, Serpentes, Reptilia, distribution, geography, herpetofauna.

Introduction

More than 4,600 different snakes are recognized today, including ~3,800 species and ~780 subspecies, distributed over all five continents (UETZ et al. 2020). Europe currently has 84 snake species most of which are either colubrids (52 species) or vipers (24) and the rest belong to other families (7 species). While the world's ~800 venomous species cause an estimated 94,000 deaths per year (CHIPPAUX 1998, KASTURIRATNE et al. 2008), Europe has relatively few medically important snakes (LONGBOTTOM et al. 2018). Nevertheless, members of the genus *Vipera* (and a few other genera) can cause serious pain and other complications (SCHROTH et al. 2003, HERMANSEN et al. 2019) that account for hundreds of snakebite envenomings but only very few fatalities every year (CURRIE 2000), hence it is important that venomous snakes can be identified quickly and easily.

While the snake body plan is simple (essentially a tube), snakes occur in a great variety of colors, patterns, and sizes. Although most European snakes display a limited set of brownish or grayish colors, some can be blue, green, or purple. Snake patterns also show a great diversity, with the most common patterns being longitudinal striping, regular and irregular crossbands, neck rings, rings on the body, chain or zigzag marking, longitudinal rows of dorsal blotches or saddles, longitudinal rows of diamond-shaped markings, and spots and checkers on the venter (BECHTEL 1978). We wondered if we can use simple descriptions of color and pattern to identify snakes or at least possible species. In other words: is it possible to identify a snake species by simply recording its color and pattern in a given locality? If not, to how many species can we narrow it down to and what other information do we need for a reliable identification? A sub-problem of this question is whether a particular snake is venomous or not. Although numerous field guides and other snake books have been published, it is often cumbersome to search them. Thus, a goal of this project was to compile data that would allow also inexperienced users to identify a snake or a least narrow down possible species, eventually using a website or mobile app for confirmation. While an app was outside the scope of this project we provide a spreadsheet that fulfills a similar purpose.

In order to classify colors and patterns of European snakes, we collected more than 600 published photographs of all terrestrial species and coded their color and pattern. We then mapped these color patterns to geographic maps to find the frequency of patterns in each grid cell. This would tell us, for instance, how many uniform brown snakes are expected in one cell and thus which species they likely are. Although we did not expect precise identifications from such a simplified approach, our goal was to provide a tool to identify a shortlist of possible species that can then be verified with additional data such as photographs or scalation data.

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In this study we excluded slow worms and glass lizards (Anguidae), although they can be easily confused with snakes by lay people. However, our dataset can easily be extended by such data (as well as additional snake patterns) and eventually we plan to implement the data of this study in a searchable online database at which time anguids will be included.

Materials and methods Image and character collection

First, we collected a list of all European snake species from the Reptile Database, which was cross-checked with the recent literature, with GENIEZ (2018) as our main reference list (Supplementary Table S1). Next, in order to collect pattern data, we collected ~350 published images from books and papers (GRUBER 2009, TUNIYEV et al. 2012, SINDA-CO et al. 2013, HOFMANN et al. 2018, TUNIYEV et al. 2018a, JABLONSKI et al. 2019), 270 images from the Reptile Data-

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base, and about a dozen photos from various websites if the aforementioned sources were insufficient (Supplementary Table S2). This approach was preferred over relying on online searches, given that such images are often much less reliably identified and often fleeting (web pages can disappear or their URLs change). While we attempted to have at least 2 images of live specimens per species, 6 rare species are represented by only one photo (e.g. *Eirenis hakkariensis* or *Vipera walser*). A complete list of images and their sources is provided in Supplementary Table S3.

