

"R-evolutionary Insights: Deep dive into SNP-based population genomics". Kioloa, March 2024

Genetic management of small populations

A/Prof Catherine Grueber
Dr Kate Farquharson



THE UNIVERSITY OF
SYDNEY

We recognise and pay respect to the Elders and communities – past, present, and emerging – of the lands that the University of Sydney's campuses stand on. For thousands of years they have shared and exchanged knowledges across innumerable generations for the benefit of all.



THE UNIVERSITY OF
SYDNEY

Species

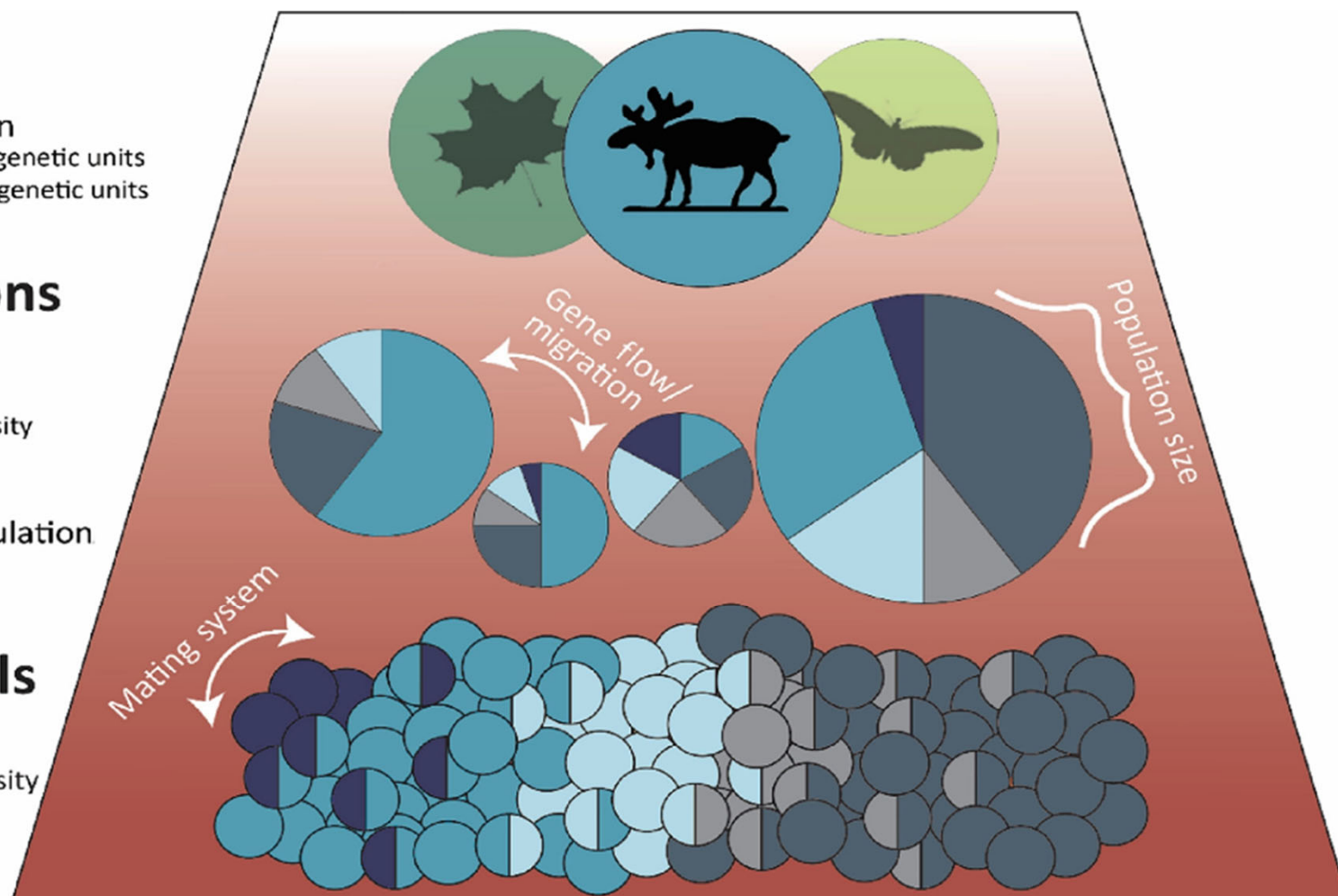
- Differentiation
 - Number of genetic units
 - Distance of genetic units

Populations

- Diversity
 - Richness
 - Heterozygosity
- Inbreeding
- Effective population size

