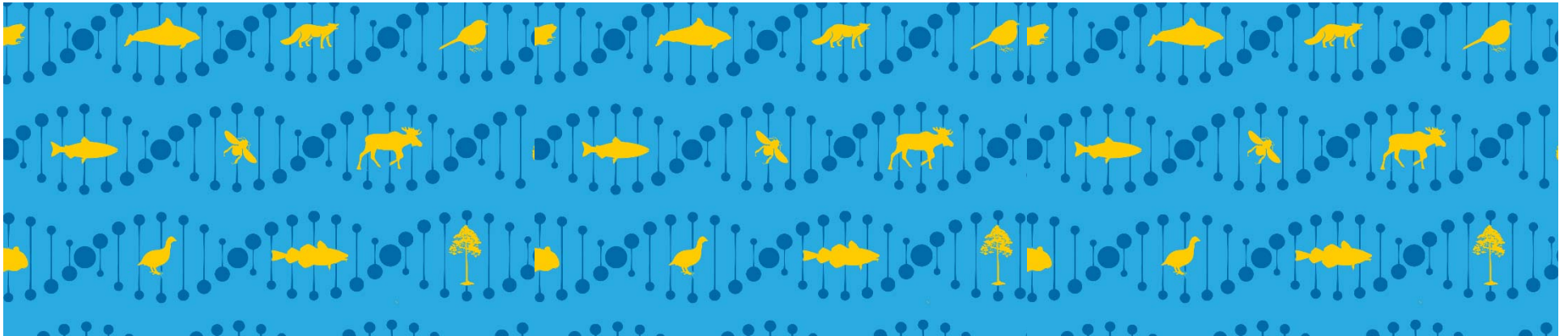


Indicators for genetic diversity in CBD Post2020 Global Biodiversity Framework

Linda Laikre

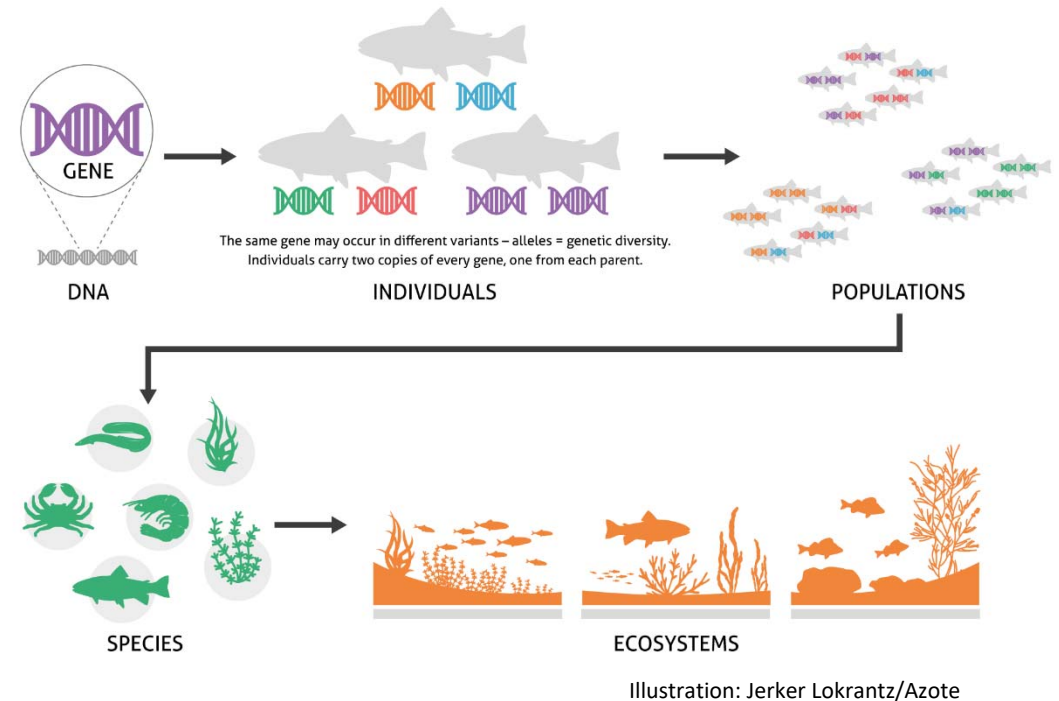
linda.laikre@popgen.su.se

Dept. Zoology, Stockholm University, Sweden



CBD: three levels of biodiversity

- Genetic diversity
- Species diversity
- Ecosystem diversity



Genetic diversity – toolbox for evolution, adaptation, survival
the basis for all biodiversity – key in rapidly changing environments

Loss of genetic diversity can have similar effects as loss of species

Genetic diversity within species equally important as species diversity



High genetic diversity

- High adaptiv capacity
- Good potential for long-term survival
- High resilience

Recent example:
Corals being able
to adapt to
warmer ocean
temperatures



Morikawa and Palumbi 2019, PNAS



Low genetic diversity

- Low adaptiv capacity
- Weak potential for long-term survival
- Low resilience

Recent example:
Wolf drastic
population decline
and spinal disorders
(Isle Royale, NA)



