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Improving the Classification of Wildlife Conservation Status to Support Nature Protection in the European Union

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ABSTRACT

Ensuring that species of conservation concern achieve favorable conservation status (FCS) is central to European Union (EU) biodiversity conservation targets. A key criterion for FCS is exceeding the favorable reference range (FRR)—the range extent needed to support long-term species stability across sufficient environmental variation. However, FRRs are often unknown, undermining their applicability. We developed a machine-learning approach based on the assumption that species with similar traits and habitats share comparable range requirements to estimate and standardize FRRs across the EU. Applied to amphibians, mammals, and reptiles, our method provided FRRs for 99.5% species of conservation concern, compared to 17.5% previously available (with satisfactory modeling performance: R^2 0.75). We compared current ranges with estimated FRRs, finding that only 34.8% of cases meet or exceed FRR expectations, notably fewer than reported in official documentation (79%). Our approach may support periodic FCS reassessments and help refine the targets of EU conservation policies.

1 | Introduction

The European Union (EU) has made notable strides in nature protection through continent-wide regulations such as the Habitats and Birds Directives, the Natura 2000 Network, and, more recently, the EU Biodiversity Strategy to 2030, which includes the Nature Restoration Regulation (Lang 2023). However, biodiversity continues to decline within the EU (European Environment Agency 2020), primarily due to inadequate coordination among EU member states, poor policy integration, insufficient funding, and limited stakeholder engagement (Hermoso et al. 2022; European Commission 2017). To address these challenges effectively, the EU must prioritize actions for threatened species based on urgency, national responsibility, and potential synergies with broader environmental and climate goals (European Commission 2021). Such an approach would also align with the Kunming-Montreal Global Biodiversity Framework, which aims to reverse ecosystem degradation through synergistic, nature-based solutions (McGowan et al. 2024).

A key component of the EU Biodiversity Strategy for 2030 is to ensure that species of conservation concern achieve or maintain a favorable conservation status (FCS; EUR-Lex 2020). In EU legislation, conservation status integrates ecological and legal aspects to assess whether a species has sufficient habitat quality and quantity to sustain it as a long-term, functional part of the landscape (Oswald et al. 2025). Species of conservation concern are listed under the Habitats Directive (European Union Council 1992), each categorized as a reporting unit, that is, the occurrence of a species within the borders of an EU member state into a

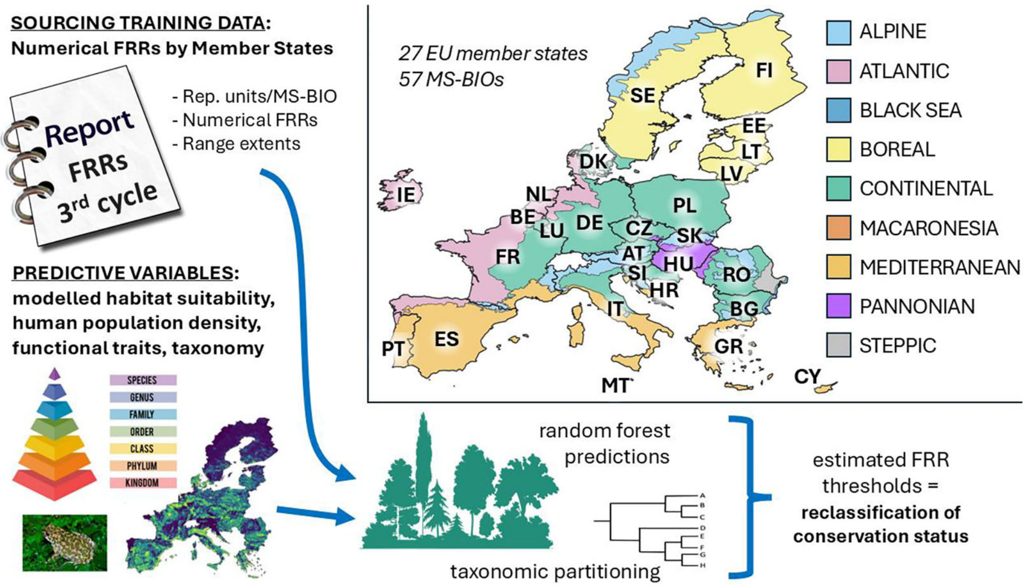

FIGURE 1 | Top right: Geography of the 57 MS-BIO areas across 27 EU member states (Table 2). Left and bottom: Summary of the methods. *Note:* Macaronesia is not included in the map. This biogeographical region covers the Spanish and Portuguese islands in the Atlantic Ocean.

specific biogeographical region (hereafter, reporting unit; MS-BIO; Figure 1). According to Article 17 of the Habitats Directive, member states must review conservation status every six years (European Environment Agency 2025). Ensuring comparability of conservation statuses across species is essential for identifying which reporting units are effectively in FCS and which are not, thereby identifying priority areas for additional protection (European Commission 2021), while avoiding misallocation of resources, such as excessive funding for charismatic taxa (Mammola et al. 2020). However, the lack of clear methodological guidance for estimating FCS—apart from a few well-monitored groups (Linnell and Boitani 2025)—forces member states to rely on subjective criteria and expert judgment, which are often inconsistent and difficult to replicate, undermining the framework's effectiveness (Bijlsma et al. 2019).

