

120 prioritaire soorten kunnen we de (genetische) toestand van hun populaties voldoende evalueren?



Joachim Mergeay & Luis Alberto Castillo Reina

RESEARCH INSTITUTE
NATURE AND FOREST

Europese Natuurherstelwet 6/11/23



Evaluatie van genetische indicatoren van het Kunming-Montreal Global Biodiversity Monitoring Framework



Joachim Mergeay & Luis Alberto Castillo Reina

RESEARCH INSTITUTE
NATURE AND FOREST

Europese Natuurherstelwet 6/11/23





THE COALITION FOR CONSERVATION GENETICS



Society for Conservation Biology

Society for Conservation Biology
Conservation Genetic Working Group

Genomic Biodiversity
Knowledge for Resilient Ecosystems



Management: SCB CGWG

Increasing awareness and use of genetic diversity in management

Interpretation: G-BIKE

Establishing the use of genomic data as standard practice for monitoring

Fostering relationships and partnerships between academia and practitioners

Raising awareness of the importance of genetic diversity

Coalition for Conservation Genetics

Developing and improving tools for genetic monitoring

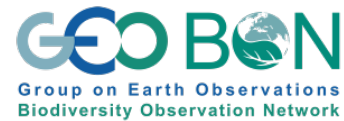
Policy: IUCN CGSG

Applying genetics to threatened species management and decision making

Development and analysis of genetic data for conservation

Research: GEO BON GCWG

Aggregating, supporting and leveraging genetic biodiversity data



CONSERVATION GENETICS
SPECIALIST GROUP

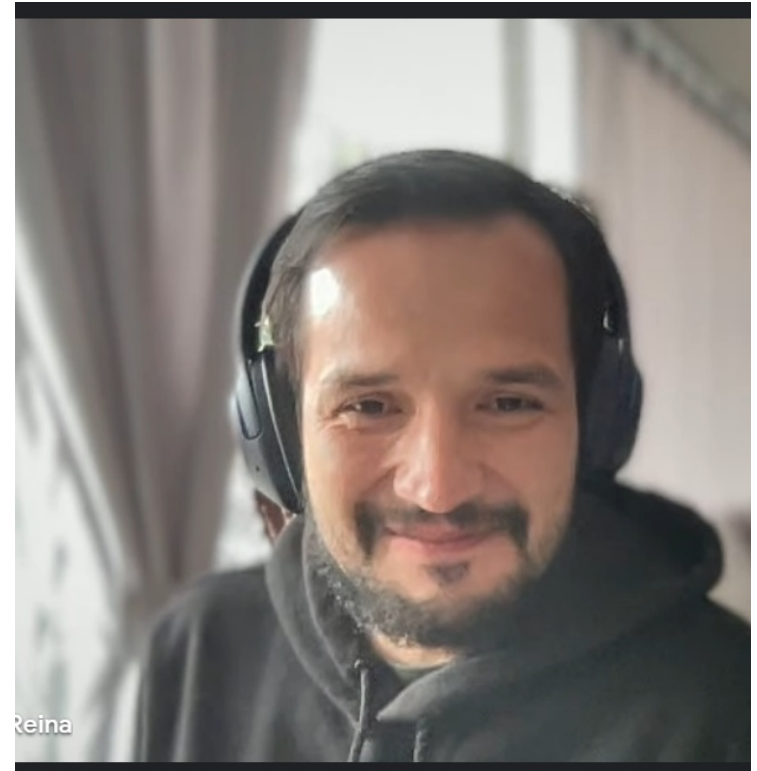
International Union for Conservation of Nature
Conservation Genetics Specialist Group

Group on Earth Observations
Biodiversity Observation Network
Genetic Composition Working Group



Plus expert advies/input/info van
soortenkenners v INBO

Wouter Van Landuyt
Sam Provoost
Jeroen Speybroeck
Dirk Maes
Geert De Knijf
Arno Thomaes
Gerlinde Van Thuyne
En vele anderen



Luis Alberto Castillo Reina en het hele
CCG-team



Kunming-Montreal GBF



2020 UN BIODIVERSITY CONFERENCE

COP 15 - CP/MOP 10-NP/MOP 4

Ecological Civilization-Building a Shared Future for All Life on Earth

KUNMING – MONTREAL

2030 Target 4

“... maintain and restore the genetic diversity within and between populations of native, wild and domesticated species to maintain their adaptive potential, including through in situ and ex situ conservation and sustainable management practices”

2050 Objective A

“...genetic diversity within populations of wild and domesticated species, is maintained, safeguarding their adaptive potential, ...”

Kunming-Montreal GBF

Biological Conservation 248 (2020) 108654



Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon



Policy analysis

Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved



Sean Hoban^{a,*,1,2}, Michael Bruford^{b,1,2}, Josephine D'Urban Jackson^b, Margarida Lopes-Fernandes^{c,1}, Myriam Heuertz^d, Paul A. Hohenlohe^e, Ivan Paz-Vinas^{z,2}, Per Sjögren-Gulve^{f,1}, Gernot Segelbacher^{g,1,2}, Cristiano Vernesi^{h,1,2}, Sally Aitkenⁱ, Laura D. Bertola^{j,1,2}, Paulette Bloomer^k, Martin Breed^l, Hernando Rodríguez-Correa^m, W. Chris Funk^{n,1,2}, Catherine E. Grueber^o, Margaret E. Hunter^{p,1,2}, Rodolfo Jaffe^q, Libby Liggins^r, Joachim Mergeay^{s,t,2}, Farideh Moharrek^{u,v}, David O'Brien^w, Rob Ogden^{x,1,2}, Clarisse Palma-Silva^y, Jennifer Pierson^{aa,2}, Uma Ramakrishnan^{ab}, Murielle Simo-Droissart^{ac}, Naoki Tani^{ad}, Lisette Waits^{ae,1,2}, Linda Laikre^{af,1}



Flanders
State of the Art

Kunming-Montreal GBF

INDICATORS

The number of populations within species with an effective population size (N_e) above 500 compared to the number below 500

The proportion of populations maintained within species

The number of species and populations in which genetic diversity is being monitored using DNA-based methods

DATA SOURCE FOR INDICATOR

Assessment of N_e from demographic or genetic data

Proxy for N_e in absence of genetic data:
10% of census size

Comprehensiveness index

livingplanetindex.org

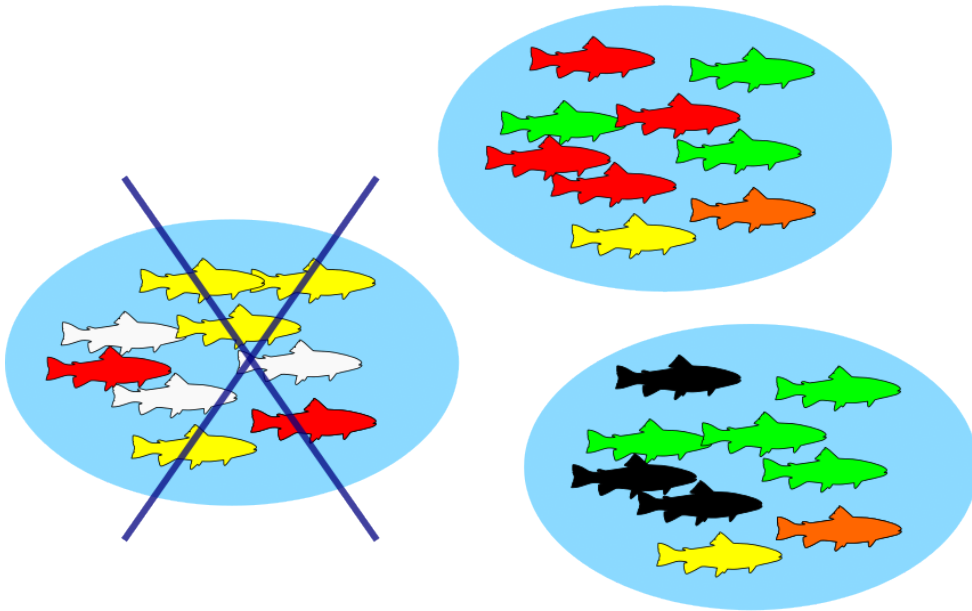
Scientific publications/
management reports

Number of submissions of genetic data to international, public databases

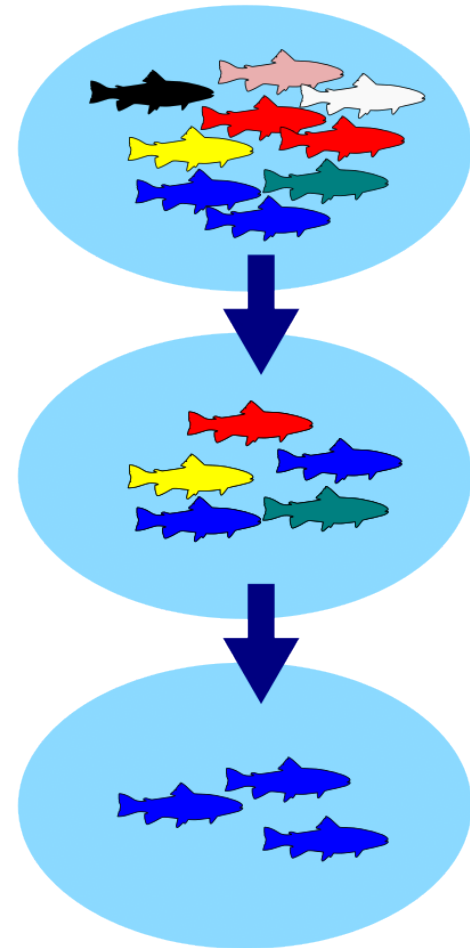
Headline Indicator A 4.0

Complementary Indicator

Loss of genetically distinct populations



Loss of diversity in small populations



PERSPECTIVE

Monitoring status and trends in genetic diversity for the Convention on Biological Diversity: An ongoing assessment of genetic indicators in nine countries

Sean Hoban^{1,2}  | Jessica M. da Silva^{3,4} | Alicia Mastretta-Yanes^{5,6} | Catherine E. Grueber⁷  | Myriam Heuertz⁸  | Margaret E. Hunter⁹ | Joachim Mergeay^{10,11} | Ivan Paz-Vinas¹²  | Keiichi Fukaya¹³ | Fumiko Ishihama¹³ | Rebecca Jordan¹⁴ | Viktoria Köppä¹⁵ | María Camilla Latorre-Cárdenas¹⁶ | Anna J. MacDonald¹⁷  | Victor Rincon-Parra¹⁸ | Per Sjögren-Gulve¹⁹  | Naoki Tani^{20,21} | Henrik Thurfjell²² | Linda Laikre¹⁵ 