Individuals

- Diversity
 - Heterozygosity
- Inbreeding



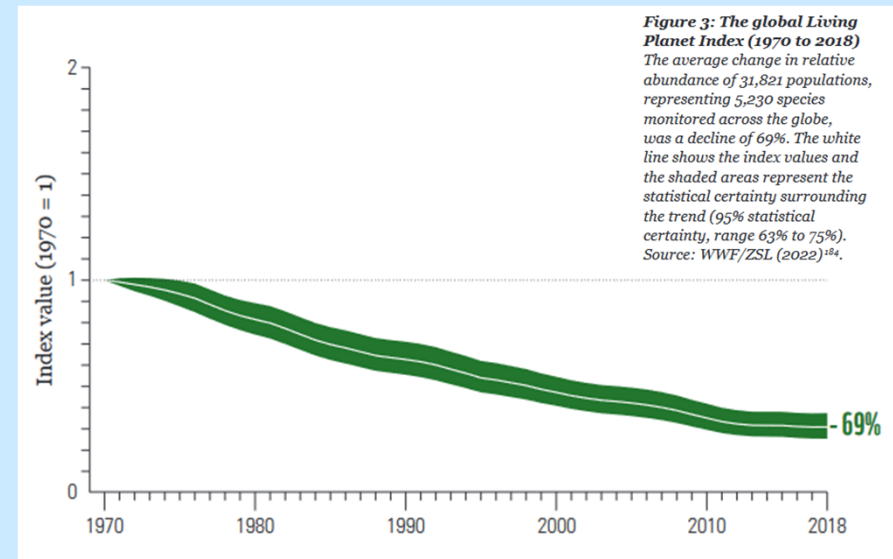
When species decline...

Genetic management concerns

Small population size leads to:

- Genetic drift
(increased genetic stochasticity)
- Inbreeding
(increased mating among relatives)
- Population fragmentation
(exacerbates these effects)

How can we measure and manage these processes?



<https://livingplanet.panda.org/>

Conservation genetics of small populations

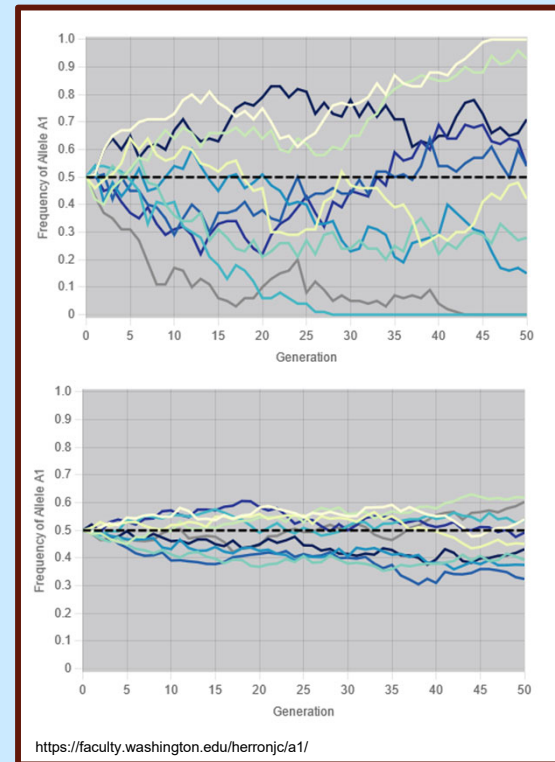
Genetic drift erodes diversity and adaptive potential

Genetic variation underpins phenotypic variation, and thus the adaptive potential of populations/species

Genetic drift has a stronger impact on small populations than larger ones

In very small populations, genetic drift is a stronger force than selection for driving genetic change.

The longer a population remains small, the longer genetic drift impacts population diversity