Hedrick et al 2019 in Animal Conservation

Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework for all species

International team of researchers provide guidelines

- IUCN Conservation Genetics Group
- GEO BON Genetic Composition Working Group
- Society for Conservation Biology's Conservation Genetics Working Group
- **COST Action G-BiKE**



The Coalition for Conservation Genetics

Received: 10 August 2021 | Revised: 13 December 2021 | Accepted: 5 January 2022
DOI: 10.1111/csp2.12635

PERSPECTIVE

Conservation Science and Practice WILEY

The Coalition for Conservation Genetics: Working across organizations to build capacity and achieve change in policy and practice

Francine Kershaw¹ | Michael W. Bruford² | W. Chris Funk³ |
Catherine E. Grueber⁴ | Sean Hoban⁵ | Margaret E. Hunter⁶ |
Linda Laikre⁷ | Anna J. MacDonald⁸ | Mariah H. Meek⁹ |
Cinnamon Mittan¹⁰ | David O'Brien¹¹ | Rob Ogden¹² |
Robyn E. Shaw¹³ | Cristiano Vernesi¹⁴ | Gernot Segelbacher¹⁵





LETTERS



Post-2020 goals overlook genetic diversity

Linda Laikre^{1,2,*}, Sean Hoban^{3,2}, Michael W. Bruford^{4,2}, Gernot Segelbacher^{5,2}, Fred W. Allen⁶

+ See all authors and affiliations

Science 06 Mar 2020:

POLICY FORUM

BIODIVERSITY

Set ambitious goals for biodiversity and sustainability

DOI: 10.1111/1365-2664.14225

POLICY DIRECTION

2022

Journal of Applied Ecology



Bringing together approaches to reporting on within species genetic diversity

David O'Brien¹ | Linda Laikre² | Sean Hoban³ | Michael W. Bruford⁴ | Robert Ekblom⁵ | Martin C. Fischer⁶ | Jeanette Hall¹ | Christina Hvilsom⁷ | Peter M. Hollingsworth⁸ | Francine Kershaw⁹ | Cinnamon S. Mittan¹⁰ | Tarek A. Mukassabi¹¹ | Rob Ogden¹² | Gernot Segelbacher¹³ | Robyn E. Shaw¹⁴ | Cristiano Vernesi¹⁵ | Anna J. MacDonald¹⁶

nature ecology & evolution

Perspective | Published: 01 March 2021

Conserving intraspecific variation for nature's contributions to people

Simone Des Roches, Linwood H. Pendleton, Beth Shapiro & Eric P. Palkovacs



ELSEVIER

Biological Conservation

Volume 248, August 2020, 108654



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 Vinas^{z, 2}, Per Sjögren-Gulve^{f, 1}, Gernot Segelbacher^{g, 1, 2}, Cristiano Vernesi^{h, 1}

Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible

SEAN HOBAN, MICHAEL W. BRUFORD, W. CHRIS FUNK, PETER GALBUSERA, M. PATRICK GRIFFITH, CATHERINE E. GRUEBER, MYRIAM HEUERTZ, MARGARET E. HUNTER, CHRISTINA HVILSOM, BELMA KALAMUJIC STROIL, FRANCINE KERSHAW, COLIN K. KHOURY, LINDA LAIKRE, MARGARIDA LOPES-FERNANDES, ANNA J. MACDONALD, JOACHIM MERGEAY, MARIAH MEEK, CINNAMON MITTAN, TAREK A. MUKASSABI, DAVID O'BRIEN, ROB OGDEN, CLARISSE PALMA-SILVA, UMA RAMAKRISHNAN, GERNOT SEGELBACHER, ROBYN E. SHAW, PER SJÖGREN-GULVE, NEVENA VELIČKOVIĆ, AND CRISTIANO VERNESI

Authors' Reply to Letter to the Editor: Continued improvement to genetic diversity indicator for CBD

Linda Laikre¹ · Paul A. Hohenlohe² · Fred W. Allendorf³ · Laura D. Bertola⁴ · Martin F. Breed⁵ · Michael W. Bruford⁶ · W. Chris Funk⁷ · Gonzalo Gajardo⁸ · Antonio González-Rodríguez⁹ · Catherine E. Grueber¹⁰ · Phillip W. Hedrick¹¹ · Myriam Heuertz¹² · Margaret E. Hunter¹³ · Kerstin Johannesson¹⁴ · Libby Liggins¹⁵ · Anna J. MacDonald¹⁶ · Joachim Mergeay^{17,18} · Farideh Moharrek^{19,20} · David O'Brien²¹ · Rob Ogden²² · Pablo Orozco-terWengel⁶ · Clarisse Palma-Silva²³ · Jennifer Pierson²⁴ · Ivan Paz-Vinas²⁵ · Isa-Rita M. Russo⁶ · Nils Ryman¹

Three pragmatic indicators possible to use in global context incl.
without genetic data (indicator 1 & 2)