A key metric for assessing the conservation status of reporting units is the favorable reference range (FRR), which defines the minimum range extent required to achieve FCS (Bijlsma et al. 2019). Conceptually, the FRR represents the spatial extent necessary to support the favorable reference population—the biological target for FCS under EU legislation—ensuring sufficient environmental variation and habitat to maintain long-term viability. Estimating FRR is species-specific and relies on population monitoring, expert knowledge, historical baselines, and modeling (Bonelli et al. 2021; D'Alessio et al. 2025). The criteria outlined in the Habitats Directive thus far have allowed using qualitative indicators instead of numerical FRRs, including in the most recent third reporting cycle (period 2013–2018). Unlike a numerical FRR, a qualitative indicator assesses whether a population's range extent is sufficient for FCS classification without defining a quantitative target. Qualitative indicators can be robust when grounded in expert knowledge, but they limit cross-species and MS-BIO comparisons (Bijlsma et al. 2019). In the third reporting cycle, most member states relied heavily on qualitative indicators, with numerical FRRs missing for most reporting units. This trend largely reflects insufficient data, often making expert opinion the main basis for assigning conservation status (van Eldik et al. 2024). Addressing gaps in numerical FRRs is both urgent and essential, as these data offer greater utility than qualitative indicators. Furthermore, qualitative indicators are set to be phased out in the upcoming fourth reporting cycle (European Environment Agency 2025), rendering the development of a robust method to establish numerical FRRs a pressing priority.

To address this need, we developed a machine-learning method based on the assumption that species with similar traits and habitats share comparable range requirements, using the limited numerical FRRs provided by member states to estimate FRRs for as many reporting units as possible. The approach creates cross-species comparisons based on habitat quality, functional traits, and taxonomy, extrapolating missing values among reported FRRs and standardizing them for better comparability. We used the numerical FRRs reported for the third reporting cycle as our primary data source. Applying this methodology, we compared current ranges with estimated FRRs to highlight cases where range extent may fall below model expectations, without implying formal reclassification of FCS. Our analysis focused on amphibians, mammals, and reptiles, but the methodology can be adapted to other taxa where similar data are available.

2 | Materials and Methods

We collated data from the third reporting cycle mandated by Article 17 of the Habitats Directive, linking taxonomy to each reporting unit (Section 2.1). Next, we generated a set of predictive variables (Section 2.2), which were combined with numerical FRRs provided by member states to estimate FRRs for as many reporting units as possible within the relevant taxa, employing machine learning and taxonomic partitioning techniques (Section 2.3). Importantly, the developed modeling framework is not designed to predict species-specific trends in the response variable, that is, FRR; rather, it extrapolates FRRs across reporting units with comparable ecological and taxonomic characteristics, akin to an extrapolation approach. Using the estimated FRRs, we compared current range extents with modeled FRRs to identify cases where ranges fall below or exceed the estimated requirements, without implying formal FCS reclassification (Figure 1). Additionally, we calculated the proportional distance (p.dist) between each reporting unit's range extent and its estimated FRR, a variable expected to become standardized in the upcoming fourth reporting cycle (European Environment Agency 2025). Finally, based on range estimates from the third reporting cycle (European Environment Agency datahub 2025), we flagged island-endemic species whose estimated FRR warrants caution due to unmodeled physical barriers, intersecting reported ranges with continental-Europe boundaries (islands excluded). All analyses were performed in R programming language v4.4.1 (R Core Team 2024).