The images were then used to code the patterns and colors. We initially used 15 colors but then simplified them to six color codes (whitish, light, brown, dark, purplish and greenish) (Fig. 1) and seven basic patterns (blotched, banded, anterior-posterior, spotted, uniform, striped and zigzag) (Fig. 2). For most patterns this was straightforward but some patterns are intermediate between patterns, e.g. some *Natrix helvetica* are intermediate between blotched and banded. These cases were coded with both patterns, so they can both be found when searching a list. For col-



Figure 1. Color terminology used in this study: Original color scheme with 15 colors that were reduced to a simpler scheme with six colors (A), and examples of species (B). Photos courtesty of PHILIPP WAGNER, DANIEL JABLONSKI, AUGUSTO CATTANEO, VLAD

ors, we coded the dominant 1–3 colors, so if a black-andwhite banded snake has a few yellow dots somewhere, they were usually ignored unless they are big enough to be easily seen from a distance. Given that brown is the most common color among European snakes, we initially differentiated light brown, brown and dark brown, but eventually merged them into a single 'brown', given that light conditions or variation among specimens may make it nearly impossible to pick the 'correct' hue. Similarly, rare colors such as purple or orange were merged into 'purplish' which is found in less than a dozen species, even when applied generously. This approach is still imperfect but simplifies data analysis and utility, and thus should be acceptable for our goals.

Mapping colors and patterns

All categorical traits were classified in binary terms, by presence or absence of each trait, although traits could adopt multiple values, e.g. black and white for color (Supplementary Table S4). We excluded the size variable from our analysis, given that size is not necessary for most identifications. Similarly, we initially considered including other characters in our analysis, such as scale type or pupil shape, but these traits are difficult to see without handling a snake.

We refer to each combination of traits as 'morphotype'. Several species may share the same morphotype, for example, *Coronella austriaca*, *Dolichophis caspius* and *Eirenis aurolineatus* can all be uniform brown. On the other hand, a species may also have numerous morphotypes, such as the Smooth Snake (*Coronella austriaca*) which can be 'whitish' (i.e. very lightly colored), brown or dark and be spotted, blotched or uniform. Hence, the number of morphotypes in a particular grid cell refers to the number of different combinations of colors and patterns. A grid cell with low species richness may therefore still have a high number of morphotypes, and a cell with high richness may have a low number of morphotypes.

Distribution maps and spatial analysis

To map the colors and patterns of the 84 European snake species, we intersected the species ranges to a 50 by 50 km grid of Europe, excluding Russia. The species ranges were obtained from ROLL et al. (2017) and supplemented by manually digitizing missing species from ŠMÍD et al. (2015), GHIELMI et al. (2016), KINDLER et al. (2017), MIZSEI et al. (2017), SALVI et al. (2018) and TUNIYEV et al. (2018b). Note that the maps in ROLL et al. (2017) are somewhat different and more complete than those in SILLERO et al. (2014), which is why we have not used the latter. The georeferencing of the distribution maps was done in QGIS ver. 3.6 and the remaining analysis were conducted in R (ver. 3.5.1) (R Core Team 2018), using the packages 'sf' (ver. 0.7-1) (PE-BESMA 2018), 'raster' (ver. 3.0-7) (HIJMANS et al. 2015), ggplot2 (ver. 3.1.0) (WICKHAM 2016), and 'rnaturalearth' (ver. 0.1.0) (SOUTH 2017).

Results

Europe has a relatively small number of snakes, given its size and climate (countries such as Mexico or India have



Natrix helvetica (spotted/blotched)

Hierophis gemonensis (anterior-posterior/spotted)

laphe quatuorlinea (striped)

Dolichophis schmidti (spotted/blotched)

Figure 2. Snake patterns used in the study. A total of seven snake patterns were used to differentiate between all snakes, namely uniform, banded, blotched, zigzag, spotted, anterior-posterior, and striped. The anterior-posterior pattern represents snakes that have different colors anteriorly and posteriorly. Blotches are large spots and spots are small (less than 3 scales in diameter). When all scales show the same pattern, they are classified as uniform. Some species may show a combination of patterns, such as both blotches and spots, or different patterns in different individuals. *Dolichophis schmidti* is a juvenile. Photos courtesy of PETER UETZ (2), DAVID JANDZIK, DANIEL JABLONSKI, PATRICK PRÉVOST, DANIEL JABLONSKI (2), OMID MOZAFFARI (top left to bottom right).