INDICATORS

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

Proposed **Headline Indicator**
A.0.4

Genetic diversity within populations

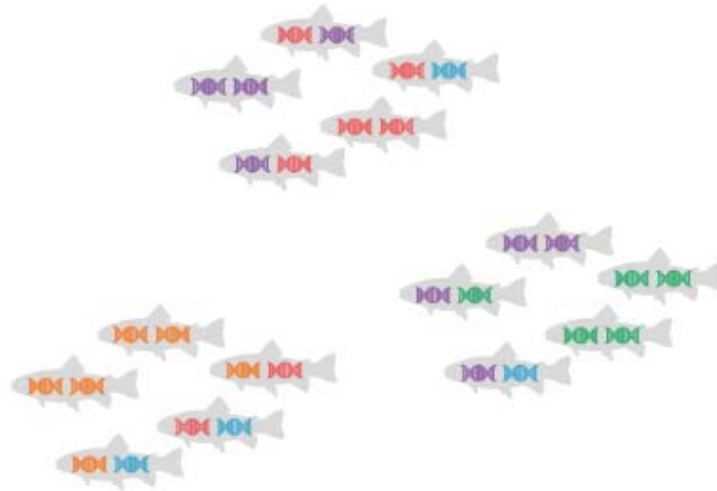
The proportion of populations maintained within species

Proposed **Component Indicator**
A.8.1

Genetic diversity between populations

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

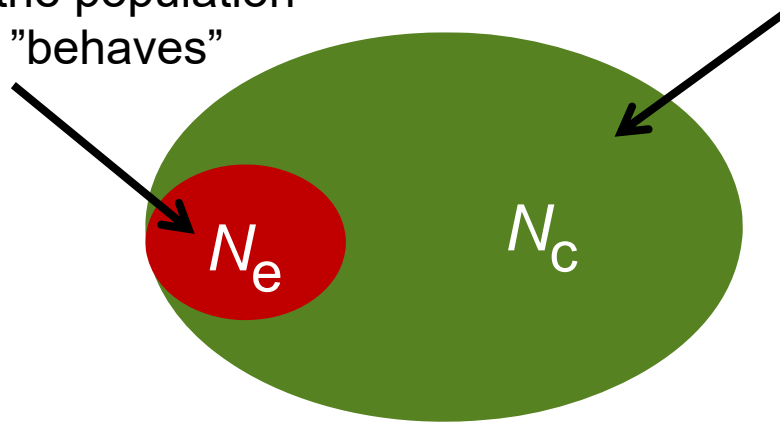
Important addition to
Component Indicators



Effective population size (N_e) – basis for indicator A.0.4

Genetically effective population size
(N_e)
the genetic size of the population -
how the population "behaves"
genetically

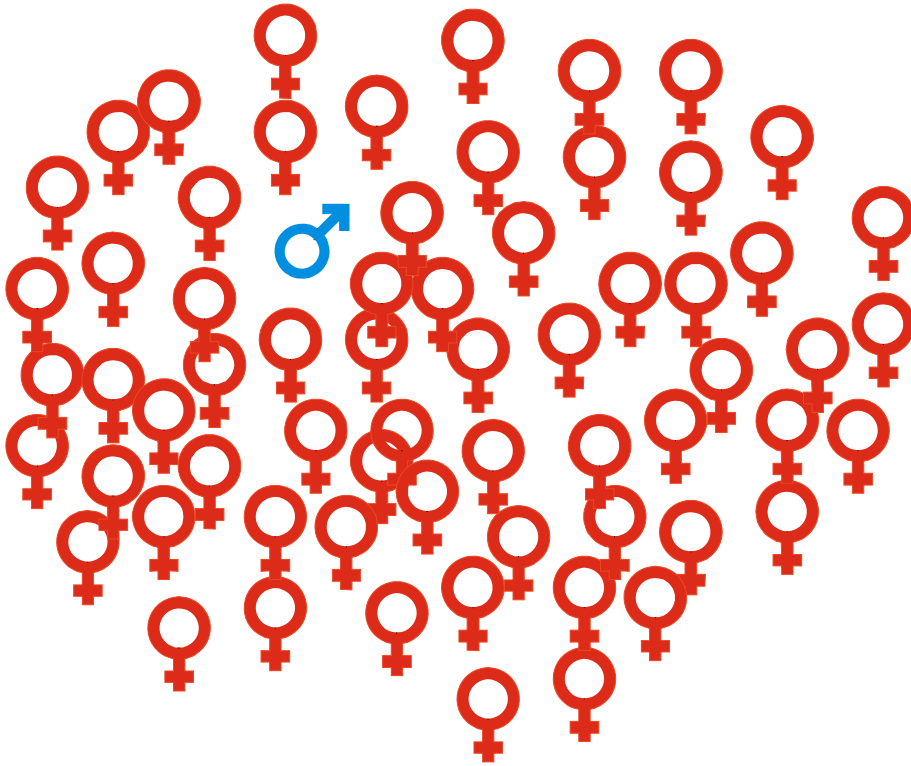
Census size (N_c) - number of mature
individuals