Conservation genetics of small populations

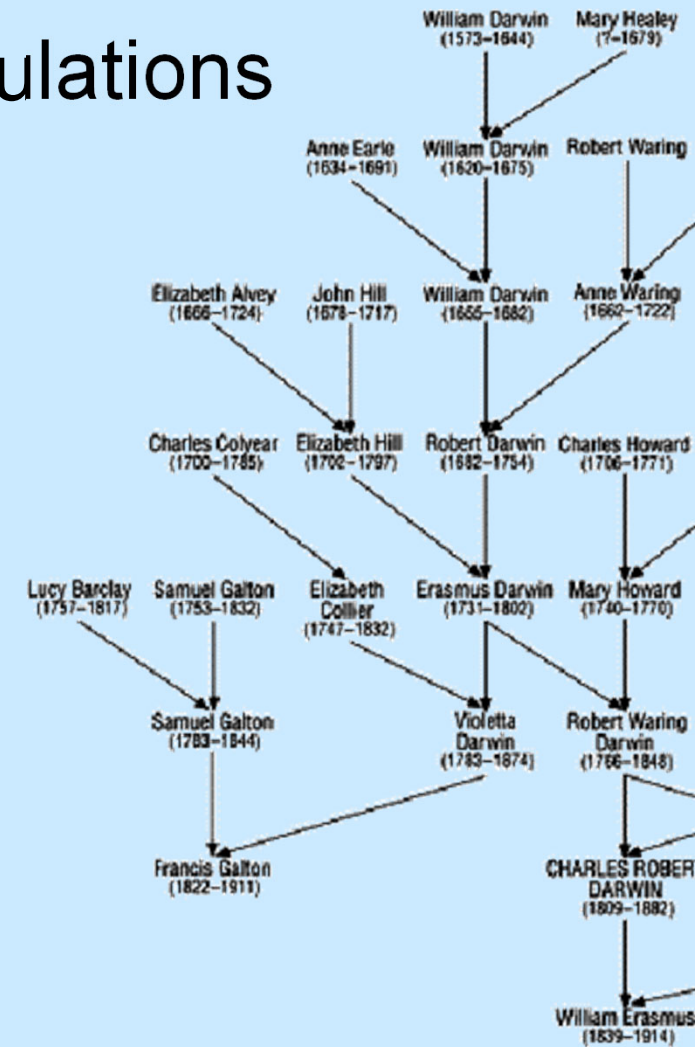
Inbreeding erodes individual fitness

Inbreeding can accumulate over generations and increase the expression of harmful recessive alleles.

Inbreeding is inevitable in small populations, even if mating is random.

Inbreeding reduces individual survival and reproductive fitness (“inbreeding depression”), ultimately risking population loss

Reduced fitness of inbred individuals is a widespread observation for normally outbreeding, diploid species.



Conservation genetics of small populations

Gene flow and fragmentation

Land-use change modifies the landscape, so that habitat patches exist in a mosaic of inhospitable environment

Population fragments may be small (drift and inbreeding)

A fragmented population is generally at greater risk than a contiguous population of the same total size

Using genetics to characterise population fragmentation can support conservation planning.



Photo: Nicholas Hartmann on Wikimedia

Measuring population genetic processes

Essential biodiversity variables

...fundamental metrics to help aggregate, harmonize, and interpret biodiversity observation data from diverse sources.

...also intended as inputs and validation to forecast the status and trends of biodiversity, and to support policy and decision making.

Genetic
diversity

Genetic
differentiation

Inbreeding

Effective
population size

Genetic diversity

Richness and evenness of genetic diversity in a population (e.g. number of alleles, and expected heterozygosity, respectively)

Genetic differentiation

Number of genetic units, and the degree of genetic differentiation among them (e.g. number of evolutionary significant units)

Inbreeding

Degree of relatedness between pairs of individuals (coancestry), mating among relatives, or identity by descent.

Effective population size

Size of an ideal population that loses genetic variation at the same rate as the focal population.




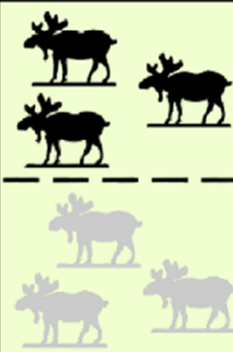
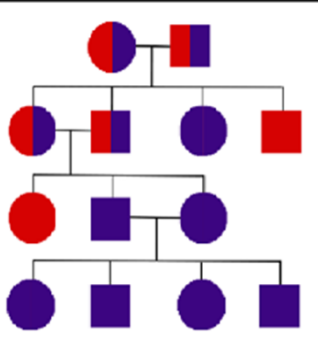
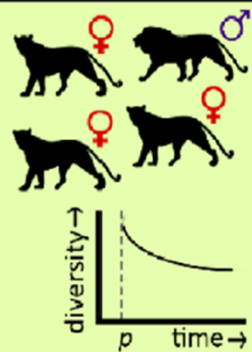


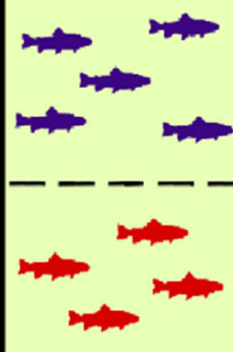
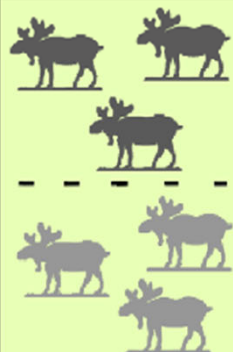
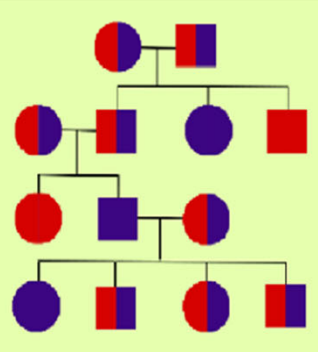
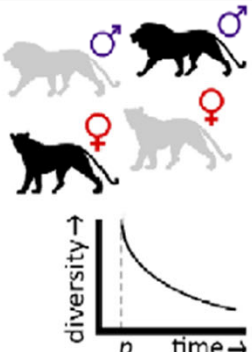
Why this combination of four metrics?