many more). Hence, the number of different species in any particular area is also moderate with about 1 to 25 species per area unit (here: $\sim 50 \times 50$ km, Fig. 3A). By combining a single color and pattern, 42 unique morphotypes are possible (6 colors \times 7 patterns), of which 39 were recorded in Europe. The range of possible snake morphotypes per grid cell observed across the continent was between 7 and 30 (Fig. 3B, with *Vipera berus* being often the only species in a grid cell, having 7 different morphotypes in our data set).

We wondered how many different morphotypes can be found in any particular grid cell. More importantly, how does the number of species relate to the number of morphotypes in a grid cell? The latter number would give the number of species that share a particular morphotype and thus indicate how difficult it is to identify a species. We find that no grid cell had more than 18 species of the same morphotype (i.e. when all colors and patterns are combined, Fig. 3).

Very few snakes are purplish or greenish, while the majority are whitish, light, brown and dark (Fig. 4). Regarding patterns, blotched is the most common pattern, followed by uniform and spotted snakes (Fig. 4).

When color and pattern combinations are taken into account, this reduces the number of possible combinations per grid cell even further (Fig. 5). For instance, the most common color/pattern combination are whitish or dark blotched snakes, and even though half of the snakes in Europe have this morphotype, no grid cell has more than 18 species with the same combination of traits and only 4% of the grid cells have more than 10 species with the same morphotype. All other combinations are much rarer (e.g. Fig. 5). For instance, green uniform snakes do not occur in most grid cells at all, and if they occur, no more than 2 such species are found in any grid cell (Fig. 5).

This suggests that we can narrow down possible species by simply recording their color, pattern and locality. The correct species can usually be identified by comparing a specimen with photos of the candidate species with the same characters (Fig. 6), even though in some cases additional data such scalation will be required for an unambiguous ID.

Supplementary Table S4 contains the color and pattern data that we compiled. It can be directly used as an ID tool by using the filters in Excel. If this data does not lead to correct IDs, we encourage readers to send us additional photos and/or color pattern data, so we can add that for future releases.

Discussion

Photos as data source

We have used an average of ~7 photos per snake species to extract color and pattern information. Photos have many limitations, including variable lighting, color distortion during image processing and the often-subjective interpretation of colors by the person who codes a color. For instance, dark brown snake may easily appear as black in a photo if the photo was taken under poor light conditions, making it look like black. We have tried to address this by using multiple photos.

Natural variation

Another source for errors is natural variation. Some rare species are known from only a few specimens and many publications illustrate only one specimen, thus ignoring sexual dimorphism or ontogenetic variation. In fact, many juveniles are strikingly different from the adults, e.g. in *Elaphe quatuorlineata*, in which juveniles are blotched and



Figure 3. Species and morphotype richness among European snakes: species richness (A), morphotype richness (B), maximum number of species with the same morphotype across European snakes (C), total number of species per country (D). The maximum number of species in a grid cell was 25, while some grid cells have up to 30 different morphotypes. The maximum number of species with the same morphotype in a cell was 18, which referred to brown blotched snakes.

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Figure 4. Number of species per color trait across Europe. See Figure 1 for an explanation of colors.

adults are striped (13 species with ontogenetic variation are indicated in Supplementary Table S1, but most are much less dramatic than in *E. quatuorlineata*).