2.1 | Gathering and Processing FRRs Reported by Member States

We downloaded the latest published version (third reporting cycle) of the dataset on the conservation status of habitats and species under Article 17 of the Habitats Directive (European Environment Agency datahub; Table S1). Reporting units from marine biogeographical regions were excluded to ensure consistency across the selected predominantly terrestrial and freshwater species. Taxonomic classification (levels: class, order, family) was assigned by matching species names with the Global Biodiversity Information Facility (GBIF) taxonomic backbone (Lane and Edwards 2007) using the R package *taxize* (Chamberlain,Szoecs, et al. 2017), without manual corrections. We retained only amphibians (class: *Amphibia*), mammals (class: *Mammalia*), and reptiles (orders: *Squamata* and *Testudines*), selecting 2943 out of 8097 reporting units. The excluded reporting units belong to other taxa, for example, vascular plants. To ensure consistency, we constrained "range extent" values and numerical FRRs to the spatial extent of the relevant MS-BIO, using a 1 km^2 raster (ETRS89-extended/LAEA Europe equal-area projection). We then standardized "range extent" and numerical FRRs as a percentage of MS-BIO area to account for MS-BIO extent variability. This procedure was necessary to make FRRs comparable across reporting units, although it implicitly gives equal weight to small and large MS–BIOs. As a result, regions representing marginal or ecologically less relevant habitats may have a disproportionate influence on model fitting—a limitation we acknowledge as a trade-off for achieving a consistent, transferable modeling framework. Finally, we extracted numerical FRRs assigned by member states, which served as training data for model estimation.

2.2 | Predictive Variables

The generated predictive variables fall into two groups: those related to (A) habitat characteristics and (B) functional traits (Table 1). Importantly, not all variables were available for every reporting unit. We compiled species occurrence data (temporal range 2013–2018, corresponding to the data gathered from the third reporting cycle) from GBIF (our query: https://doi.org/10.15468/dl.gxfms8), using the R package *rgbif* (Chamberlain, Ram, et al. 2017). These records were used to define median human population density at species' realized distributions within each MS–BIO and to train independent climate- and land-use-suitability models using an ensemble of machine-learning algorithms (Naimi and Araújo 2016) (Appendix S1 and Appendix S2 for details; ODMAP Protocol, Zurell et al. 2020). The suitability models provided median predicted climate and land-use suitability, calculated as the central tendency across all grid cells within an MS-BIO. Spatial projections were omitted to reduce computational load, as the aim was to compare environmental characteristics MS-BIOs rather than predict fine-scale distributions. Instead, we summarized conditions statistically within each combination reporting unit/MS-BIO. To complement the central metrics calculated as median, we also computed the Gini index for population density and suitability values as an indicator of spatial inequality (Farris 2010), reflecting whether suitability is evenly distributed or concentrated in a few areas. We then calculated the percentage of suitable areas within an MS-BIO by converting climate- and land-use-based modeling outputs into binary form, using the 10th percentile training-presence threshold—the minimum suitability value encompassing 90% of known occurrences—as the cutoff for suitability. This approach excludes potential outliers and mislocated records, yielding conservative estimate of suitable habitat extent (Liu et al. 2005).

For functional traits, we used the databases "AmphiBIO" (Oliveira et al. 2017) for amphibians, "COMBINE" (Soria et al. 2021) for mammals, "ReptTraits" (Oskyrko et al. 2024) for reptiles, and Mancini et al. (2025) for both amphibians and reptiles. The selected traits—body mass (g, $\log_{10}$-scaled for mammals), litter size (mean offspring per litter or eggs per clutch), and generation length (average parental age; Pacifici et al. 2013)—were chosen for their broad taxonomic coverage, demographic processes relevance, and importance in extinction-risk analyses (Foden et al. 2019).

2.3 | Estimating FRRs and Comparing Them to Current Range Extents

We developed a series of random forest (RF) regression models with subsequent taxonomic partitioning (Figure 1) to predict FRR for as many reporting units as possible, including those already assigned by member states. RF models were built separately for each taxonomic group (mammals, amphibians, reptiles), as functional traits are not comparable across these groups, with numerical FRRs provided by member states as the response variable. Predictive variables included habitat characteristics and functional traits (Table 1). The available data for these variables varied across reporting units, depending on the availability of occurrence records, the performance of the habitat suitability models (Appendix 1), and the completeness of functional trait data. To account for potential variability in the training data, stemming from different member states assigning FRRs without explicit methodological coordination, we added "member state" as an extra variable in each model. Rather than treating it as a categorical factor (which could cause overfitting due to few levels in some member states), we transformed it into a numerical variable by calculating each member state's effect size using Cohen's d metric with Hedges' correction (Cohen 2013). Effect

TABLE 1 | Predictive variables used in the random forest (RF) models to estimate favorable reference ranges (FRRs).