The effective population size determines the rate of loss of genetic
diversity

The effective population size (N_e) is usually much smaller
than the census size (N_c)

Sex ratio affects N_e



Non-equal sex ratio

1 male

99 females

$N_c = 100$

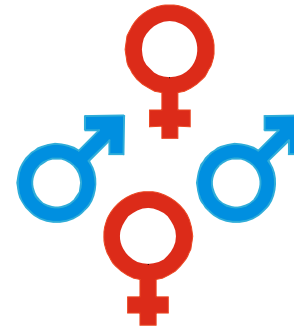
$$N_e = \frac{4 \cdot N_m \cdot N_f}{N_m + N_f}$$

Equal sex ratio

2 males

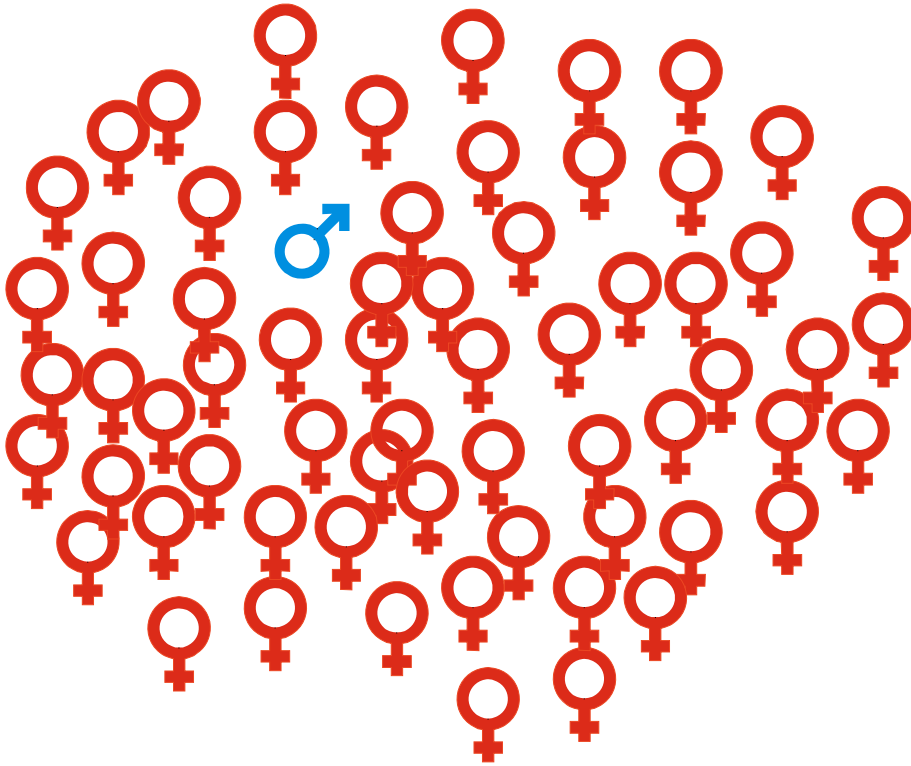
2 females

$N_c = 4$



N_m = number of mature males; N_f = number of mature females

Sex ratio affects N_e



Non-equal sex ratio

1 male

99 females

$N_c = 100$

$$N_e = 3.96 \approx 4$$

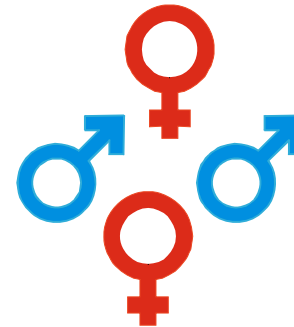
$$N_e = \frac{4 \cdot 1 \cdot 99}{1 + 99} = 3.96$$