In addition, some species are highly variable by nature (e.g. Eirenis persicus) or may have rare color variants or mutations. Hence it is practically impossible to describe every single variant and thus to identify every single snake using our approach. In addition, snakes can also show combinations of pattern types, either by having co-occurring patterns along the snake such as in *Platyceps najadum* that are typically blotched anteriorly and uniform posteriorly. In this analysis we only considered common morphotypes as documented in the cited books or papers, thus excluding combinations not in our photo library. If a species was observed to be green spotted in one specimen and brown uniform in another, we excluded other random combinations, such as brown spotted or green uniform. This approach is likely to cause an underestimation of possible morphotypes but will avoid an overestimation by inferring all possible combinations.

Geographic localities

Using range maps is often critical to identify species and dramatically narrows down the number of species when combined with colors and patterns. However, polygons are incomplete descriptions of ranges, often ignoring habitat, elevation, or abundance data. While such data can be integrated in niche models (ELITH & LEATHWICK 2009), this is rarely done with polygons. In addition, ranges are often incompletely known as shown by the numerous range extensions that are published regularly. Projects such as citizen science programs can improve this situation to some extent although they have their own limitations such as erroneous identifications (BIRD et al. 2014). Most importantly, polygons are impossible to search by simple text searches, requiring more sophisticated search algorithms. Hence, we included a list of $(200 \times 200 \text{ km})$ grid cells and the species occurring in each cell in Supplementary Table S5. We are also working on an implementation of an online search tools for our data but this was beyond the scope of this study.

C.Whitish Uniform



B.Whitish Blotched

Figure 5. Species richness of particular color patterns: Number of species by morphotype (A), brown and uniform species (B), purplish and uniform species (C), brown and spotted species (D), and greenish and spotted species (E).

A. Species per color and pattern



Hemorrhois ravergieri

Natrix natrix





Dolichophis schmidti

Figure 6. Species identification using color and pattern (A) and geography (B), and possible snake species (C). Hemorrhois ravergieri matches the pattern in (A) best but *Natrix tessellata* (here a somewhat untypical specimen from Israel) or *Dolichophis schmidti* are possible alternatives. Photos in (C) courtesy of Peter Uetz, DANIEL JABLONSKI, DAVID JANDZIK, PETER UETZ, PATRICK PRÉVOST, DAVID JANDZIK (2), RIYAD SADEK, OMID MOZAFFARI (top left to bottom right).

Hemorrhois nummifer

Outlook: other applications of color pattern data

Our data should be useful for many other applications, such as phylogenetic or ecological studies. Many colors and patterns have a strong phylogenetic signal (data not shown), given that similar species are usually related (although processes such as mimicry may obscure such relationships). Good examples are the species of Vipera which all display some zigzag pattern. However, while there are some studies illuminating the role of color patterns in ecology (e.g. (ALLEN et al. 2013)) it often remains unclear what the selective pressures and adaptations are that certain color pattern combinations provide in nature. More studies are required to illuminate their role in a larger number of species. Finally, while species identification may be automated by artificial intelligence and machine learning (as in iNaturalist's Seek app), these tools do not provide any way to export traits for other applications or analyses.

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References

- ALLEN, W. L., R. BADDELEY, N. E. SCOTT-SAMUEL & I. C. CUTHILL (2013): The evolution and function of pattern diversity in snakes. – Behavioral Ecology, **24**: 1237–1250.
- BECHTEL, H. B. (1978): Color and pattern in snakes (Reptilia, Serpentes). Journal of Herpetology, **12**: 521–532.
- BIRD, T. J., A. E. BATES, J. S. LEFCHECK, N. A. HILL, R. J. THOM-SON, G. J. EDGAR, R. D. STUART-SMITH, S. WOTHERSPOON, M. KRKOSEK & J. F. STUART-SMITH (2014): Statistical solutions for error and bias in global citizen science datasets. – Biological Conservation, 173: 144–154.
- CHIPPAUX, J. P. (1998): Snake-bites: appraisal of the global situation. – Bulletin of the World Health Organization, **76**: 515.
- CURRIE, B. J. (2000): Snakebite in tropical Australia, Papua New Guinea and Irian Jaya. Emergency Medicine, 12: 285–294.
- ELITH, J. & J. R. LEATHWICK (2009): Species distribution models: ecological explanation and prediction across space and time.
 Annual Review of Ecology, Evolution, and Systematics, 40: 677–697.
- GENIEZ, P. (2018): Snakes of Europe, North Africa and the Middle East: A photographic guide. – Princeton University Press, Princeton.
- GHIELMI, S., M. MENEGON, S. J. MARSDEN, L. LADDAGA & S. UR-SENBACHER (2016): A new vertebrate for Europe: the discovery of a range-restricted relict viper in the western Italian Alps. –