Category	Name	Data source and elaboration
Habitat characteristics	Median climate suitability	GBIF occurrence records combined with climate data (cc. 1 km resolution; annual mean 1979–2018; source: Copernicus Climate Change Service, 2025) reduced via principal component analysis. Median value calculated as the central tendency of climate suitability across all grid cells within the relevant MS-BIO (all details in Appendix 1)
	Climate suitability inequality	Gini index of climate suitability values modeled across the relevant MS-BIO
	Median land use suitability	GBIF occurrence records combined with land cover data (100 m resolution; 2018 figure; source: Copernicus Land Monitoring Service, 2025) transformed to a continuous scale. Median value calculated as the central tendency of land-use suitability across all grid cells within the relevant MS-BIO (Appendix 1)
	Land use suitability inequality	Gini index of land-use suitability values modeled across the relevant MS-BIO
	Available suitable habitat	Percentage of 1000 randomly extracted 1 km^2 cells classified as suitable in the binary climate and land-use suitability models within the relevant MS-BIO
	Median human population density	GBIF occurrence records interpolated with population density data map (5 km resolution; 2020 figure; source: Copernicus Emergency Management Service, 2025). Median value extracted across the relevant MS-BIO
	Human population density inequality	Gini index of population density values at occurrence record points within the MS-BIO
Functional traits	Body mass	Measured or estimated (via trait-based correlation) in grams (log10-scaled for mammals)
	Litter size	Measured or estimated (via trait-based correlation) as the number of individuals (eggs for amphibians and reptiles) per reproductive event
	Generation length	Measured or estimated (using taxonomy) as the average age of parents of the current cohort, in days

Note: For both habitat characteristics and functional traits variables, the assumption is that reporting units with similar functional and life-history traits, occurring in comparable environments, are expected to have similar range extent needs to secure sufficient resources for long-term viability.

size quantifies the standardized magnitude of mean differences among groups, providing a comparable measure across datasets.

In the multiple RF model runs, we progressively reduced predictors from the complete set to a minimum of five, allowing FRR estimations even with incomplete data. Before running each model, we checked for variable collinearity and excluded variables with a variance inflation factor > 5 (Zuur et al. 2010). Each iteration prioritized models based on performance, measured by Nagelkerke R^2 or, when performance was equal, by the lower number of predictors used, thus favoring models with broader cross-species comparability. RF models were trained using the *R package RandomForest* (Breiman et al. 2018), with hyperparameter tuning of "ntree" (number of decision trees; tested range 100 to 500, increment by 100), "mtry" (number of features considered for each split; 2 to number of predictors −1, by 1), and "nodesize" (minimum number of observations in a terminal node; tested 1, 5, and 10), to optimize out-of-bag error. Given limited training data, parameters were kept within recommended ranges to prevent overfitting (Probst et al. 2019). To quantify predictive uncertainty, we calculated the mean squared prediction error and adjusted each prediction by adding or subtracting this value (Lu and Hardin 2021), yielding a prediction interval around each FRR estimate.

For cases where the RF models did not return estimates, we applied taxonomic partitioning following Pacifici et al. (2013), assigning remaining FRRs based on the mean of already estimated FRRs within the relevant taxonomic group in the MS-BIO. Priority was given to estimates from populations within the same family, followed by order and class, with estimation error calculated as the standard deviation from the mean.

Reporting units whose estimated FRR was lower than or equal to their current range extent were considered to meet the estimated requirement, while others were flagged as below FRR or labeled "N/D" (not determined) when estimation was impossible. Estimated FRRs were converted from the percentage of MS-BIO occupied area to km^2 and capped at the MS-BIO extent. Finally, in accordance with the guidelines for the fourth reporting cycle (European Environment Agency 2025), we calculated the proportional deviation between the estimated range and FRR for all reporting units below the estimated requirement.

3 | Results

3.1 | Estimated FRRs

We estimated a total of 2929 (99.5%) FRRs (Table S2), compared to the 521 (17.7%) numerical FRRs available in the third reporting cycle (Table S1). Our predictions covered nearly all amphibians (579/580), all mammals (1847/1847), and most reptiles (503/516). The predictive performance of the RF regressions was good to optimal, with an overall mean Nagelkerke's R^2 of 0.754 (maximum 0.872 in Romania-Black Sea, minimum 0.667 in Spain-Macaronesia; Table 2). RF regressions performed particularly well for amphibians (0.905) and reptiles (0.924), while results for mammals (0.669) were relatively less satisfactory. The majority of numerical FRRs were derived from RF regressions (82.7%), followed by family-level partitioning (7.5%), order-level partitioning (6.1%), and class-level partitioning (3.2%; Figure 2). 69 reporting units (2.4%) were identified as island endemic (Table S2).

3.2 | Comparison Between Current Ranges and Estimated FRRs

Based on our estimates, 1024 of 2943 reporting units (34.8%) meet or exceed their estimated FRR, indicating range adequacy relative to FCS requirements. Considering RF prediction errors and taxonomic partitioning variability, this ranges from 939 (31.9%) to 1,099 (37.3%) (Table S2). In contrast, the official Report (Table S2) indicates 69.1% as meeting FCS criteria when combining numerical FRRs and qualitative indicators. Discrepancies are most notable in Fennoscandia, Italy, and Eastern Europe, especially for amphibians and reptiles (Figure 3). Among reporting units below their estimated FRR, reptiles show the largest mean proportional deviation between current range and FRR (−67.8%), followed by amphibians (−64.2%) and mammals (−63.4%). A high share of reporting units exceeds a −75% deviation, especially among amphibians and mammals. France, Italy, and Romania exhibit the highest numbers of reporting units below their estimated FRR thresholds (Table 3).