Equal sex ratio

2 males

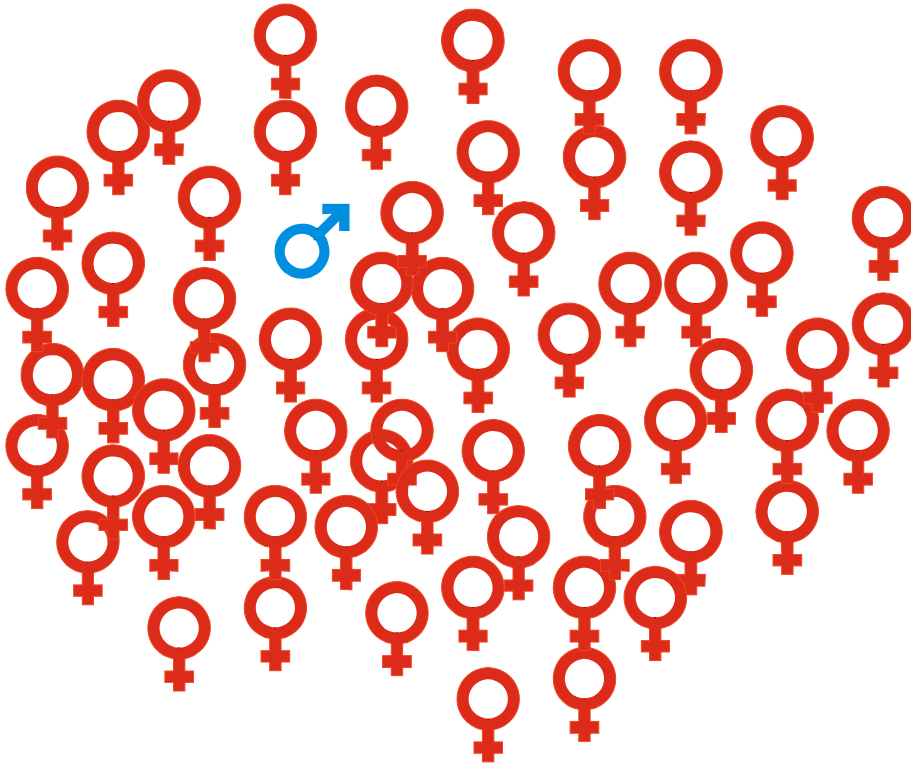
2 females

$N_c = 4$



N_m = number of mature males; N_f = number of mature females

Sex ratio affects N_e



Non-equal sex ratio

1 male

99 females

$N_c = 100$

$$N_e = 3.96 \approx 4$$

$$N_e = \frac{4 \cdot 2 \cdot 2}{2 + 2} = 4$$

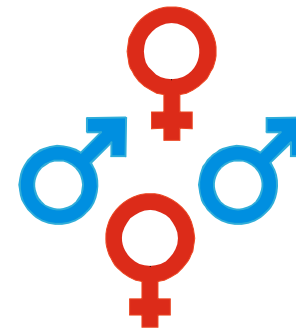
N_m = number of mature males; N_f = number of mature females

Equal sex ratio

2 males

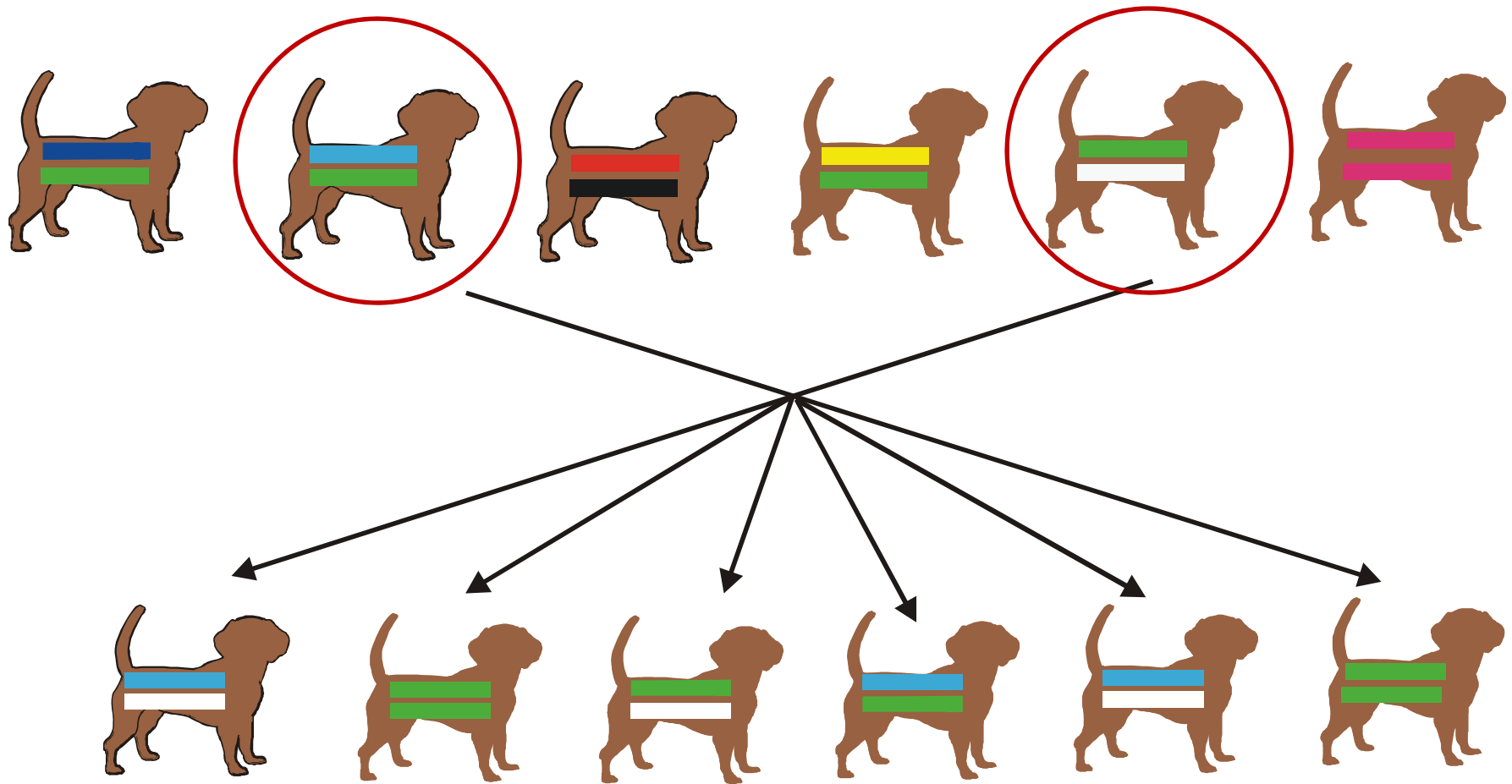
2 females

$N_c = 4$



$$N_e = 4$$

Variation in number of offspring affects N_e



If few of adult individuals reproduce and contribute offspring loss of genetic diversity will be faster than if many contribute