Journal of Zoological Systematics and Evolutionary Research, **54**: 161–173.

- GRUBER, U. (2009): Die Schlangen Europas: Alle Arten Europas und des Mittelmeerraums. – Franckh-Kosmos, Stuttgart.
- HERMANSEN, M. N., A. H. KRUG, E. TJØNNFJORD & M. BRA-BRAND (2019): Envenomation by the common European adder (*Vipera berus*): a case series of 219 patients. – European Journal of Emergency Medicine, **26**: 362–365.
- HIJMANS, R. J., J. VAN ETTEN, J. CHENG, M. MATTIUZZI, M. SUMNER, J. A. GREENBERG, O. P. LAMIGUEIRO, A. BEVAN, E. B. RACINE & A. SHORTRIDGE (2015): Package 'raster'. R package version 2.5-8. – Available from: https://cran.r-project.org/ web/packages/raster/index.html, accessed 15 September 2021.
- HOFMANN, S., K. MEBERT, K.-D. SCHULZ, N. HELFENBERGER, B. GÖÇMEN & W. BÖHME (2018): A new subspecies of Zamenis hohenackeri (STRAUCH, 1873) (Serpentes: Colubridae) based on morphological and molecular data. – Zootaxa, 4471: 137– 153.
- JABLONSKI, D., O. KUKUSHKIN, A. AVCI, S. BUNYATOVA, Y. KUM-LUTAŞ, Ç. ILGAZ & D. JANDZIK (2019): The biogeography of *Elaphe sauromates* (Pallas, 1814), with a description of a new rat snake species. – PeerJ, 7: e6944.
- KASTURIRATNE, A., A. R. WICKREMASINGHE, N. DE SILVA, N. K. GUNAWARDENA, A. PATHMESWARAN, R. PREMARATNA, L. SA-VIOLI, D. G. LALLOO & H. J. DE SILVA (2008): The global burden of snakebite: a literature analysis and modelling based on regional estimates of envenoming and deaths. – PLoS Medicine, **5**: e218.
- KINDLER, C., M. CHÈVRE, S. URSENBACHER, W. BÖHME, A. HILLE, D. JABLONSKI, M. VAMBERGER & U. FRITZ (2017): Hybridization patterns in two contact zones of grass snakes reveal a new Central European snake species. – Scientific Reports, 7: 1–12.
- LONGBOTTOM, J., F. M. SHEARER, M. DEVINE, G. ALCOBA, F. CHAPPUIS, D. J. WEISS, S. E. RAY, N. RAY, D. A. WARRELL & R. R. DE CASTAÑEDA (2018): Vulnerability to snakebite envenoming: a global mapping of hotspots. – The Lancet, **392**: 673–684.
- MIZSEI, E., D. JABLONSKI, S. A. ROUSSOS, M. DIMAKI, Y. IOAN-NIDIS, G. NILSON & Z. T. NAGY (2017): Nuclear markers support the mitochondrial phylogeny of *Vipera ursinii-renardi* complex (Squamata: Viperidae) and species status for the Greek meadow viper. – Zootaxa, **4227**: 75–88.
- PEBESMA, E. (2018): Simple features for R: standardized support for spatial vector data. – The R Journal, **10**: 439–446.
- R Core Team (2018): R: A language and environment for statistical computing.
- ROLL, U., A. FELDMAN, M. NOVOSOLOV, A. ALLISON, A. M. BAUER, R. BERNARD, M. BÖHM, F. CASTRO-HERRERA, L. CHIRIO & B. COLLEN (2017): The global distribution of tetrapods reveals a need for targeted reptile conservation. Nature Ecology & Evolution, 1: 1677–1682.
- SALVI, D., J. MENDES, S. CARRANZA & D. J. HARRIS (2018): Evolution, biogeography and systematics of the western Palaearctic *Zamenis* ratsnakes. – Zoologica Scripta, **47**: 441–461.
- SCHROTH, M., J. JÜNGERT, M. SCHREIBER, G. GERBER-ZUPAN, S. ZINK & W. RASCHER (2003): Life-threatening snakebites by Vipera berus. – Intensive Care Medicine, 29: 1615–1615.
- SILLERO, N., J. CAMPOS, A. BONARDI, C. CORTI, R. CREEMERS, P.-A. CROCHET, J. C. ISAILOVIĆ, M. DENOËL, G. F. FICETOLA & J. GONÇALVES (2014): Updated distribution and biogeography