4 | Discussion

Despite several conceptual frameworks proposed to improve coordination among EU member states in the definition of FRR targets (Bijlsma et al. 2019; van Eldik et al. 2024), provided numerical FRRs remain scarce and likely inconsistent as also noted in previous reports (Hochkirch et al. 2013). This is largely because no alternative methodologies have been adopted beyond species-specific approaches that require extensive ecological expertise and long-term monitoring data. In this study, we presented a generalized framework based on the assumption that species with similar traits and habitat associations tend to have comparable range requirements, using cross-species comparisons of traits, habitat structure, and taxonomic partitioning to substantially expand the availability of FRRs for species of conservation concern in the EU. Compared to the third reporting cycle, our method covers FRR for over 80% more reporting units. At its core are machine-learning-based regression models, which achieved strong predictive performance, particularly in countries like Germany and Sweden, where species-specific numerical FRRs were available to train the models. Notably, model performance was lower for mammals, likely reflecting their greater ecological plasticity and generalist habitat use, which may weaken the relationship between traits, habitat structure, and range extent. This suggests that the framework may perform better for taxa with narrower ecological niches, while FRRs for generalists should be interpreted with caution.

With FRRs now assigned to nearly all reporting units, our findings differ markedly from previous assessments of wildlife conservation status in the EU. While FRRs provided by member states—based largely on qualitative indicators—suggested that 69.1% of reporting units met FCS criteria, our analysis indicates that only 34.8% of reporting units have current ranges meeting or exceeding their estimated FRRs. When accounting for model uncertainty, the estimate ranges from 31.9% to 37.3%, underscor-

TABLE 2 | Estimated FRRs and mean Nagelkerke's R^2 from RF regressions for each MS-BIO (all taxa included).

MS-BIO	FRRs	R^2	MS-BIO	FRRs	R^2	MS-BIO	FRRs	R^2
AT-ALP (0/62)	62	0.78	ES-MED (4/85)	85	0.81	MT-MED (0/16)	16	0.72
AT-CON (1/62)	62	0.78	FI-ALP (0/9)	9	0.68	NL-ATL (0/43)	42	0.74
BE-ATL (0/39)	38	0.72	FI-BOR (0/30)	29	0.72	PL-ALP (0/47)	46	0.69
BE-CON (0/38)	37	0.70	FR-ALP (0/73)	73	0.77	PL-CON (2/52)	51	0.74
BG-ALP (69/70)	70	0.77	FR-ATL (0/64)	64	0.81	PT-ATL (20/46)	46	0.72
BG-BLS (66/72)	72	0.75	FR-CON (1/64)	64	0.79	PT-MAC (2/6)	5	0.67
BG-CON (85/90)	90	0.77	FR-MED (0/81)	81	0.79	PT-MED (22/56)	56	0.79
CY-MED (0/32)	31	0.71	GR-MED (0/112)	112	0.78	RO-ALP (0/56)	56	0.70
CZ-CON (0/61)	61	0.75	HR-ALP (0/63)	63	0.72	RO-BLS (0/20)	20	0.87
CZ-PAN (2/52)	52	0.69	HR-CON (0/65)	65	0.73	RO-CON (0/74)	74	0.74
DE-ALP (12/40)	40	0.72	HR-MED (0/76)	76	0.75	RO-PAN (0/31)	31	0.78
DE-ATL (14/45)	44	0.81	HU-PAN (0/67)	67	0.76	RO-STE (0/58)	58	0.75
DE-CON (28/58)	58	0.82	IE-ATL (13/15)	15	0.76	SE-ALP (11/12)	12	0.74
DK-ATL (0/22)	22	0.79	IT-ALP (0/73)	73	0.75	SE-BOR (34/34)	33	0.78
DK-CON (0/32)	32	0.81	IT-CON (0/69)	69	0.76	SE-CON (36/39)	38	0.80
EE-BOR (1/32)	32	0.71	IT-MED (0/94)	94	0.78	SI-ALP (25/64)	64	0.73
ES-ALP (1/54)	54	0.72	LT-BOR (0/37)	36	0.71	SI-CON (20/71)	71	0.75
ES-ATL (2/60)	60	0.80	LU-CON (12/38)	37	0.71	SK-ALP (0/60)	60	0.71
ES-MAC (16/23)	23	0.67	LV-BOR (22/40)	39	0.68	SK-PAN (0/59)	59	0.72

Note: Numbers in brackets indicate numerical FRRs provided by member states relative to the total number of reporting units per MS-BIO.