Proposed indicators of genetic diversity

1

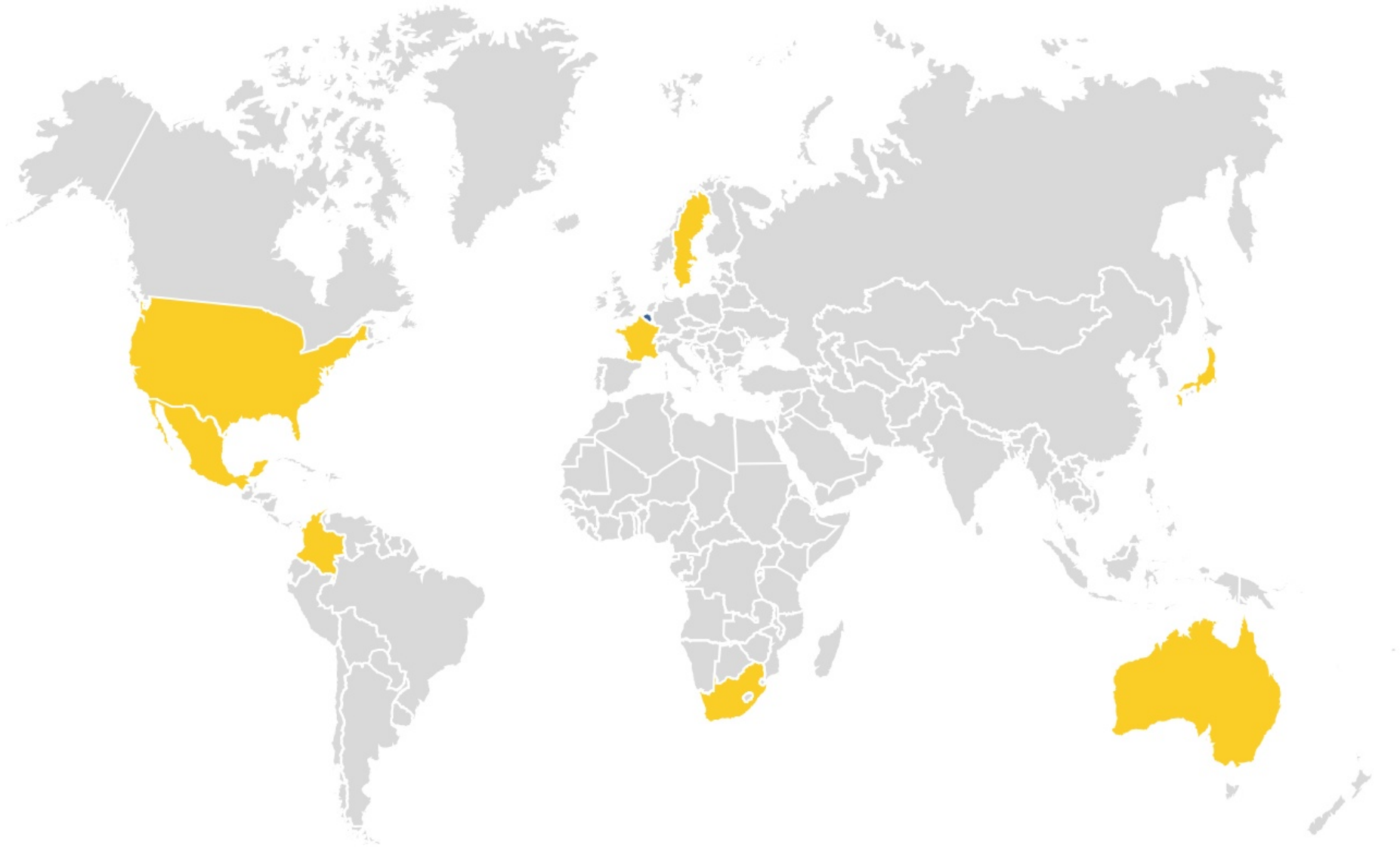
Number of populations within species with **effective population size (Ne) above 500** versus those with Ne below 500

2

The proportion of distinct **populations maintained** within species

3

Number of species and populations in which genetic diversity is being **monitored using DNA based methods**



Policy Brief SBSTTA 25, Nairobi 15-19-10/23

Genetic diversity indicators for the Global Biodiversity Framework are developed, tested and ready for implementation

POLICY BRIEF

SUMMARY

Genetic diversity is a vital part of populations, species and ecosystem resilience - and can be monitored and reported on using simple indicators that do not need DNA analysis and have data available. Genetic diversity indicators can be compiled for 100+ species per country quickly, and have national and local benefits. Assessment of 900 species of plants and animals across nine countries has shown: (a) most populations are maintained BUT (b) in most species, many populations are too small and are losing genetic diversity. Guidance and support for indicator implementation are available.

The Kunming-Montreal GBF requires conserving genetic diversity of all species

- Genetic diversity helps species adapt to changing conditions, contributes to ecosystem resilience, and improves ecological restoration success.
- Genetic diversity is declining due to habitat loss, fragmentation, overharvest, and other human activities.

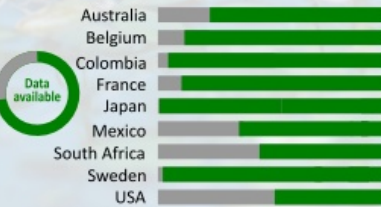
Parties to the CBD are now required to report progress on conserving genetic diversity using indicators of genetic status

- The proportion of populations within species with an effective population size $N_e > 500$ (Headline indicator A.4.0).
- The proportion of populations maintained within species.

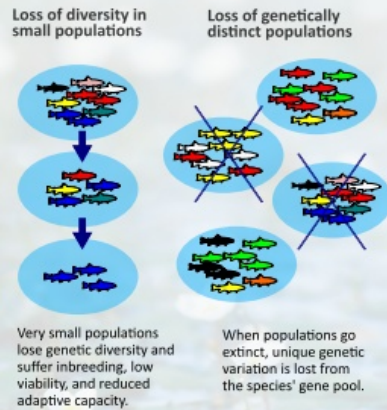
Genetic diversity is variation at the DNA level, but DNA data are not essential to assess genetic diversity indicators. The indicators use reliable proxies for genetic diversity change.

Why should genetic diversity be monitored using indicators?

Genetic diversity indicators are useful conservation tools, even beyond the CBD, to guide conservation action, endangered species management, and help communicate with the public about genetic threats.



Green bars show proportion of species with enough data available - which is the majority of species.



Genetic diversity indicators have been used in nine countries across the world including megadiverse countries- and the genetic diversity situation is critical!

- Indicators were assessed for >900 species from Australia, Belgium, Colombia, France, Japan, Mexico, Sweden, South Africa, and USA. 72% of species had data for at least one of the indicators.
- The indicators are affordable and feasible with existing data and require limited time.
- They are applicable and comparable in all countries, taxonomic groups, and ecosystems.
- The indicators show many populations are at a threshold of dramatic genetic diversity decline unless swift action is taken.

Turn the page to read more.



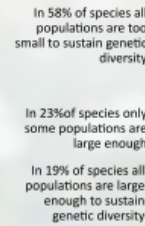
90% of populations of *Luronium natans* (Belgium) are too small to maintain genetic diversity

What type of data are needed and is the process practical for most countries?

- Useful information includes current or recent population sizes, and number of current and lost populations - even rough estimates (e.g., less than 1000, many thousands).
- Data can be gathered from experts, existing research or management reports, agency databases, NGOs, local knowledge, citizen science data (e.g., iNaturalist), or GIS based estimates.
- Populations can be defined using geographic isolation, genetic knowledge, ecoregion/ habitat differences, dispersal radius, or other information.
- If there is uncertainty, multiple estimates can be used.

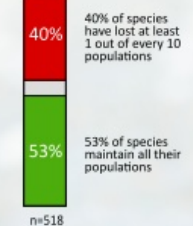
HEADLINE indicator A.4

% of populations within species with $N_e > 500$



Complementary indicator

% of populations maintained



Fewer than 5000 individuals remain of *Capensibufo rosei* (South Africa), with only 2 of the 6 populations maintained.

What are the capacity needs?

- Personnel (ideally with knowledge of biodiversity databases, national reporting, management plans, etc.) compile the information- about 400 hours to do 100 species.
- If coordinated with Red Listing efforts, this time can be greatly reduced.
- The country does not need DNA-based genetic research or infrastructure. All data can come from non-genetic sources.
- Hundreds of species can be analyzed with the genetic diversity indicators much faster and more affordably than DNA based studies.
- Still, DNA based projects do provide more detailed and accurate information on species' genetic health.

Guidance for the indicators is available

- Help is available to advise on how to calculate and report the indicators and include them in National Reports and National Biodiversity Strategy and Action Plans, and use them for national or local policy and management. Use the QR codes below!

Next steps?

- UNEP metadata is complete. More support is being developed. Additional written and video guidance will be available by January 2024.
- We suggest the CBD Glossary should now include more genetic terms to help Parties in their reporting.



The genetic diversity indicators have also been estimated in crop wild relatives such as this wild cotton (*Gossypium hirsutum*, Mexico).



Follow the QR link for details of the approach



THE COALITION FOR CONSERVATION GENETICS

Visit our website for more information



Follow the QR link for details of the approach



THE COALITION FOR CONSERVATION GENETICS

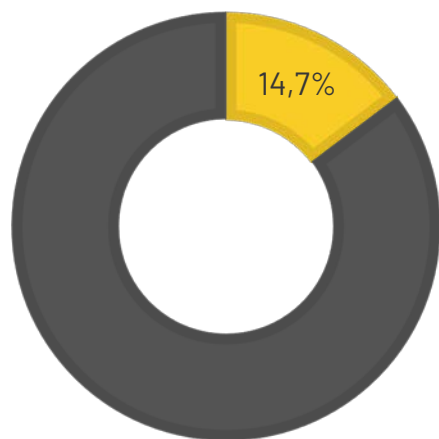
Visit our website for more information



Biodiversity in Belgium

30 x 30 Goal
All signatory countries
Global Biodiversity Framework

PERCENTAGE OF LAND COVERED BY PROTECTED AREAS



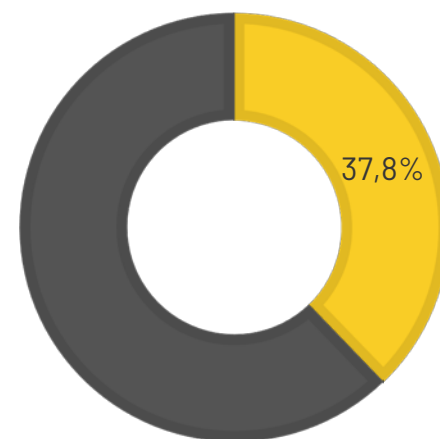
What



By 2030 at least 30%



PERCENTAGE OF MARINE WATERS COVERED BY PROTECTED AREAS

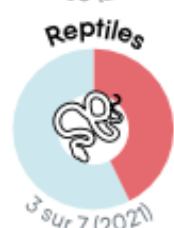
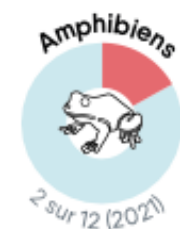