of amphibians and reptiles of Europe. – Amphibia-Reptilia, **35**: 1–31.

- SINDACO, R., A. VENCHI & C. GRIECO (2013): The reptiles of the western Palearctic. 2. Annotated checklist and distributional atlas of the snakes of Europe, North Africa, Middle East and Central Asia, with an update to vol 1. – Edizioni Belvedere, Latina.
- ŠMÍD, J., G. MARTINEZ, J. GEBHART, J. AZNAR, J. GALLEGO, B. GÖÇMEN, P. DE POUS, K. TAMAR & S. CARRANZA (2015): Phylogeny of the genus *Rhynchocalamus* (Reptilia; Colubridae) with a first record from the Sultanate of Oman. – Zootaxa, 4033: 380–392.
- SOUTH, A. (2017): rnaturalearth: World map data from Natural Earth. R package version 0.1. 0. – Availabale from: https:// cran.r-project.org/web/packages/rnaturalearth/README. html, accessed 15 Sepetmber 2021.
- TUNIYEV, B., A. AVCI, Ç. ILGAZ, K. OLGUN, T. PETROVA, S. Y. BODROV, P. GENIEZ & A. TEYNIÉ (2018a): On taxonomic status of shield-head vipers from Turkish Lesser Caucasus and East Anatolia. – Proceedings of the Zoological Institute RAS, 322: 3–44.
- TUNIYEV, B., G. IREMASHVILI, T. PETROVA & M. KRAVCHENKO (2018b): Rediscovery of the steppe viper in Georgia. – Proceedings of the Zoological Institute RAS, 322: 87–107.
- TUNIYEV, S., A. AVCI, B. TUNIYEV, A. AGASIAN & L. AGASIAN (2012): Description of a new species of shield-head vipers – *Pelias olguni* sp. nov. from basin of upper flow of the Kura river in Turkey. – Russian Journal of Herpetology, **19**: 314–332.
- UETZ, P., P. FREED & J. HOŠEK (2020): The reptile database. Available from: http://www.reptile-database.org, accessed 20 March 2020.
- WICKHAM, H. (2016): ggplot2: Elegant graphics for data analysis. Springer, New York.

Supplementary data

The following data are available online:

Supplementary Figure S1. 200 \times 200 km grid cells used in Table S5.

Supplementary Table S1. Checklist of European snake species, by country, compared to the list in GENIEZ (2018).

Supplementary Table S2. Image sources for this project

Supplementary Table S3. All images used in this study, with their source.

Supplementary Table S4. All species with their color and pattern combinations and map source.

Supplementary Table S5. Snake species and their traits mapped to grid cells (Figure S1).