TABLE 3 | Number of reporting units with range extents below the estimated FRR threshold by member state (totals in brackets) and proportional deviation (p.dev) between current range and estimated FRR, grouped by taxon—amphibians (Amp.), mammals (Mam.), reptiles (Rep.)—and organized by p.dev intervals.

	p.dev. < −0.25			p.dev. −0.25 to −0.50			p.dev. −0.50 to −0.75			p.dev. −0.75 to −1.00		
EU member states	**Amp.**	**Mam.**	**Rep.**	**Amp.**	**Mam.**	**Rep.**	**Amp.**	**Mam.**	**Rep.**	**Amp.**	**Mam.**	**Rep.**
Austria (110)	1	6	1	2	12	5	6	15	10	14	38	0
Belgium (29)	1	3	0	2	1	0	1	5	1	3	12	0
Bulgaria (117)	5	17	11	4	16	7	3	14	13	11	10	6
Croatia (116)	4	12	2	3	10	2	1	20	13	5	40	4
Cyprus (9)	/	1	1	/	1	0	/	1	2	/	2	1
Czech Rep. (43)	2	4	0	1	3	1	3	4	4	3	18	0
Denmark (38)	3	3	2	4	3	0	4	4	0	1	14	0
Estonia (16)	3	3	0	6	0	0	2	1	1	13	7	0
Finland (18)	1	1	/	0	1	/	0	7	/	1	7	/
France (247)	5	22	4	7	34	6	9	36	16	34	71	3
Germany (91)	9	17	1	4	10	0	5	9	8	5	22	1
Greece (84)	1	5	2	1	6	7	4	4	23	9	10	12
Hungary (46)	0	7	1	1	5	2	0	8	4	5	11	2
Ireland (5)	0	1	/	0	1	/	0	1	/	1	1	/
Italy (182)	5	11	1	7	21	4	7	14	28	27	50	7
Latvia (7)	0	0	0	0	1	0	2	0	1	5	5	1
Lithuania (7)	2	0	0	0	0	0	1	0	1	2	1	0
Luxembourg (10)	0	0	/	0	0	/	3	0	/	0	7	/
Malta (10)	/	0	0	/	1	0	/	3	1	/	4	1
Netherlands (23)	3	1	0	1	3	1	0	3	1	4	6	0
Poland (66)	3	2	0	3	8	1	1	14	1	4	29	0
Portugal (60)	1	16	2	0	8	0	1	15	4	1	10	2
Romania (172)	3	7	8	3	12	7	2	21	16	5	77	11
Slovakia (116)	1	6	0	7	18	7	4	17	6	10	39	1
Slovenia (51)	2	7	0	3	12	2	2	7	7	5	2	2
Spain (40)	3	5	4	6	19	8	2	12	26	13	33	8
Sweden (139)	2	7	0	3	12	2	0	7	7	4	2	2

Note: Colors indicate the p.dev interval with the highest number of reporting units below their estimated FRR per taxon and member state: green = amphibians, orange = mammals, blue = reptiles.

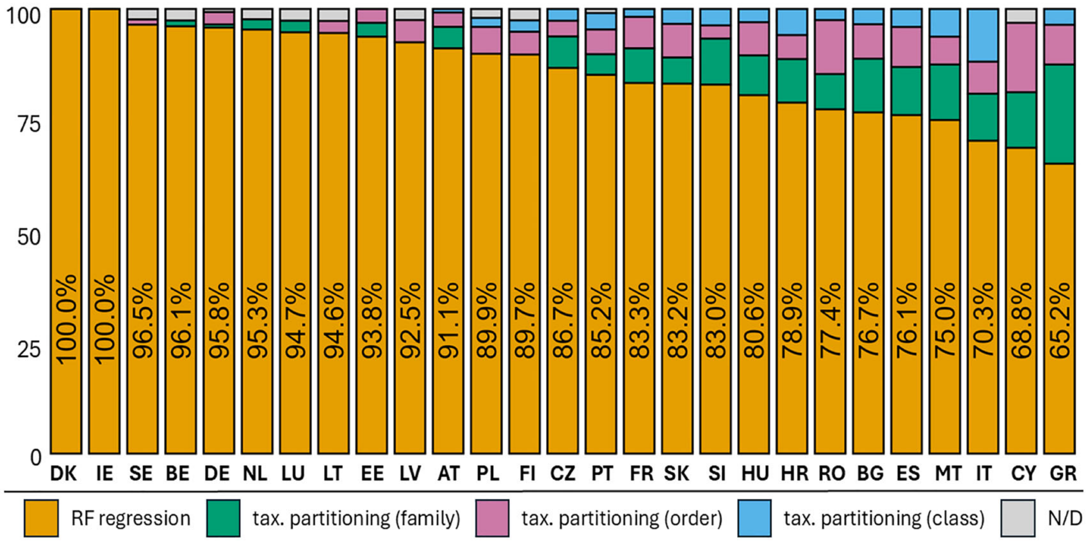

FIGURE 2 | Percentage of estimated FRRs over the total number of reporting units per member state by methodology. Member states are ordered left to right by decreasing contribution of the RF regressions (percentage reported on the bar), which is the primary modeling approach.