European Environmental Agency, 2023

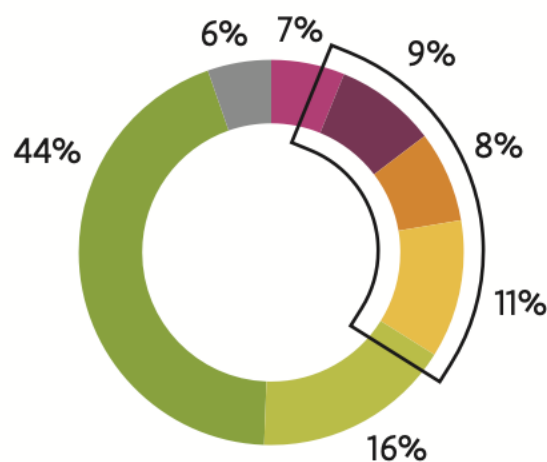
© 2023 WWF

Biodiversity in Belgium

Wallonie

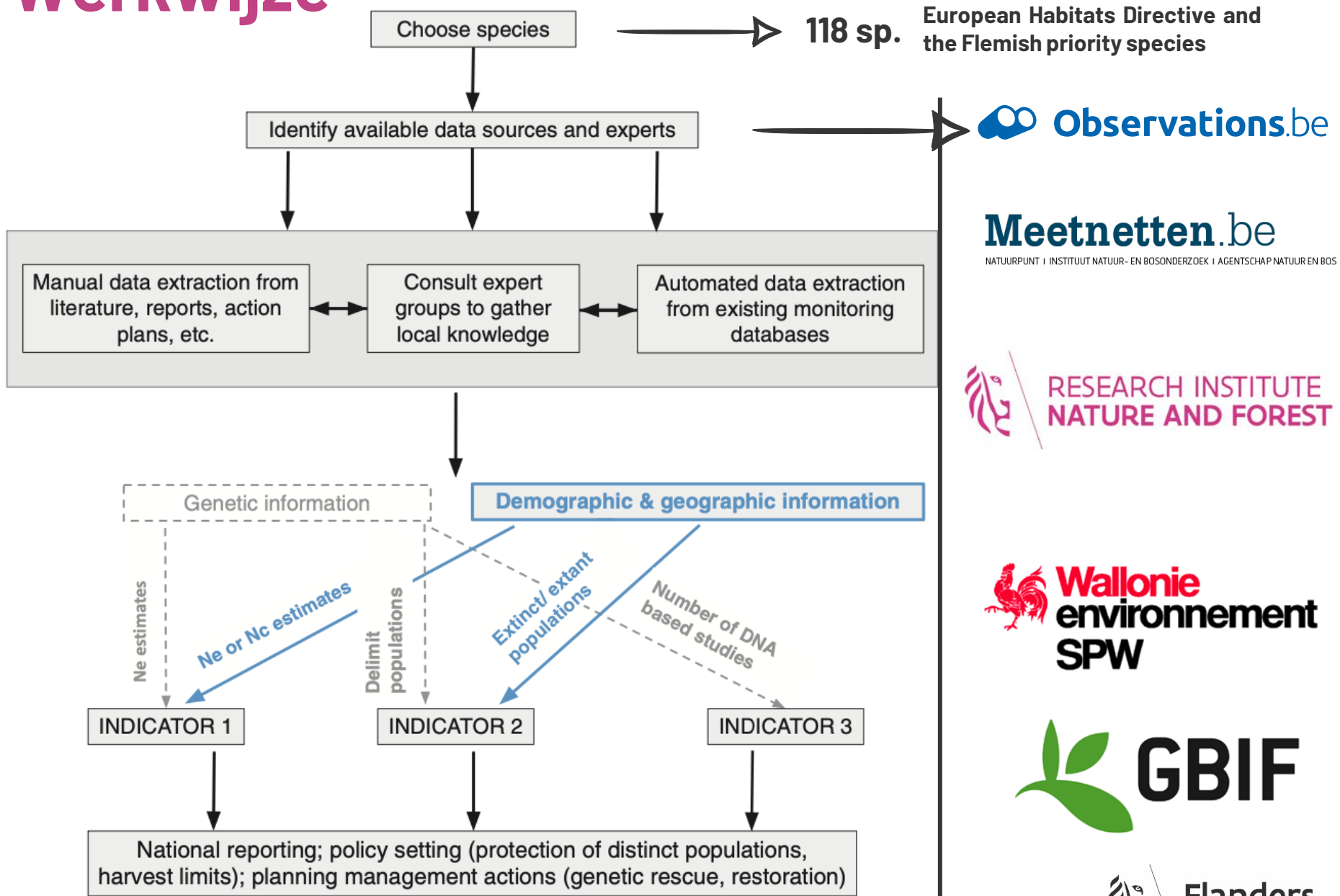


Vlaanderen



- Regionally extinct
- Critically endangered
- Endangered
- Vulnerable
- Near threatened
- Least concern
- Data deficient

Werkwijze



Hoban et al., 2023

 **Observations.be**

Meetnetten.be
NATUURPUNT | INSTITUUT NATUUR- EN BOSONDERZOEK | AGENTSCHAP NATUUR EN BOS

 **RESEARCH INSTITUTE
NATURE AND FOREST**

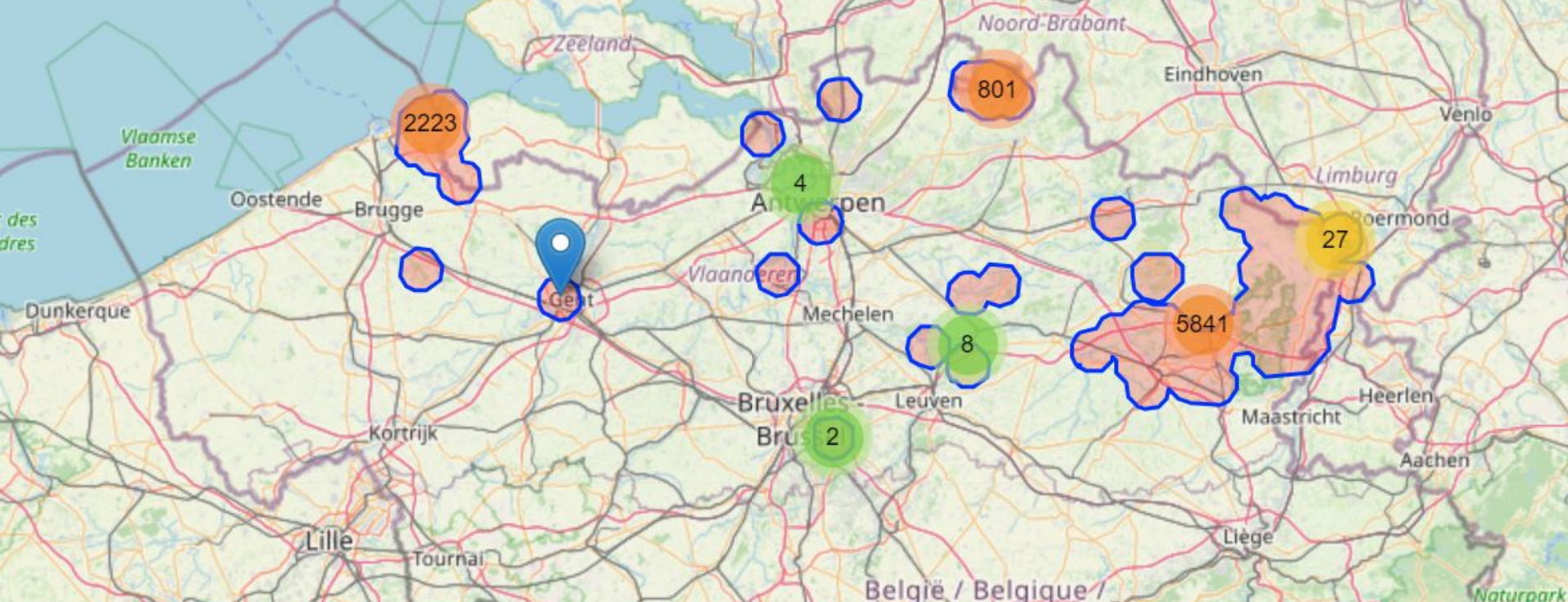
 **Wallonie
environnement
SPW**

 **GBIF**

 **Flanders
State of the Art**



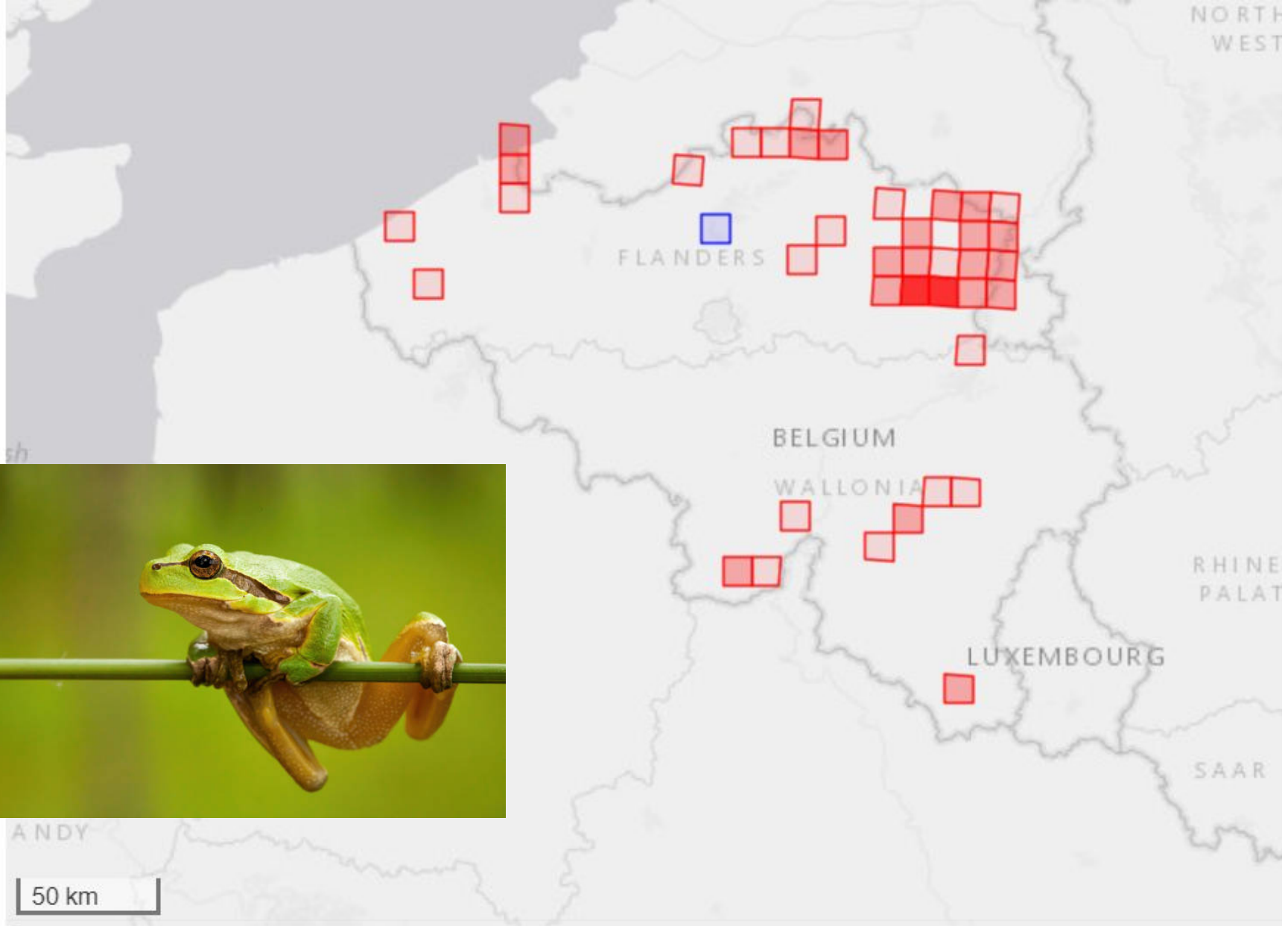
1. Data primarily sourced from observations.be databases for the period 2012-2022
2. Georeferencing for map creation.
3. Literature reviews determined species dispersion ranges.
4. Buffers around georeferenced points based on species' ranges.
5. Merged overlapping buffers for dispersion polygons.
6. Polygons as population representations.
7. Validation via additional references and expert consultations.