A well-established scientifically accepted rule-of-thumb:

$N_e \geq 500$ Maintains sufficient levels of genetic variation for adaptation

e.g., Franklin 1980; Frankel & Soulé 1981, Ryman & Allendorf 2002; Jamieson & Allendorf 2012

Our proposed indicator 1 for genetic diversity of all species:

Headline Indicator A.0.4

Indicator 1

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

Laikre et al 2020; Hoban et al 2020

CBD/WG2020/3/3/Add.1

Three pragmatic indicators possible to use in global context incl.
without genetic data (indicator 1 & 2)

INDICATORS

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

Proposed **Headline Indicator**
A.0.4



Trial application in
Sweden
Costa Rica
South Africa
Mexico

The proportion of populations maintained within species

Proposed **Component Indicator**
A.8.1



Trial application in
Sweden
Costa Rica
South Africa
Mexico

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

Suitable **Component Indicator**



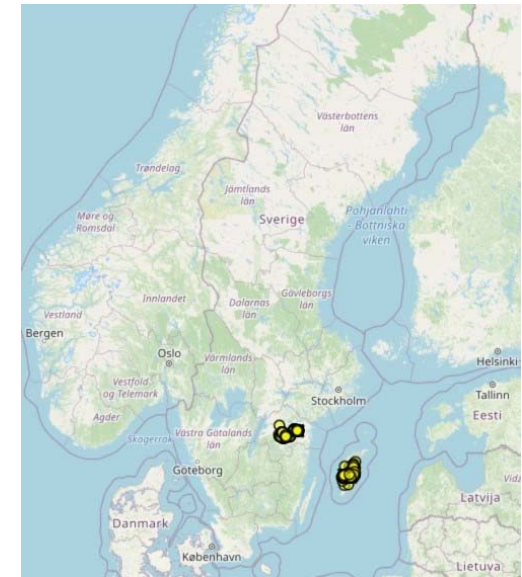
Applied/elaborated
Switzerland
<http://gendiv.ethz.ch>
Scotland [Hollingsworth et al. 2020](#)
Sweden



Example from Sweden: Applying A.0.4 and A.8.1



Photo: © Karl-Olof Bergman



- The butterfly *Lopinga achine* **NT**

- (1) the conservative N_e/N_c "0.1 rule" \Rightarrow census size $N_c = 5000$
 metapopulation sizes: **> 6100** (Östergötland) + **c. 7000** (Gotland)
- (2) **100% distinct metapop.s remain**, recovery program exist

Taxon	# $N_e > 500$ (i.e, $N_c > 5000$)	# $N_e < 500$	Remain. pop.
<i>Lopinga</i> butterfly	2 pop. (100%)	0 pop.	100%

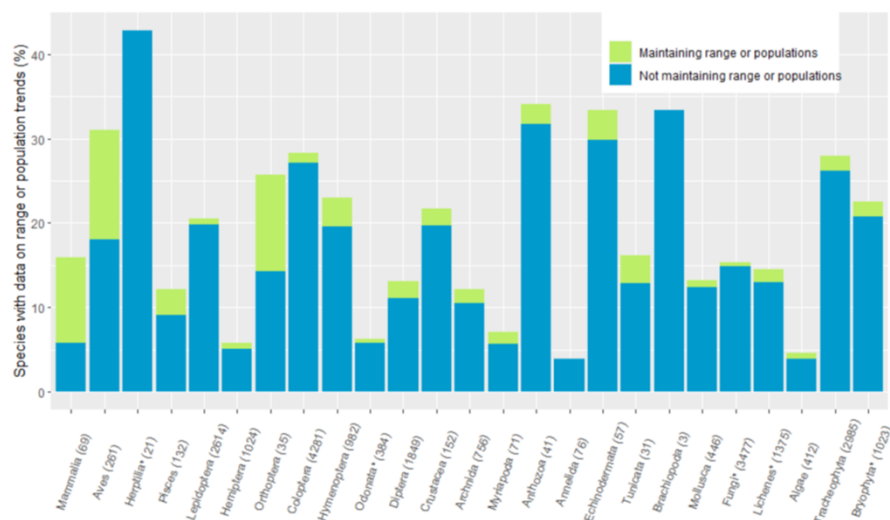
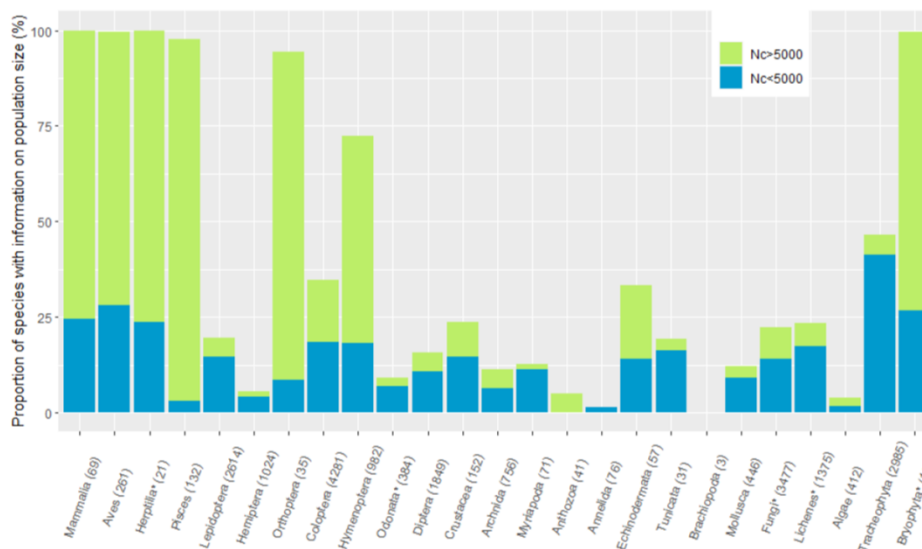
Indicators A.0.4 and A.8.1 and our 3 applied in Sweden using Red List data