Decline indicates loss of adaptive capacity and/or increased levels of inbreeding

Loss of independent evolutionary or demographic units; Increased differentiation indicates more fragmentation (reduced gene flow) between units

Increased inbreeding increases the chance of expression of deleterious alleles, reducing fitness

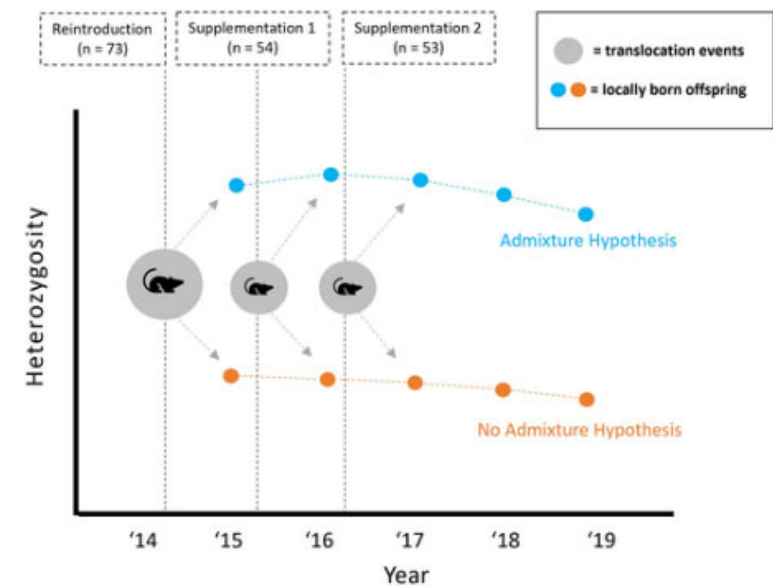
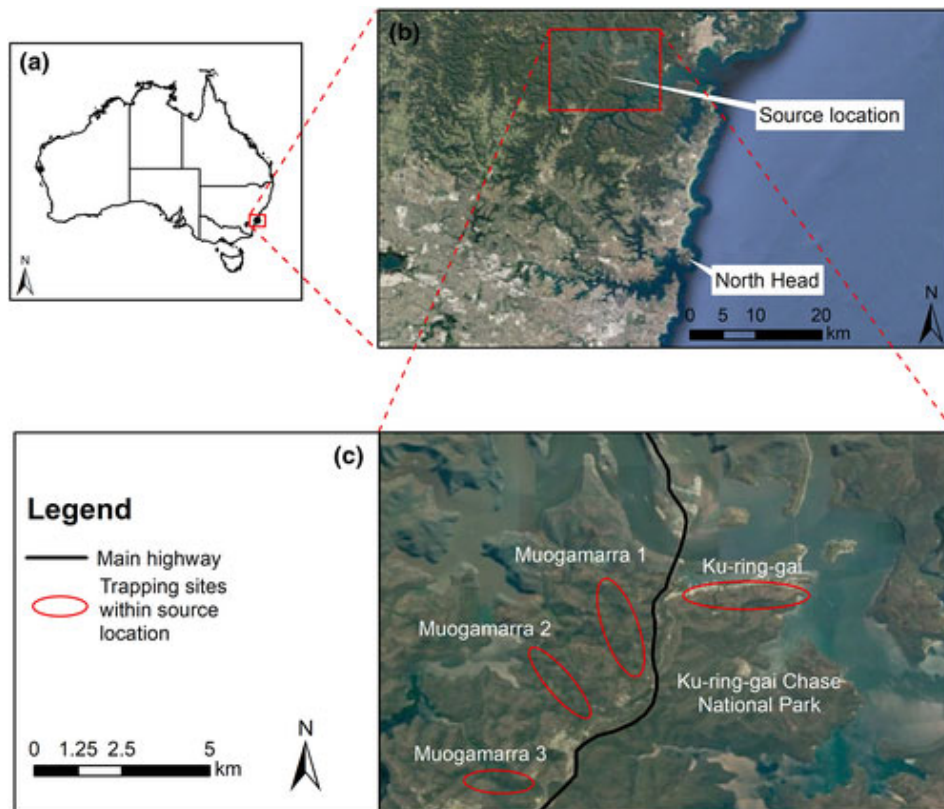
Lower N_e increases genetic drift, inbreeding, and future loss of genetic variation

	Genetic diversity		Genetic differentiation		Inbreeding	Effective population size
	Richness	Heterozygosity	Number of genetic units	Distance genetic units		
High						
Low						