ANDY

50 km



Summed 4785 maximum number of individuals in 40 cells (min: 1 median: 5 max: 1500). Tl

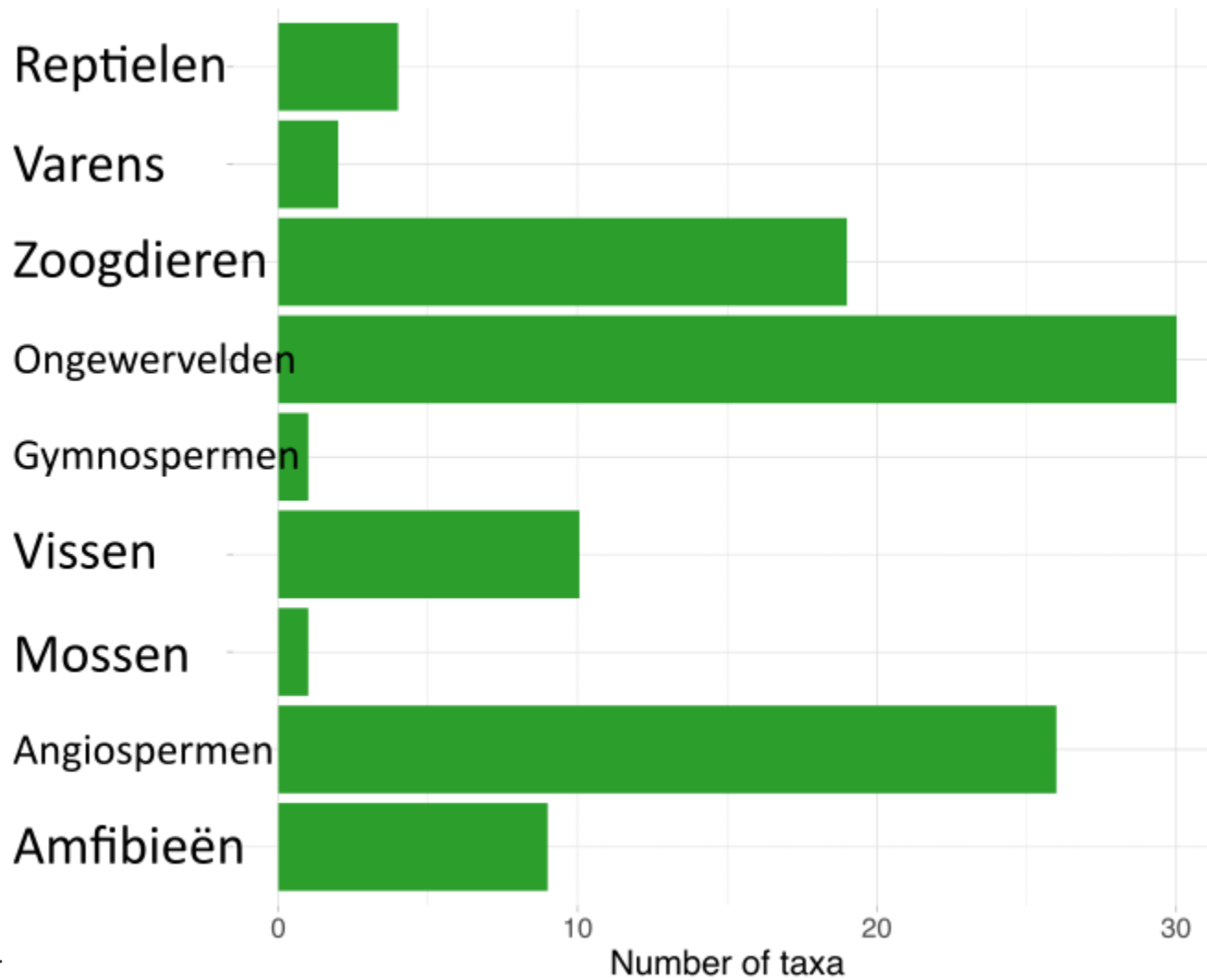
■ Natural occurrence ■ Only escapes

art



1968-1978

118 soorten



Proposed indicators of genetic diversity

1

Number of populations within species with **effective population size (Ne) above 500** versus those with Ne below 500

2

The proportion of distinct **populations maintained** within species

3

Number of species and populations in which genetic diversity is being **monitored using DNA** based methods

Results

Effective population size (N_e) above 500

1

Data availability

Population size data availability

Population level Species or subspecies level Insufficient data



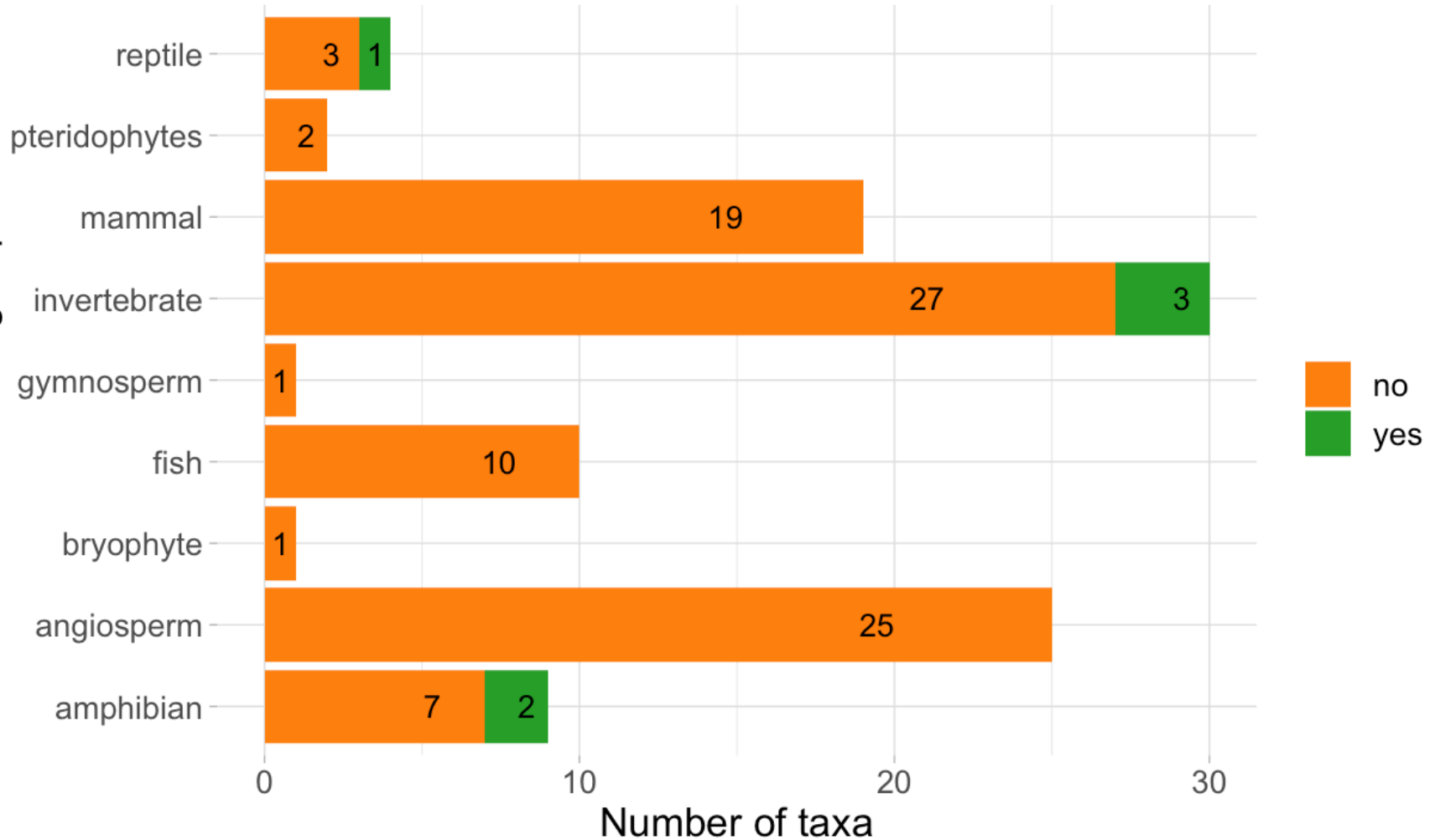
Results

Effective population size (N_e) above 500

1

Data availability

N_e available (from genetic data)



