### Supplementary information for

# Setting temporal baselines for biodiversity: the limits of available monitoring data for capturing the full impact of anthropogenic pressures

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## **Supplementary Methods**

Selection of biodiversity monitoring schemes in the Global Population Dynamic Database In addition to DaEuMon and the Participatory Monitoring Networks in Europe database (PMN), the Global Population Dynamic Database (GPDD) was used in this study to measure the temporal baseline for biodiversity monitoring in Europe. The GPDD compiles population timeseries data such as counts, indices, or percentage cover at the global scale. To enable comparison with the DaEuMon and PMN databases, we selected from GPDD only those monitoring schemes conducted in Europe ("Europe" as "Continent" entry, with the exclusion of Russian Federation and Belarus as "Country") and which have recorded population counts and harvest catches as data type ("SamplingProtocol" filtered as "Count" and "Harvest ").

### Bias associated with biodiversity monitoring databases

Geographical and taxonomic bias has been identified in DaEuMon<sup>1</sup> and in GPDD<sup>2</sup>. For instance, DaEuMon under-represents fish, while GPDD partly corrects for this taxonomic bias (DaEuMon: 3%, GPDD: 19%, PMN: 10%, total in the three databases: 9%). In contrast, GPDD under-represents amphibians and plants, while these biases are reduced when GPDD is combined with PMN and DaEuMon (for Amphibians: GPDD: 1%, DaEuMon: 6%, PMN: 13%, total in the three databases: 9%; for Plants: GPDD: less than 1%, DaEuMon: 15%, PMN: 18%, total in the three databases: 15%, see Suppl. Fig. 1). Despite such heterogeneity, general conclusions on the starting years of monitoring schemes and their relative taxonomic representation remained consistent overall between all data sources (i.e. a strong under-representation and very recent starts for reptiles and molluscs, and to a lesser extent for plants and insects).

Anthropogenic	Taxonomic groups								
pressures	Amphibian	Birds	Fish	Insect	Mammals	Molluscs	Plants	Reptiles	
CO2	72.71	63.01	56.30	66.88	68.01	81.53	71.52	71.52	
Temperature	77.69	68.62	62.06	72.29	73.35	85.59	76.60	76.60	
Human	68.14	57.59	50.69	61.70	62.94	78.38	66.79	66.79	
Forest	88.82	84.23	80.28	85.94	86.51	92.89	88.82	88.24	
Pasture	82.43	75.63	70.81	78.36	79.16	88.50	81.60	81.60	
Crop	82.02	75.09	70.19	77.87	78.68	88.22	81.17	81.17	
Furan	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	
Diox	70.73	58.37	50.48	63.15	64.59	83.03	69.14	69.14	
Nitrogen	66.89	46.42	35.37	53.87	56.23	91.32	64.03	64.03	
Phosphorus	74.91	64.24	57.07	68.44	69.69	85.00	73.57	73.57	

**Supplementary Table S1.** Level that anthropogenic pressures had already reached when biodiversity monitoring started for each taxonomic group. The level of each anthropogenic pressure is expressed as a percentage of the known range of that pressure (see Methods for details).

**Supplementary Table S2.** Post-hoc multiple pair-wise comparisons for categories with significant heterogeneity. The t-test statistics and the p-values of single pair-wise comparisons performed with the Conover-Iman test adjusted through the Benjamini-Hochberg procedure are reported for categories showing heterogeneity after a significant Kruskal-Wallis test (see Methods). Significant pair-wise differences are indicated in bold.

		Taxonomic groups							
		Amphibian	Birds	Fish	Insect	Mammals	Molluscs	Plants	
Birds	t-test	-3.35							
	p-val	0.003							
Fish	t-test	-3.87	-1.38						
	p-val	0.002	0.112						
Insect	t-test	-1.73	1.77	2.61					
	p-val	0.078	0.077	0.018					
Mammals	t-test	-1.94	1.73	2.59	-0.15				
	p-val	0.062	0.074	0.017	0.439				
Molluscs	t-test	1.15	2.48	2.91	1.89	1.96			
	p-val	0.154	0.020	0.009	0.064	0.065			
Plants	t-test	-0.45	3.36	3.83	1.46	1.69	-1.36		
	p-val	0.353	0.004	0.001	0.107	0.075	0.112		
Reptiles	t-test	0.24	2.37	2.96	1.40	1.50	-0.90	0.55	
	p-val	0.422	0.025	0.009	0.114	0.103	0.215	0.328	

	_	Type of data						
		CMR	Count	Occurrence	Phenology			
Count	t-test	-2.97						
	p-val	0.015						
Occurrence	t-test	-2.49	0.03					
	p-val	0.032	0.4873					
Phenology	t-test	-0.76	1.25	1.12				
	p-val	0.320	0.265	0.219				
Population structure	t-test	-1.96	-0.35	-0.34	-1.12			
	p-val	0.083	0.453	0.407	0.262			

**Supplementary Figure S1.** Taxonomic bias associated with different sources of biodiversity information, shown as the relative contributions of different taxonomic groups in each source of biodiversity information used, extracted from three databases for Europe a) DaEuMon (N = 452 schemes), b) PMN (N = 326 schemes), and c) GPDD (N = 177 schemes) and d) one for North America <sup>3</sup>; N = 311 schemes); shown here for comparison only), or combinations of databases: e) DaEuMon, PMN and GPDD, f) all four databases.



**Supplementary Figure S2.** Relative proportions of each data type collected by biodiversity monitoring schemes over time: per decade from 1950 onward (left) and per year from 1990 onward (right). The number of schemes considered is indicated above each bar.



□Population structure □Phenology ■CMR ■Occurrence ■Count

**Supplementary Figure S3.** Examples of the identification of the value of anthropogenic pressure when biodiversity monitoring schemes start, provided for each pressure. The intersect between the starting year of a biodiversity monitoring scheme (dashed black line) with the regression trend of the anthropogenic pressure (plain bold red line) was projected to the intersect on the pressure axis (i.e. y-axis) to determine the pressure value for that year.



## **Supplementary References:**

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- 2. Inchausti P, Halley J. On the relation between temporal variability and persistence time in animal populations. *J Anim Ecol* **72**, 899-908 (2003).
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