Australian example of EBVs in use: bush rat reintroduction at North Head



Photo: Australian Wildlife Conservancy



Australian example of EBVs in use: bush rat reintroduction at North Head

Genetic
diversity

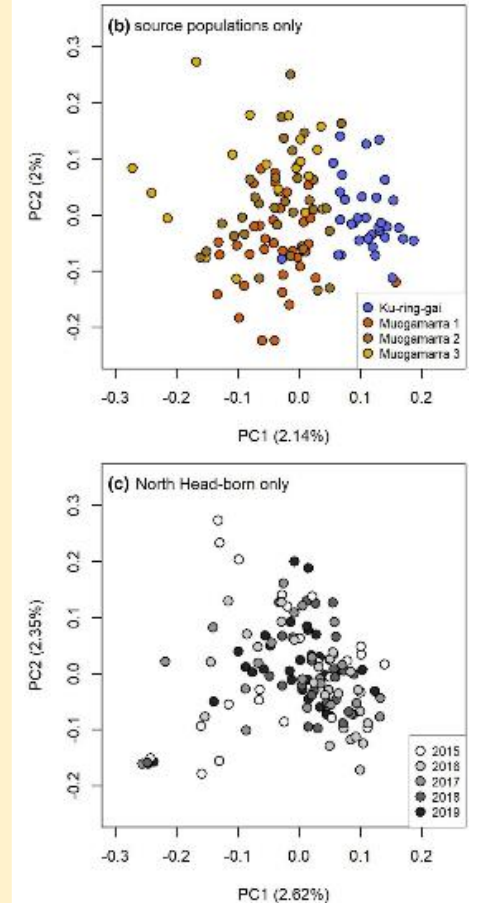
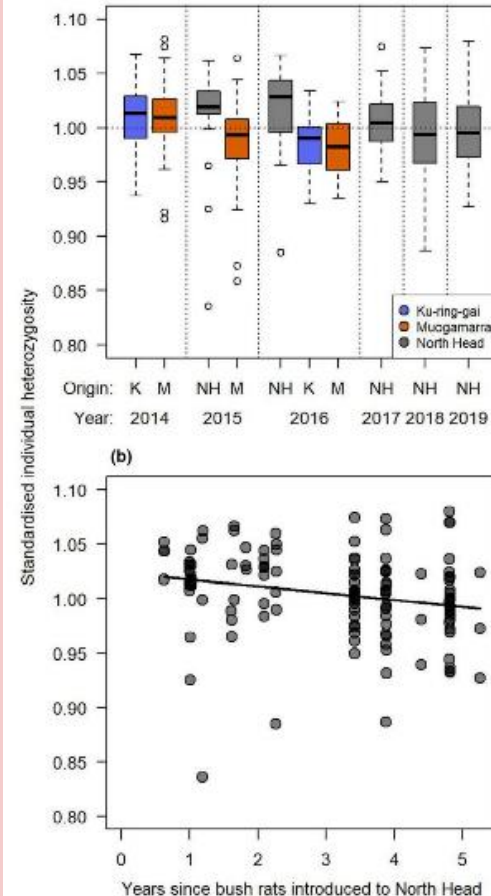
Genetic
differentiation

Inbreeding

Effective
population size

Table 2 Diversity measures for bush rat populations in Sydney, based on SNPs obtained via reduced-representation sequencing (DArTseq)

Population	N_{ind}^a	N_E (95% CI) ^b	Within-population kinship (SD)			
			N_{pairs}^c	Genomic SNPs ^d	Genic SNPs ^d	Exonic SNPs ^d
Ku-ring-gai (all)	33	119.90 (118.99; 120.83)	528	0.0224 (0.0265)	0.0253 (0.0294)	0.0355 (0.0442)
Ku-ring-gai 2014	14	74.11 (73.12; 75.11)	91	0.0264 (0.0336)	0.0260 (0.0349)	0.0343 (0.0451)
Ku-ring-gai 2016	19	85.47 (84.56; 86.39)	171	0.0218 (0.0287)	0.0285 (0.0336)	0.0382 (0.0474)
Muogamarra (all)	88	244.80 (243.27; 246.35)	3828	0.0137 (0.0201)	0.0154 (0.0213)	0.0268 (0.0358)
Muogamarra 1, 2014	36	136.42 (135.41; 137.45)	630	0.0158 (0.0256)	0.0170 (0.0264)	0.0312 (0.0414)
Muogamarra 2, 2015	31	113.78 (112.92; 114.64)	465	0.0177 (0.0281)	0.0193 (0.0295)	0.0310 (0.0428)
Muogamarra 3, 2016	21	111.25 (109.90; 112.62)	210	0.0216 (0.0303)	0.0248 (0.0270)	0.0328 (0.0427)
North Head (all)	129	115.08 (114.79; 115.38)	8256	0.0149 (0.0252)	0.0162 (0.0261)	0.0312 (0.0418)
North Head 2015	25	32.72 (32.61; 32.84)	300	0.0219 (0.0422)	0.0214 (0.0436)	0.0392 (0.0518)
North Head 2016	25	61.99 (61.63; 62.36)	300	0.0185 (0.0308)	0.0207 (0.0332)	0.0261 (0.0389)
North Head 2017	24	123.07 (121.69; 124.47)	276	0.0149 (0.0236)	0.0162 (0.0247)	0.0336 (0.0413)
North Head 2018	25	85.24 (84.56; 85.93)	300	0.0165 (0.0284)	0.0155 (0.0271)	0.0351 (0.0481)
North Head 2019	30	79.79 (79.33; 80.25)	435	0.0171 (0.0332)	0.0174 (0.0343)	0.0314 (0.0455)