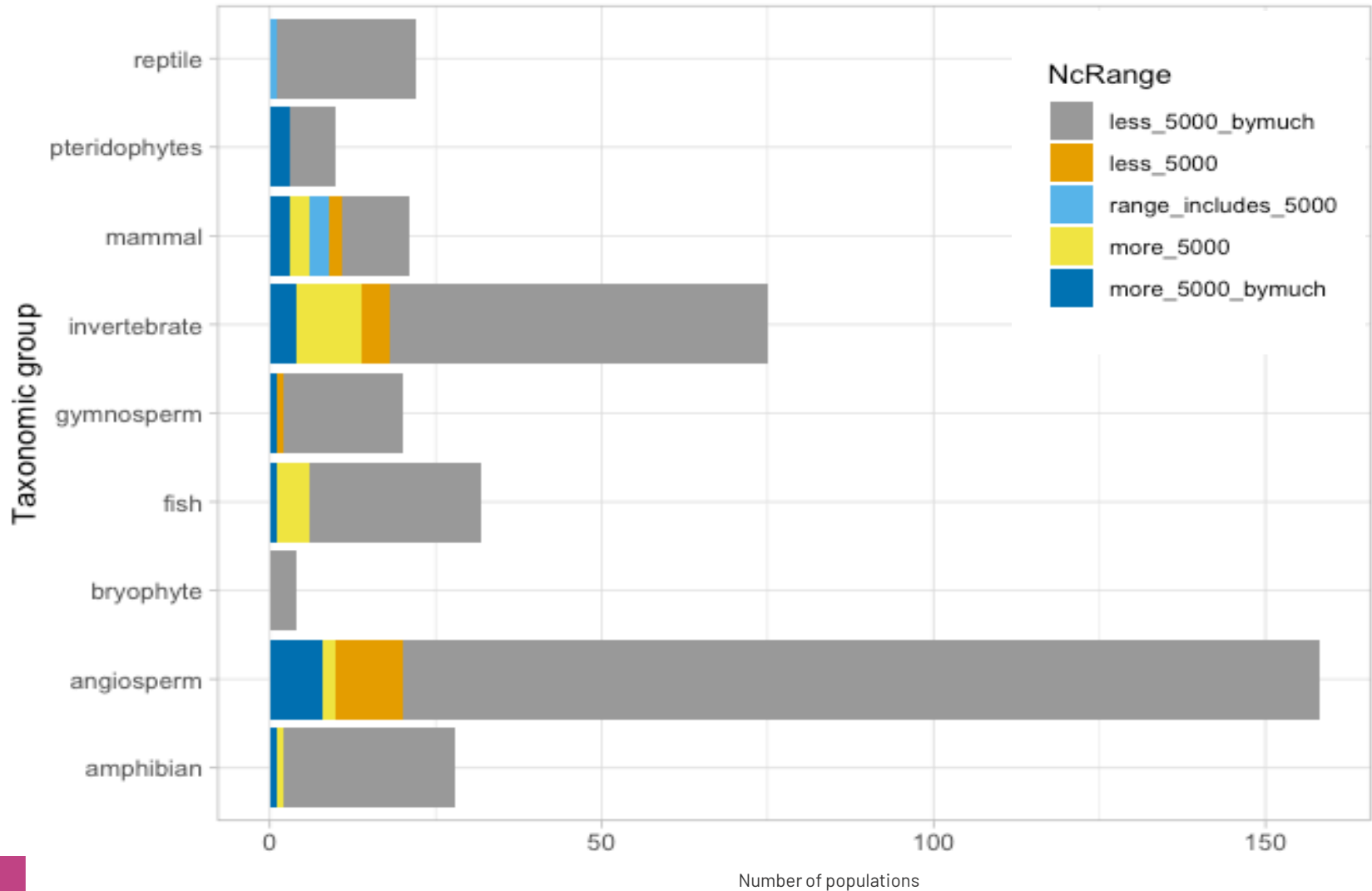
Results

Effective population size (N_e) above 500

1

Population sizes

Population size by N_c Range

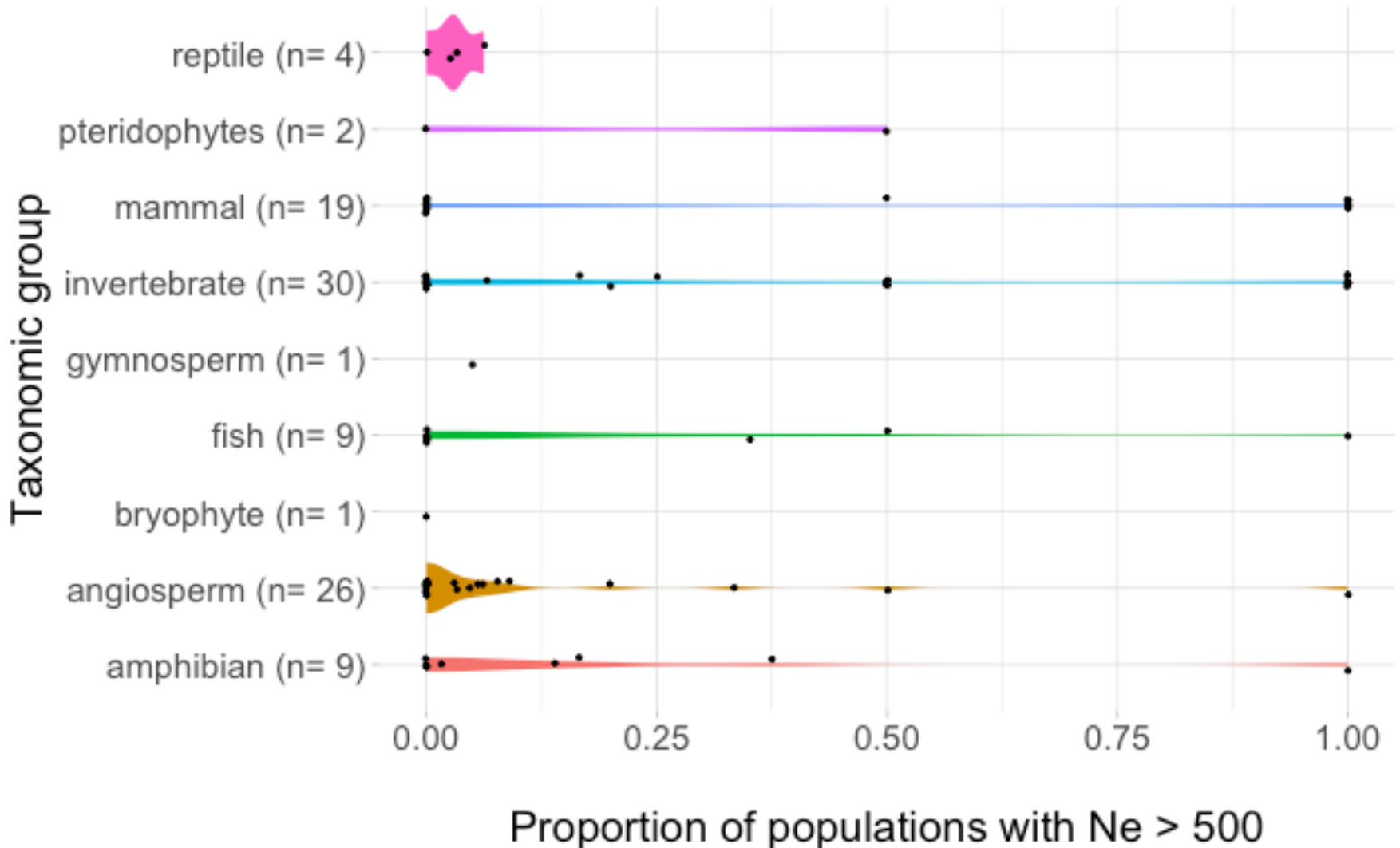


Results

Effective population size (N_e) above 500

1

Population sizes



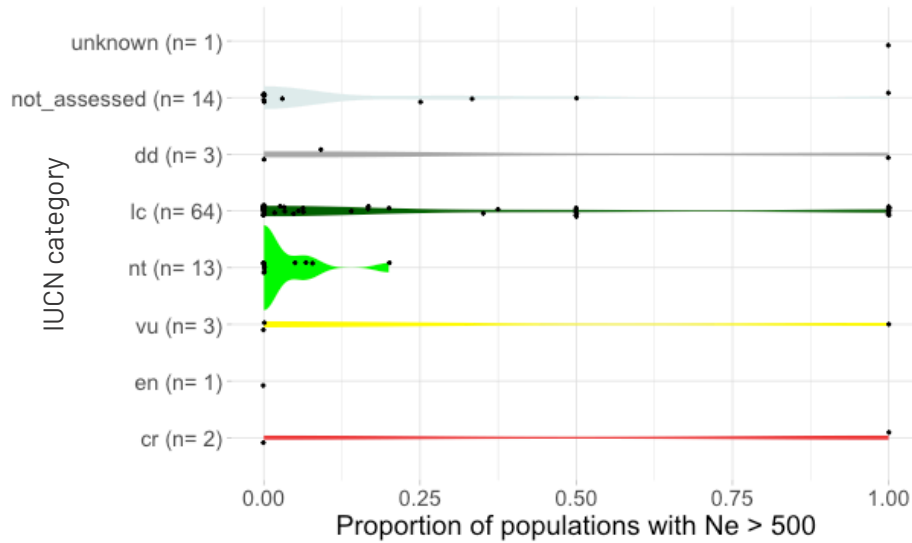
Results

Effective population size (N_e) above 500

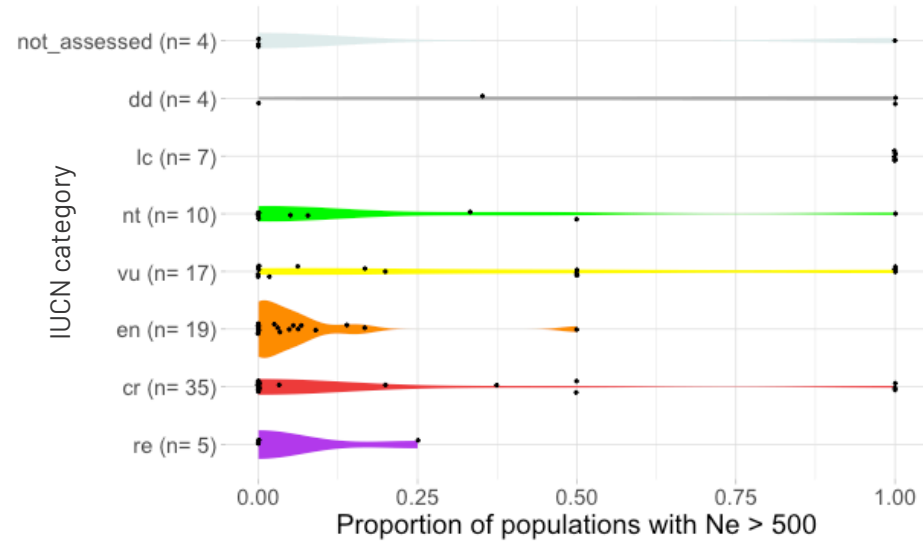
1

Comparison IUCN

Global Red List



Regional Red List



Proposed indicators of genetic diversity

1

Number of populations within species with **effective population size (Ne) above 500** versus those with Ne below 500