ing the robustness of the results. These findings are consistent with growing evidence of widespread biodiversity decline across Europe, with only limited exceptions among mammalian and avian species (Burns et al. 2021; Warren et al. 2021; Ledger et al. 2022). Bijlsma et al. (2019) reported a similar discrepancy for the second reporting cycle (period 2012–2017), noting that, when qualitative indicators were included, approximately 60% of reporting units were considered to be in FCS, whereas using only numerical FRRs, most reporting units appeared to have ranges smaller than their FRRs. Amphibians and mammals represent a large share of reporting units with ranges below estimated FRRs; however, reptiles show the greatest deviation from their FRRs (−67.8% on average). More broadly, across all three taxa, a substantial proportion of reporting units fall below their estimated range requirements, suggesting that numerous populations—particularly those endemic to specific regions—may have been severely affected by long-term habitat fragmentation, especially in Southern and Central Europe, where such processes have persisted for centuries (Kaplan et al. 2009). For these populations, protection of existing habitats alone may be insufficient to meet range requirements consistent with FCS objectives. Active habitat restoration, combined with long-term habitat protection, may be necessary (Araújo and Alagador 2024). Alternatively, for populations with highly localized ranges, the FRR framework itself may need reconsideration, as conventional range-based targets may not fully capture ecological realities.

Importantly, our approach is not intended to replace species-specific expert assessments but to complement them. Its main limitation lies in the need for a sufficiently large number of numerical FRRs provided by member states to serve as training data. The framework also relies on the key assumption that species with comparable traits and habitat associations share similar range requirements; however, ecological interactions and evolutionary history may cause deviations from these patterns. As such, the method's efficiency and reliability would benefit from closer coordination with national experts, who should focus on providing the most ecologically robust numerical FRR values possible. These experts could then apply our framework to estimate FRRs for species where ecological knowledge or long-term monitoring remains limited. As demonstrated, even with a starting dataset covering only 17% of species of conservation concern, the method can predict FRRs for almost all species, with strong model performance. Additional limitations include gaps in species occurrence data and missing functional ecological information, which can make some estimations unreliable. Furthermore, although estimates were capped to MS-BIO extension, FRRs for island endemics may be inflated when MS-BIO areas include both island and mainland portions; we flagged such cases to enable proper interpretation. Another limitation arises from harmonizing FRRs and range extents at the MS-BIO level, which risks assuming uniform ecological requirements across diverse regions. Although this was necessary to secure adequate training data, it may produce less reliable estimates for species strongly dependent on region-specific conditions. Future refinements could incorporate finer-scale ecological data or spatial structure, improving alignment with FCS assessments while maintaining the model's comparability across member states. While alternative approaches—such as historical range reconstructions (Pacifici et al. 2019), climate-resilient baselines (Willis et al. 2010), or abundance-based models (D'Alessio et al. 2025)—hold conceptual value, they require data largely unavailable for most EU species of conservation concern.

This work provides a practical tool to complement species-specific estimates of FRRs and advance conservation practice in the EU. Critically, it offers robust numerical FRR estimates, helping to reduce the longstanding overreliance on qualitative assessments—valuable replacements when quantitative data are missing but widely acknowledged as potentially imprecise or subjective, and now excluded from EU reporting guidelines (European Environment Agency 2025). The method also addresses persistent inconsistencies arising from divergent interpretations of the FCS concept, including its occasional mischaracteriza-