Ecological Indicators: in revision

Practical application of indicators for genetic diversity in CBD post-2020 Global Biodiversity Framework implementation -examples from an information intensive country using existing data.

Henrik Thurffjell^{1*}, Linda Laikre², Robert Ekblom³, Sean Hoban⁴, Per Sjögren-Gulve⁵
¹ Swedish Species Information Centre, Swedish University of Agricultural Sciences SE-75007 Uppsala, Sweden. henrik.thurffjell@slu.se

- Red List data are useful for calculating the indicators for genetic diversity.
- Genetic indicators can be calculated for at least hundreds of species per country.
- Genetic threats and current Red List assessments are complementary.



More detailed assessment for mammals and herptiles

A.0.4: 65% of species have $N_e > 500$

A.8.1: 73% maintenance

DNA-based monitoring: 12% are being monitored

Similar assessments using A.0.4 and A.8.1 are now ongoing in several countries (e.g. Mexico, South Africa, France, Belgium, Japan)

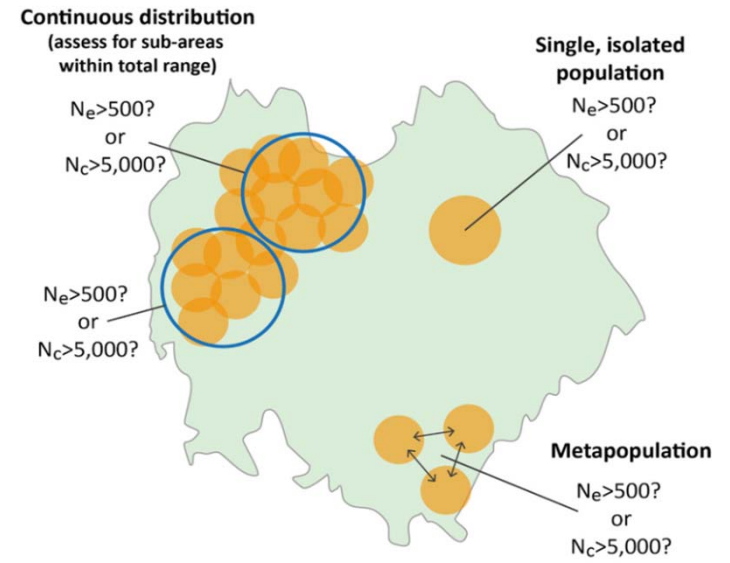
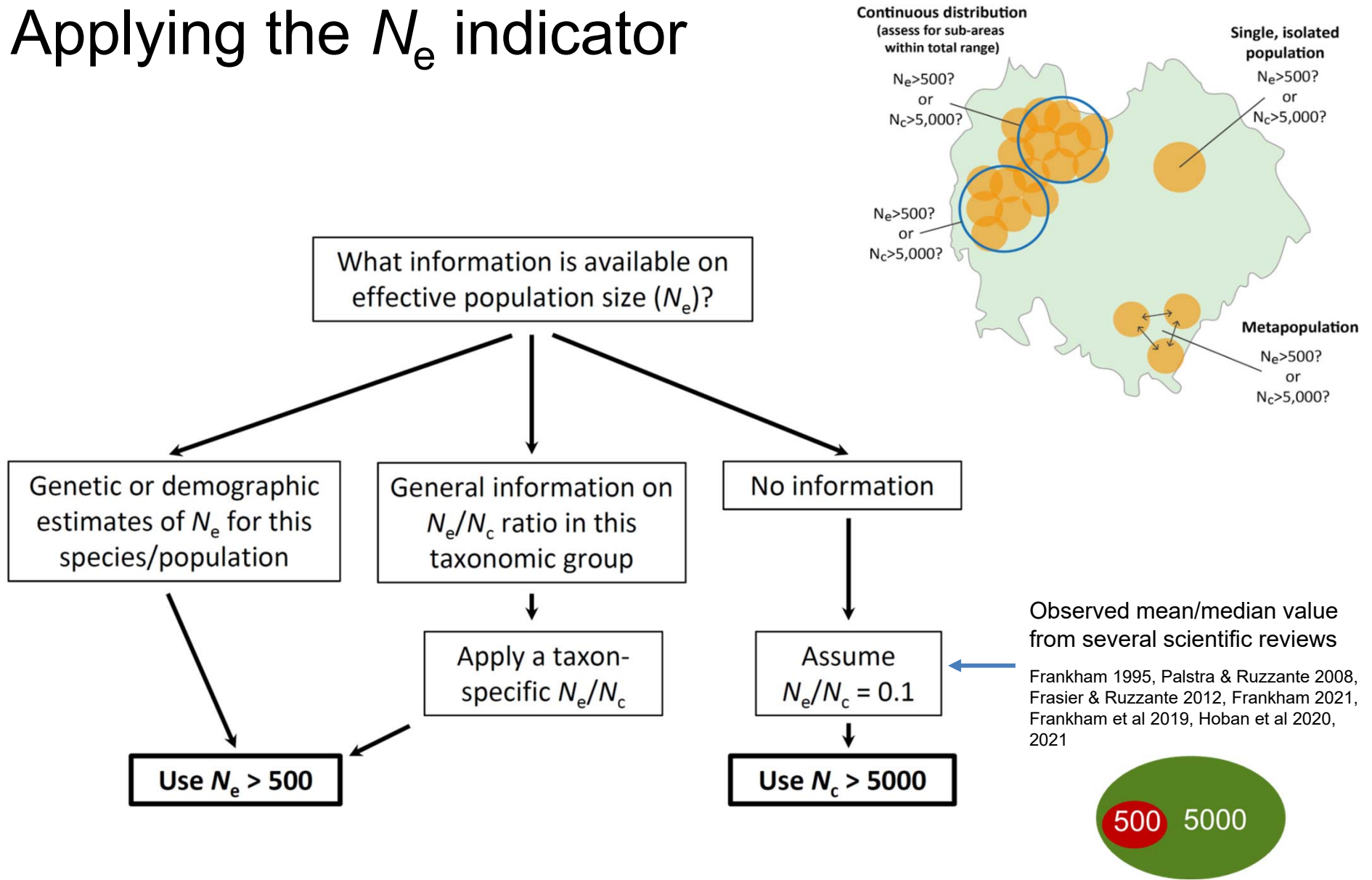
A manual for assessments will be available during 2022-2023

The indicators can be applied using existing data
Costs involved are limited



Extra slides

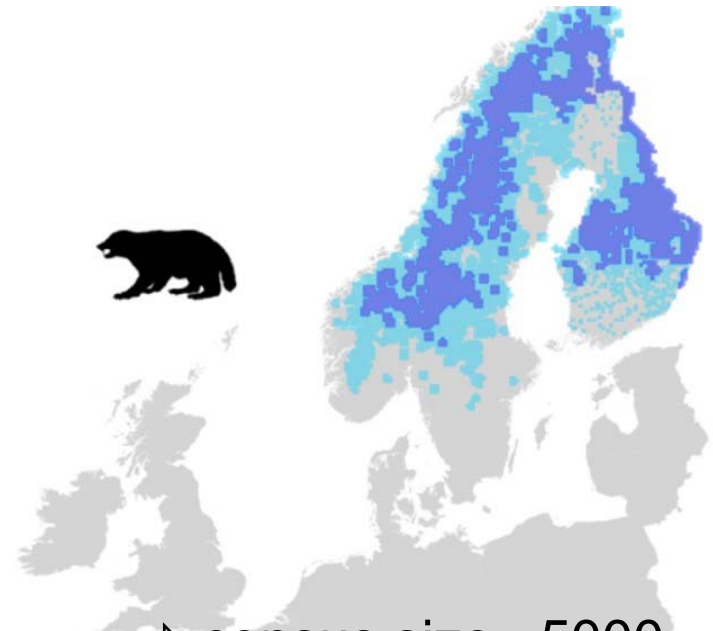
Applying the N_e indicator



The wolverine *Gulo gulo* VU



Photo: © Kimmo Pöri



(1) the conservative N_e/N_c "0.1 rule"

⇒ census size 5000

- genomic & simulation studies: $N_e/N_c = 0.248$ ⇒ census size = 2018
- (meta)population size year 2019 (SE+NO+FI): ⇒ total $N_c = 1398$

(2) 100% of populations remain, increasing, management plans exist

- Increased genetic monitoring + co-management btw countries.