2

The proportion of distinct **populations maintained** within species

3

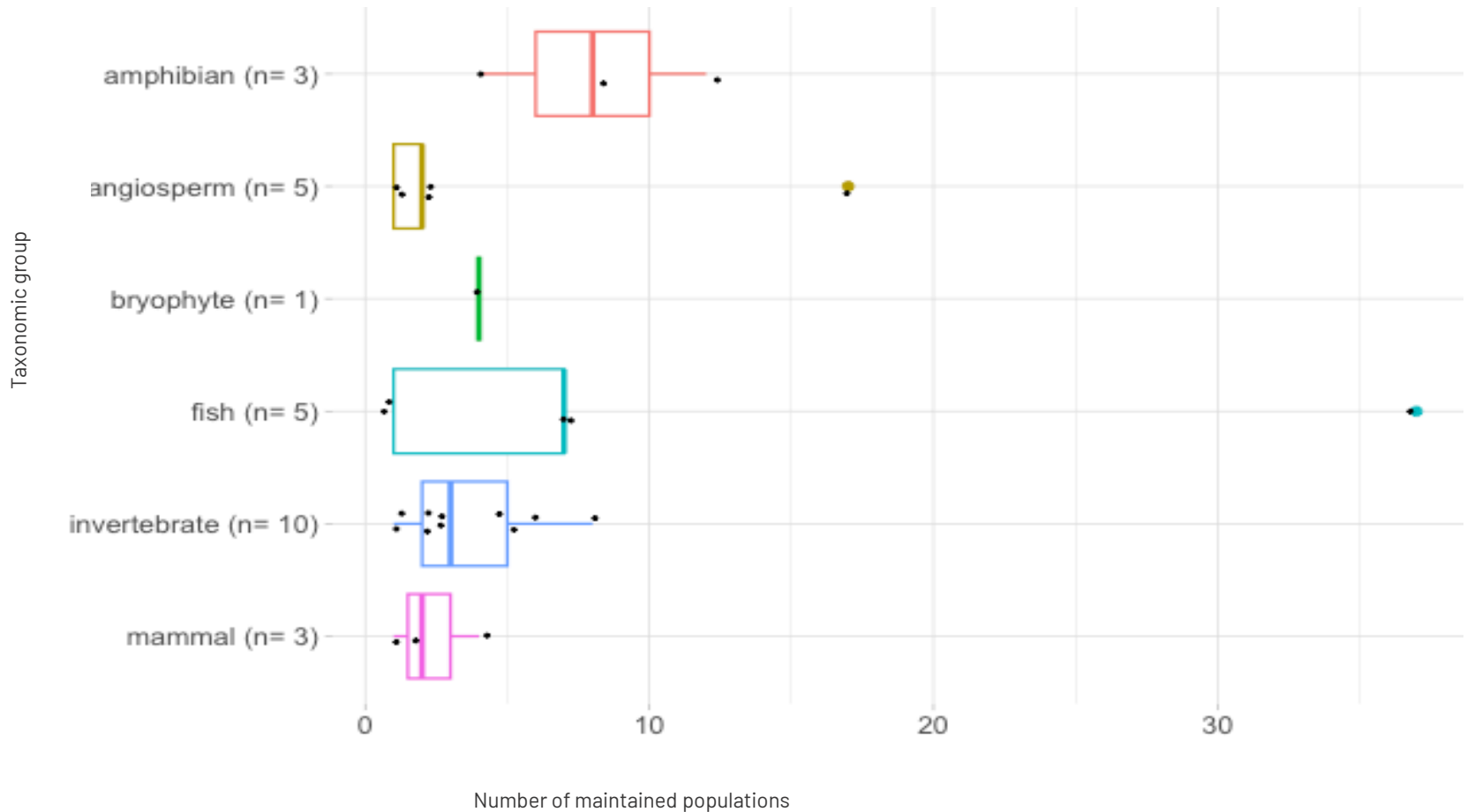
Number of species and populations in which genetic diversity is being **monitored using DNA** based methods

Results

Populations
maintained

2

Data availability – Number of Populations

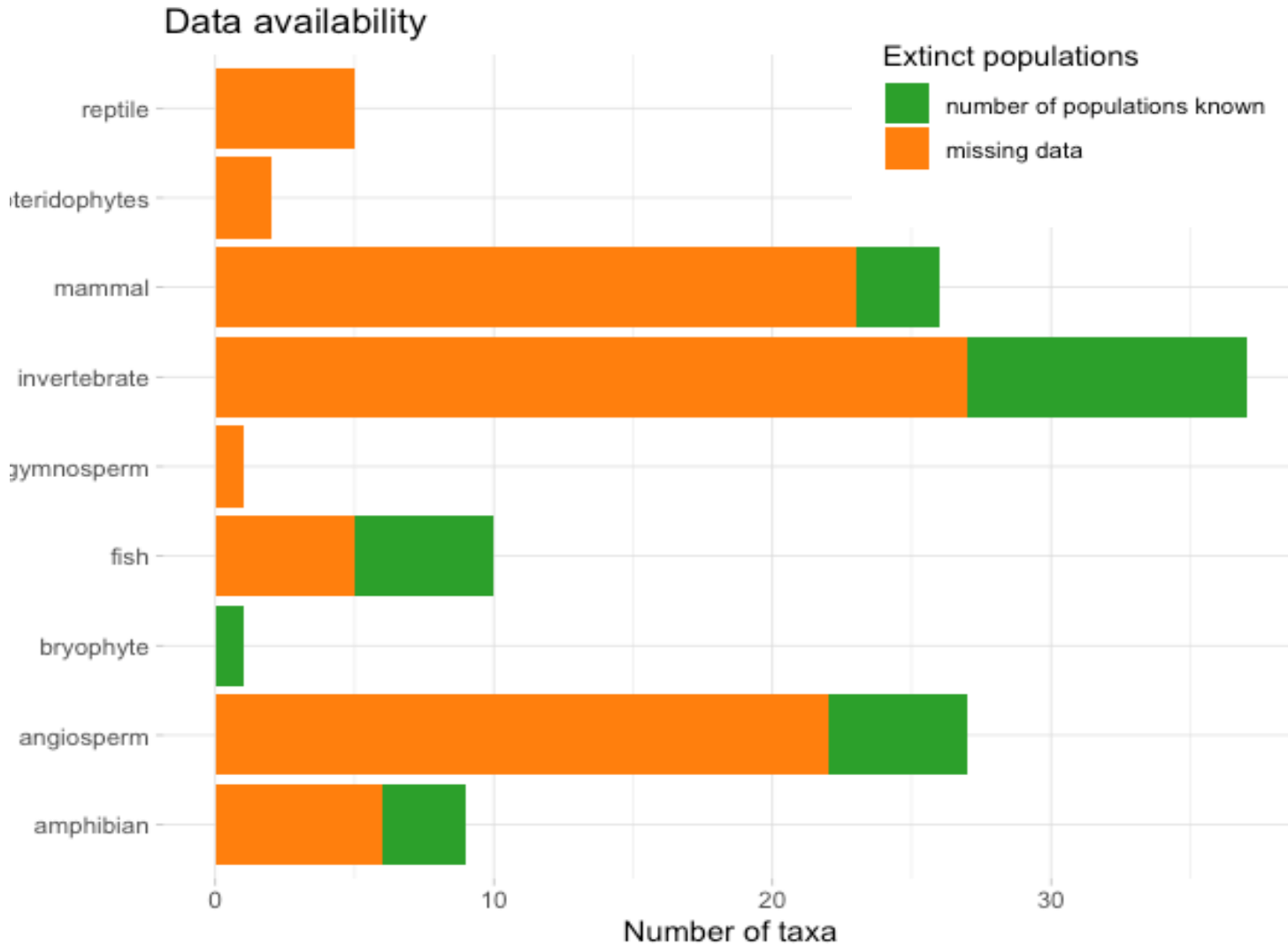


Results

Populations
maintained

2

Data availability – Number of Populations

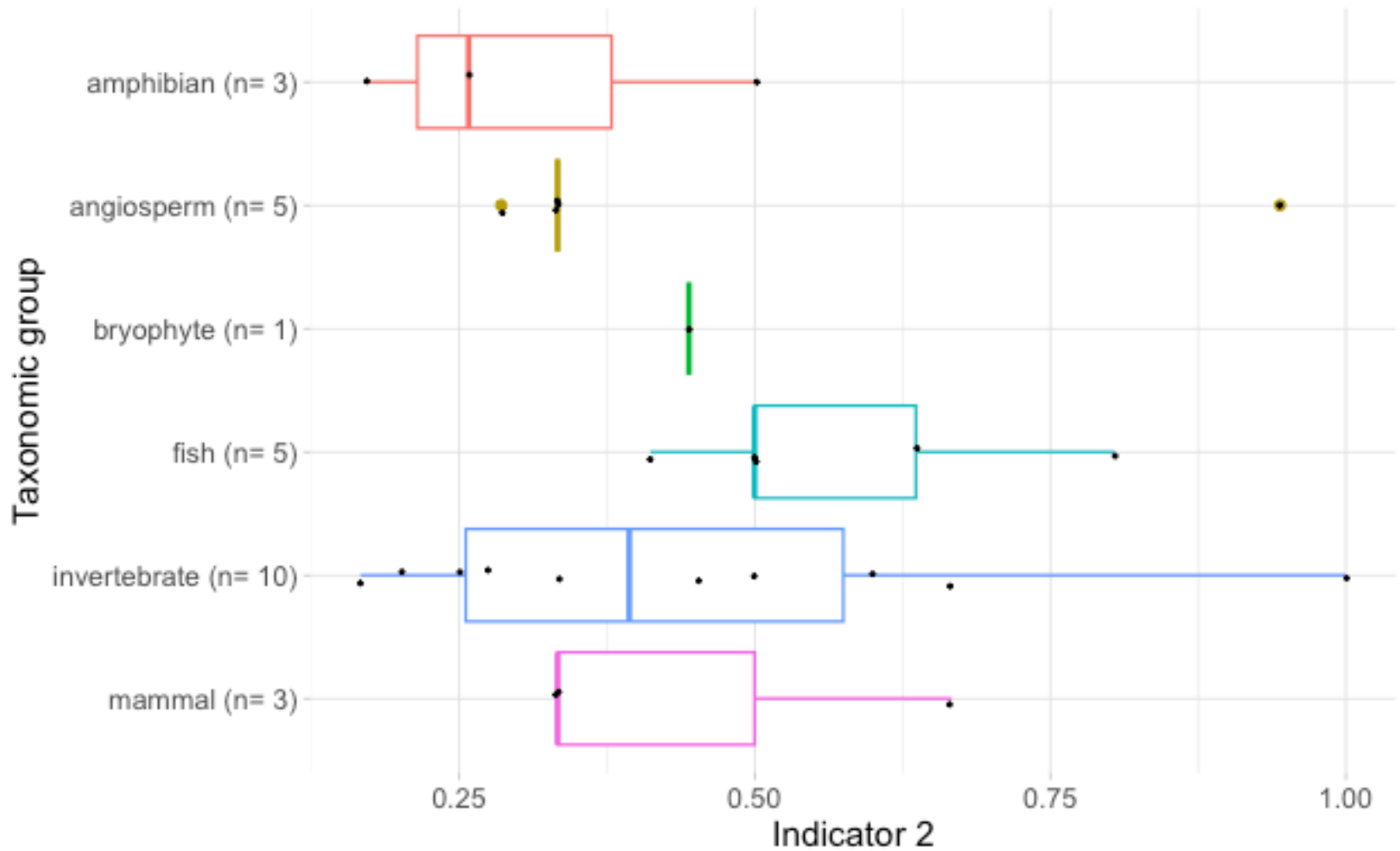


Results

Populations maintained

2

Proportion of populations maintained



Proposed indicators of genetic diversity

1

Number of populations within species with **effective population size (Ne) above 500** versus those with Ne below 500