Genetic management

Conservation objectives to prevent extinction

Maintain adaptive potential (maintain genetic diversity) of the species and its populations

Maintain individual and population fitness (minimize inbreeding)

Reduce the effects of genetic drift and inbreeding via increasing effective population size (N_E)

- ✓ Is genetic management necessary?
- ✓ How big do populations need to be to be self-sustaining?
- ✓ What is the relevant timescale for monitoring?
- ✓ When weighing our options, how much loss is too much?

Managing genetic diversity

Options for action

In the main, the objectives are to increase the population size (N_E) and/or connectivity among population fragments.

- Remove / decrease threats to improve demographic parameters
- Increase or improve habitat
- Increase connectivity among populations (either natural or human-mediated movement = translocations)
- Use captive facilities or a breeding program to support population recovery



Photo: NZ Department of Conservation

Managing genetic diversity

Monitoring to support planning

Quantify and predict what might happen if we “do nothing” (generate a null hypothesis)

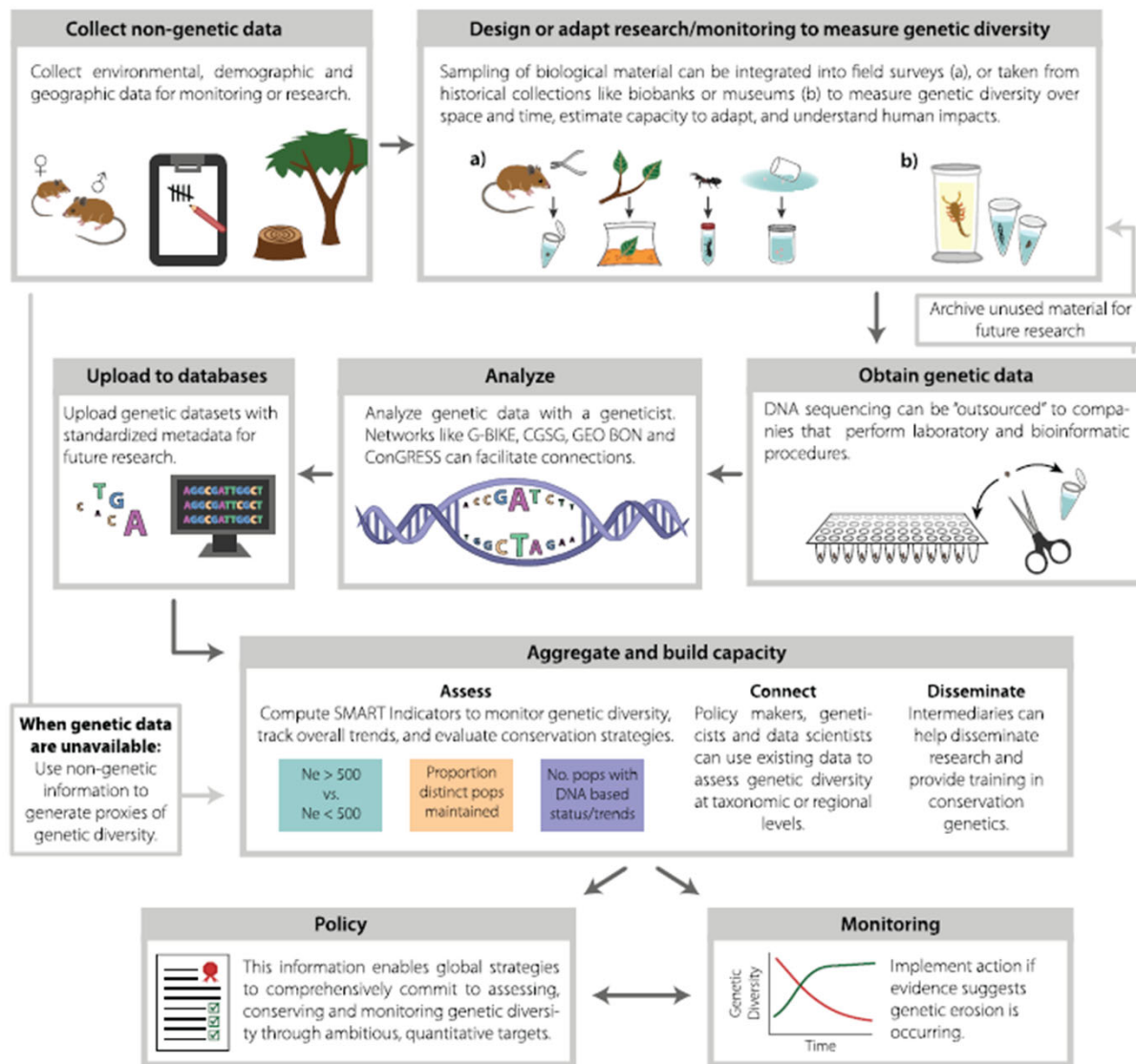
Rank populations in terms of their genetic vulnerability (risk assessment)

Identify relatively healthy populations that could serve as source populations

Answer specific conservation management questions:

- ✓ Would translocations help achieve genetic management goals?
- ✓ When do translocations need to occur?
- ✓ How many individuals should be translocated?
- ✓ Where should individuals be translocated to/from?
- ✓ Which individuals should be translocated?