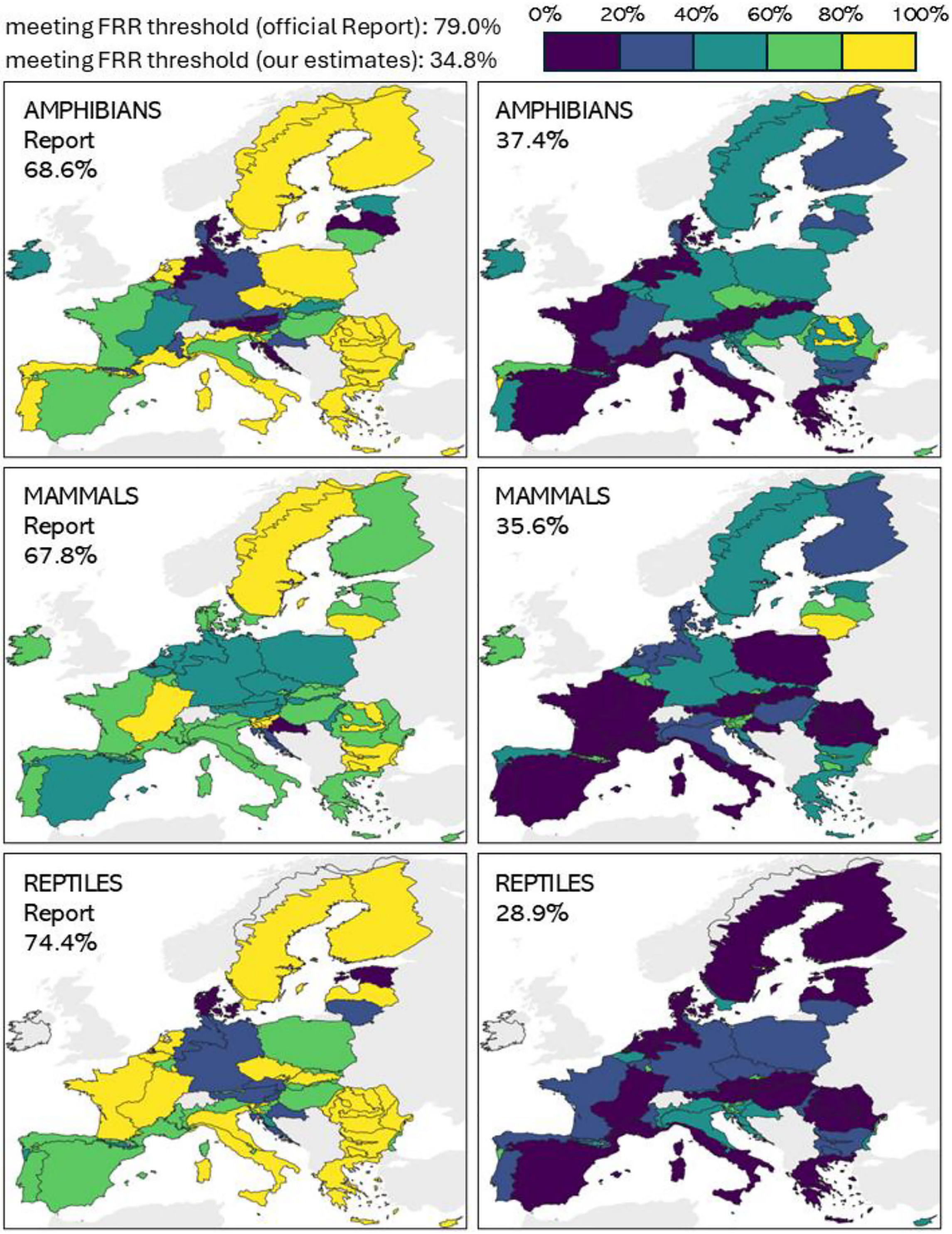

FIGURE 3 | Left: Proportion of reporting units meeting the FRR threshold according to the official Article 17 Report. Right: Proportion of reporting units whose current ranges meet or exceed the estimated FRR threshold according to our model. Top-left panel: Overall proportion across all reporting units and taxa.

tion as the minimum viable population (Epstein et al. 2016; Trouwborst et al. 2017) or disproportionate influence from species charisma (Brambilla et al. 2013). A key innovation of our framework is the integration of quantified model uncertainty alongside FRR estimates, offering pragmatic flexibility. Rather than defining single, fixed thresholds, the associated prediction intervals provide a range of possible FRR targets. This range can guide management decisions and allow member states to coordinate conservation actions across taxa within realistic upper and lower bounds, depending on ecological contexts and policy ambitions. Overall, FRRs should be regarded not as fixed thresholds but as indicative spatial metrics reflecting the area likely required to maintain viable populations over the long term.

Author Contributions

Marco Davoli, Martin Jung, and Michela Pacifici conceptualized the study and developed the methodology. Marco Davoli conducted the analyses and drafted the manuscript. All authors provided critical feedback on the methodology and manuscript.

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Data Availability Statement

The files necessary to reproduce the analyses, including the original data, Tables S1 and S2, and the R scripts used, are available on FigShare (https://doi.org/10.6084/m9.figshare.29119265).

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.

Supplementary AppendixS1: conl70039-sup-0001-AppendixS1.docx **Supplementary AppendixS2**: conl70039-sup-0002-AppendixS2.docx **Supplementary TableS1**: conl70039-sup-0003-TableS1.xlsx **Supplementary TableS2**: conl70039-sup-0004-TableS2.csv