2

The proportion of distinct **populations maintained** within species

3

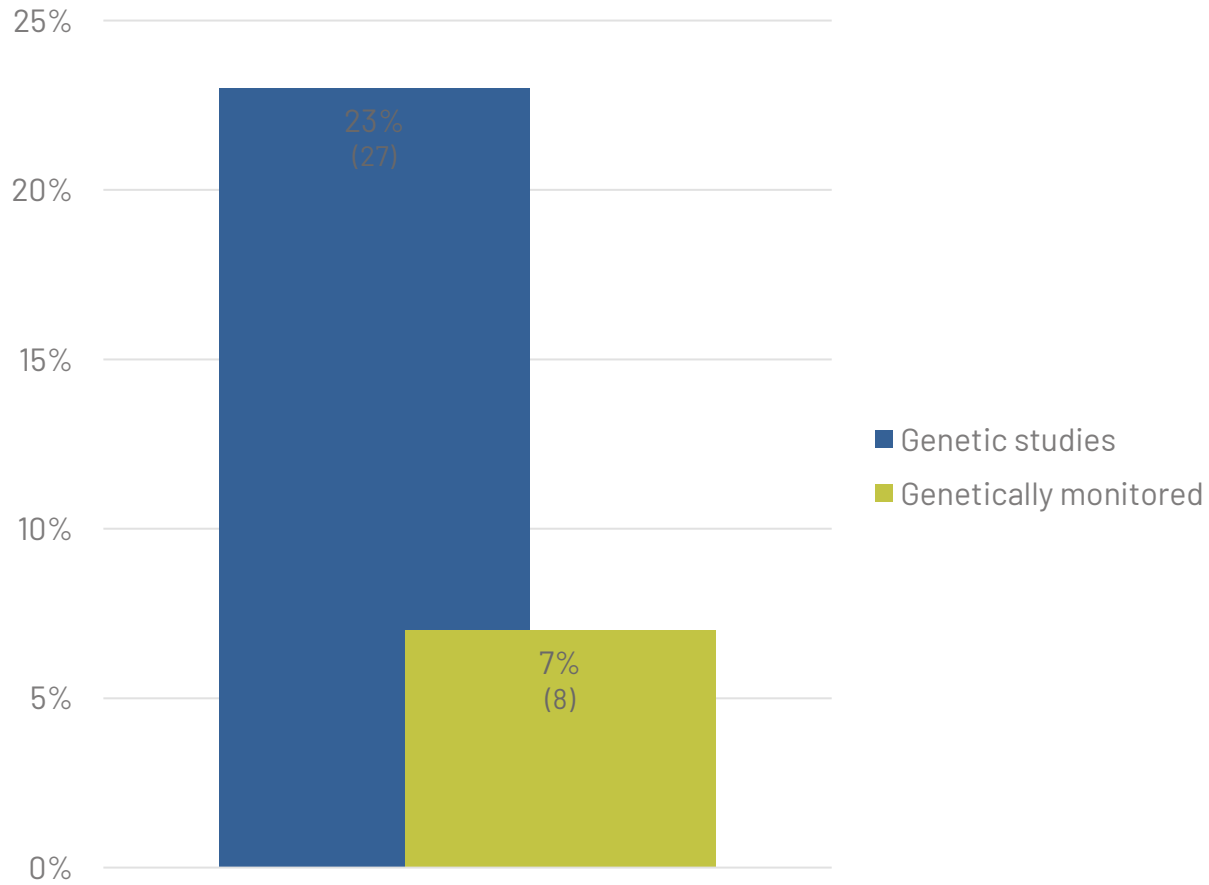
Number of species and populations in which genetic diversity is being **monitored using DNA** based methods

han et al., 2020; Frankham, 2022; Laikre et

Results

3

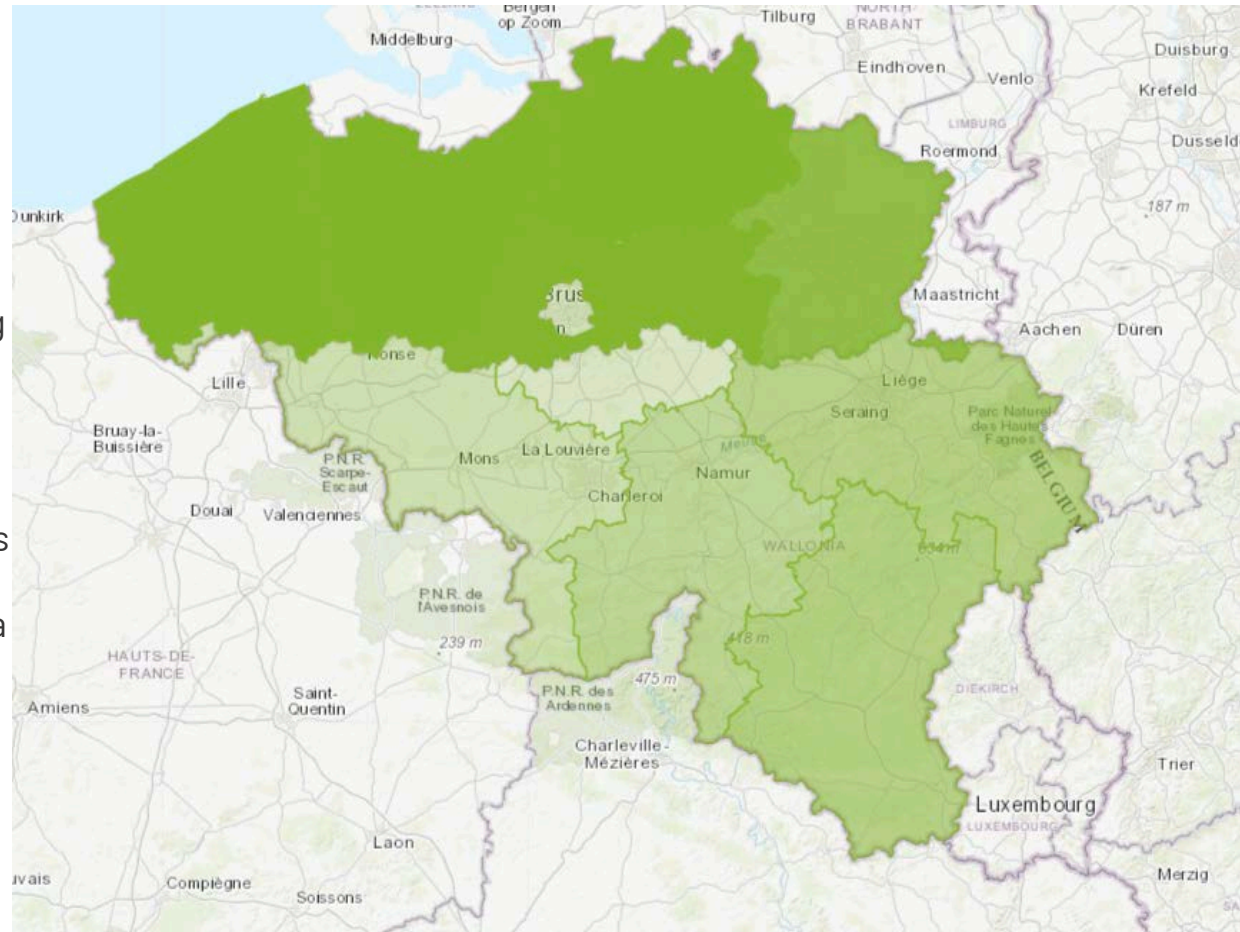
DNA monitored species



Perspectives

- Citizen science bias & afstemming
- Maintained populations
- Insufficient Species Data necessitates genetic assessments
- Validation with actual genetic data (*rana arvalis*)

Number of observers for all species groups in 2022



CC-BY-NC. Observations.be

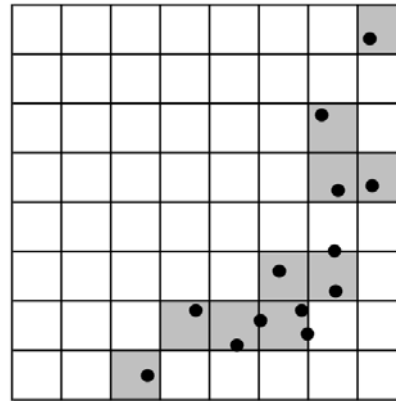
Citizen science, smartphones and AI

- Every citizen is a data provider
- Smartphones are globally becoming ubiquitous
- Inaturalist, Obsidentify, ...
- Ask users to provide numbers as much as possible!

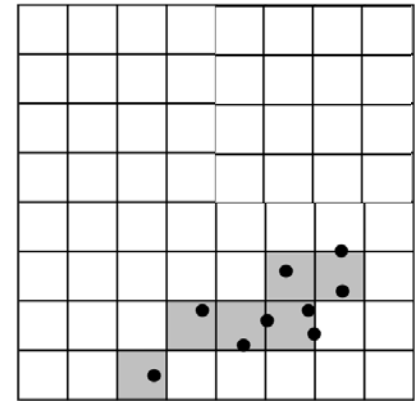


Perspectives

- Citizen science bias & afstemming
- Maintained populations
- Insufficient Species Data necessitates genetic assessments.
- Validation with actual genetic data (*rana arvalis*)



Time 1
A00 = 160 km²
#Pop = 13



Time 2
A00 = 96 km² (-40%)
#Pop = 9 (-30%)