Managing genetic diversity

Monitoring to test outcomes

Population level:

- Determine whether our “do nothing” (null hypothesis) predictions are borne out
- Determine whether actions are having the desired effect on population parameters

Individual level:

- Identify individual-level variables contributing to survival/reproduction
- Determine whether migration among populations is occurring

Design follow-up management needed to stay on track towards goals
Use lessons learnt from previous activities to plan future ones



Today's example study system

Tasmanian devil

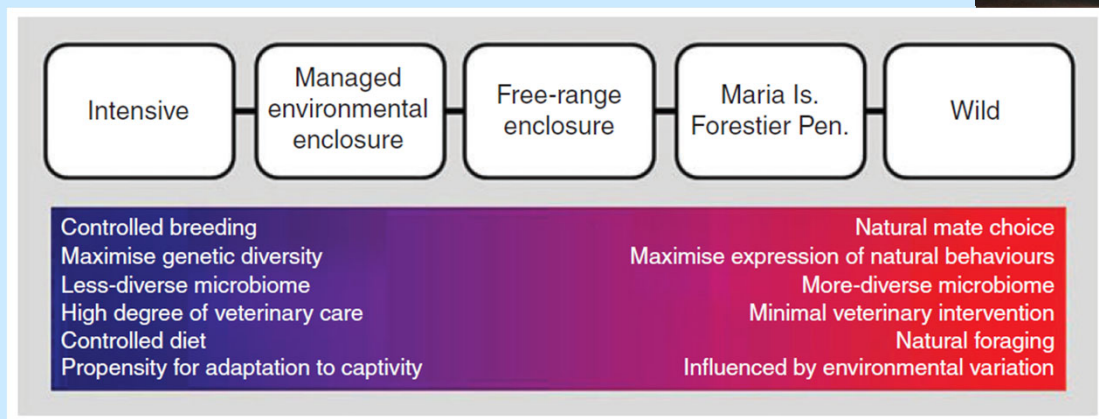


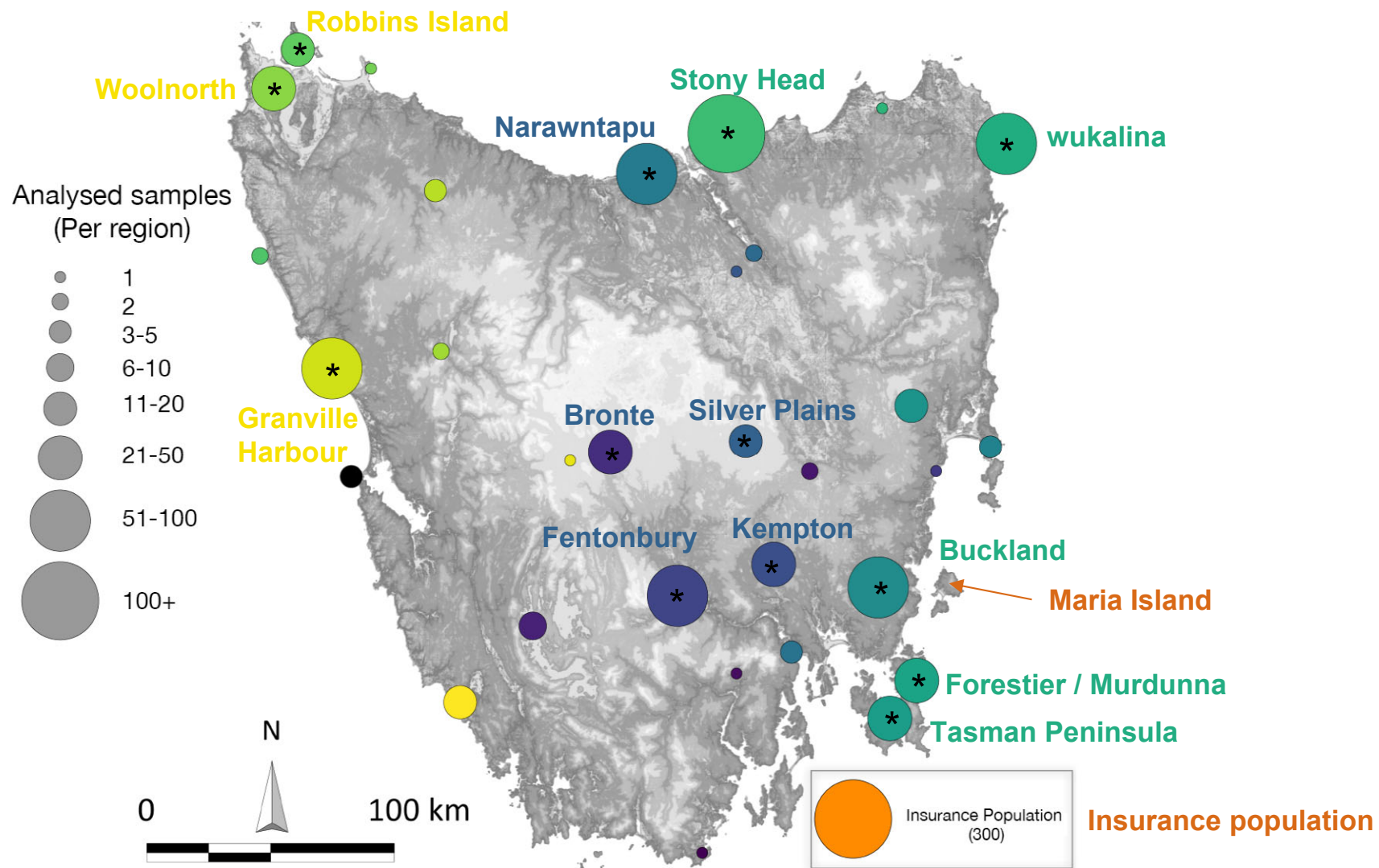
Photo: CEG



Article

Restoring faith in conservation action: Maintaining wild genetic diversity through the Tasmanian devil insurance program