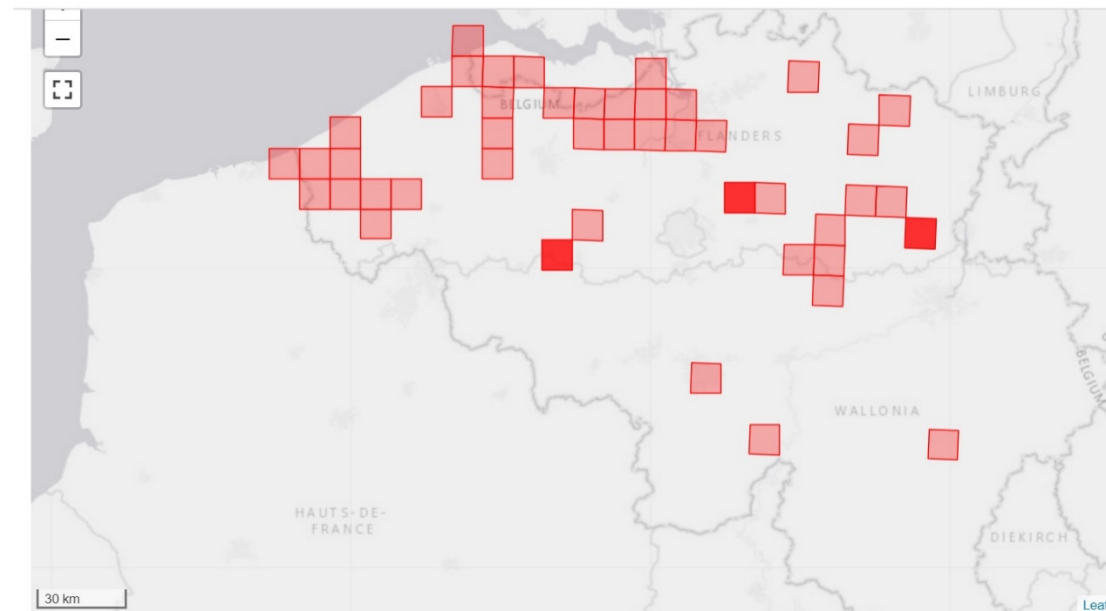
Perspectives

- Citizen science bias & afstemming
- Maintained populations
- Insufficient Species Data necessitates genetic assessments.
- Validation with actual genetic data (*rana arvalis*)



Rollin Verlinde - Vilda. <https://www.ecopedia.be/>

Crocidura leucodon

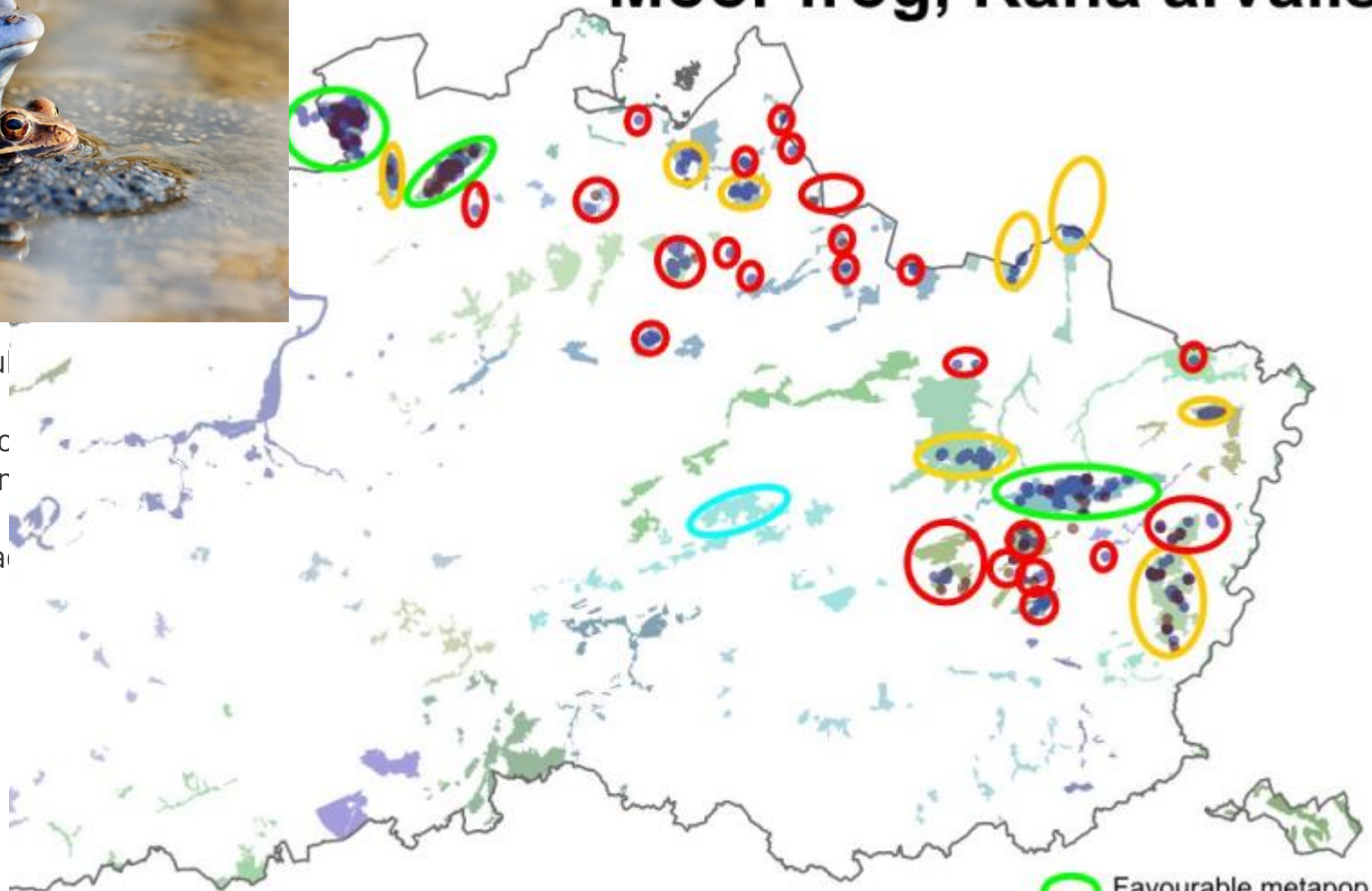


Opgeteld 67 maximum individuen in 45 cellen (min: 1 median: 1 max: 5). Deze soort is vervaagd, individuele waarnemingen en heatmaps zijn nie



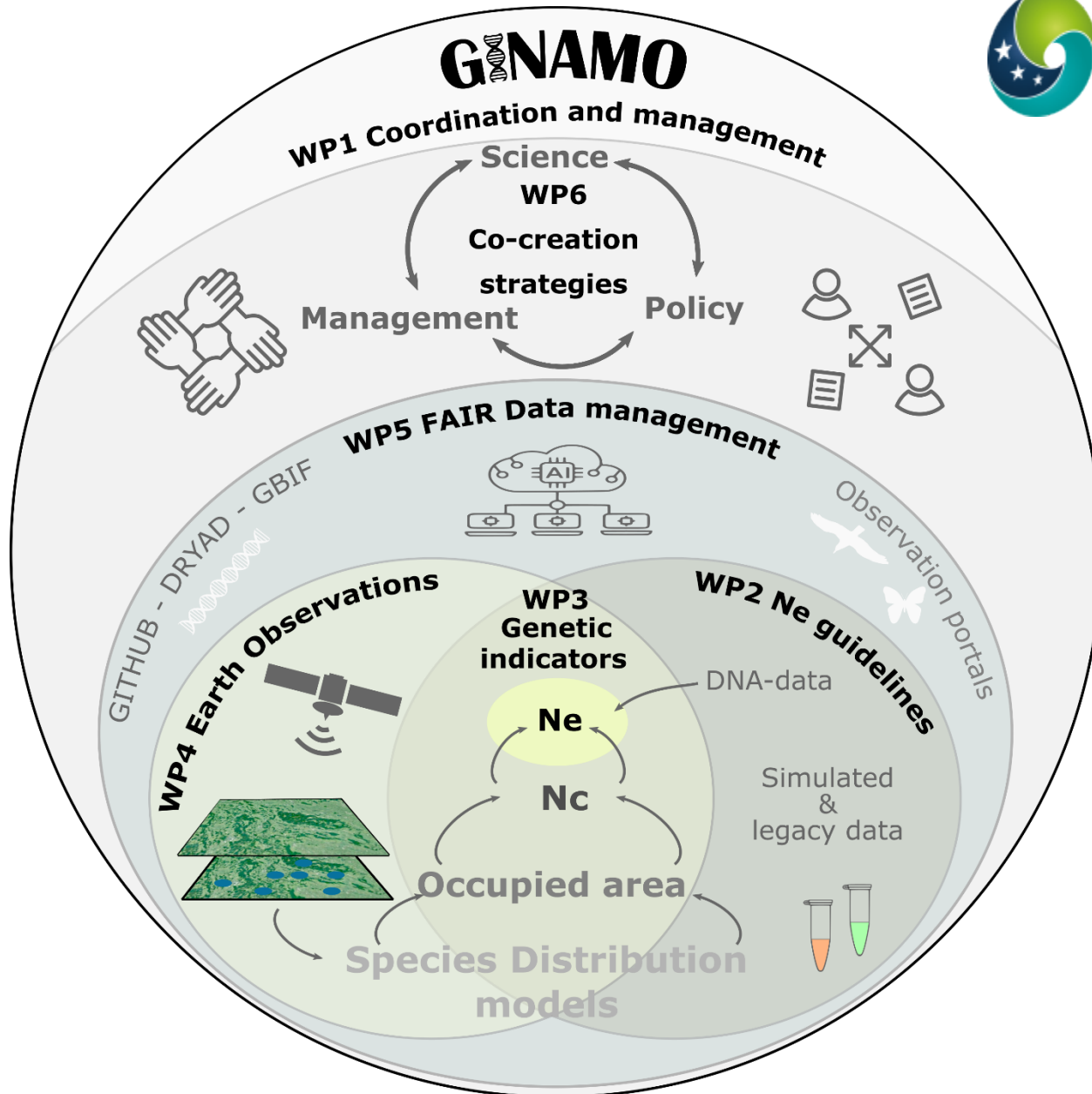
Moor frog, *Rana arvalis*

- Maintained popul
- Insufficient Spec necessitates ger
- Validation with a (*rana arvalis*)



- Favourable metapop
- Unfavourable
- favourable potential
- uncertain

Genetic Indicators for Nature Monitoring



Genetic Indicators for Nature Monitoring



Genetic or census data

Occurrence data
e.g. GBIF

Vegetation habitat
mapping

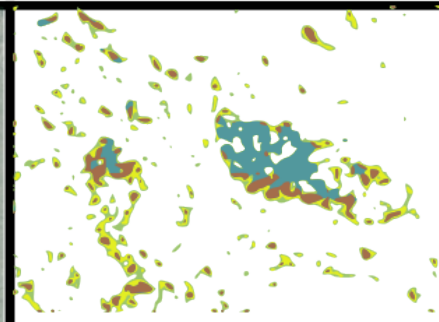
Remote sensing
habitat mapping



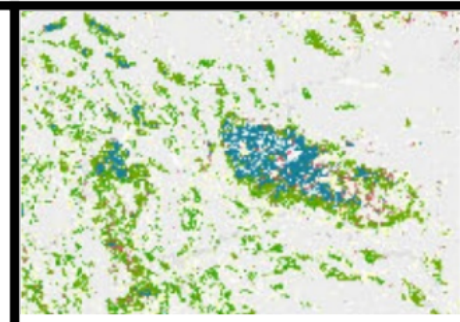
$N_e > 500?$
 $N_c > 5000?$



$\hat{N}_c = \text{area} \times \hat{\text{density}}$



Pot $N_c = \text{area} \times \hat{\text{density}}$



Pot $N_c = \text{area} \times \hat{\text{density}}$