Katherine A. Farquharson,^{1,5} Elspeth A. McLennan,^{1,5} Yuanyuan Cheng,¹ Lauren Alexander,¹ Samantha Fox,^{2,3} Andrew V. Lee,^{2,3} Katherine Belov,¹ and Carolyn J. Hogg^{1,4,6,*}



Today's example study system

Tasmanian devil

Objectives of the published study

- Quantify the current genetic diversity of Tasmanian devils across their entire range
- Investigate whether the genetic diversity of the insurance population is representative of the species

Objectives of today's activity

- Replicate some of the analyses, including some EBVs for a subset of populations
- Discuss the findings in relation to devil management
- Consider the implications of sampling/study design for addressing these kinds of questions

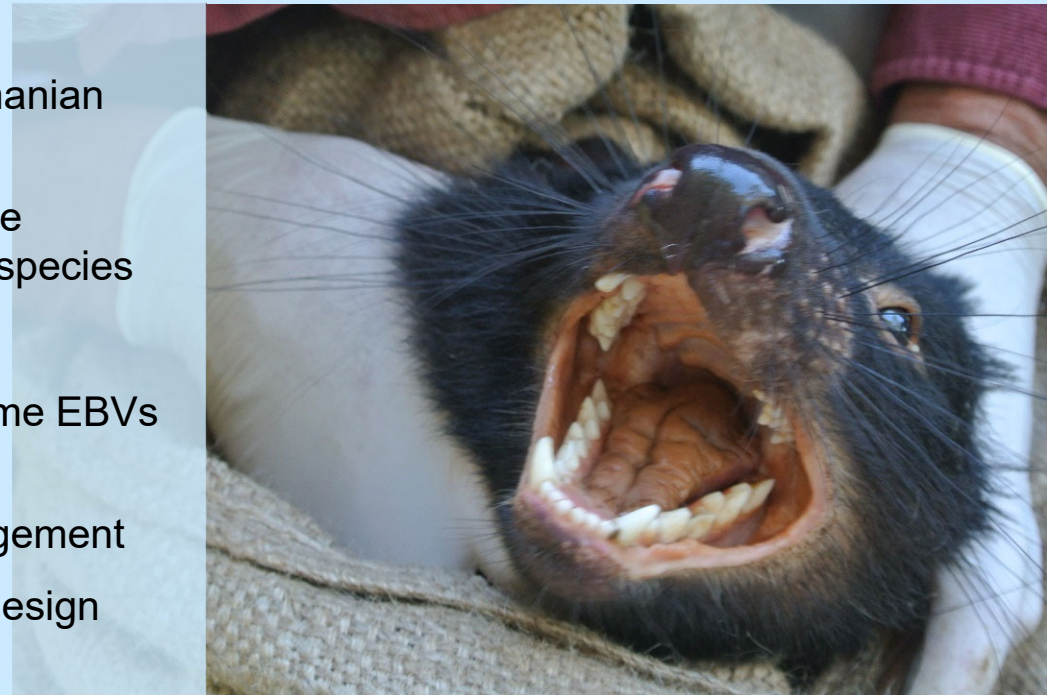


Photo: CEG