Extensive population decline in the Tasmanian devil predates European settlement and Devil Facial Tumour Disease

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Tasmanian devils
(*Sarcophilus harrisii*)

- Largest extant marsupial carnivore
- Top–predator
- Specialised scavenger
- Endemic to Tasmania
- Low genetic diversity at mitochondrial, nuclear and MHC genes
- Extinction threatened due to spread of Devil Facial Tumor Disease (DFTD)

Genetic diversity and population structure of the endangered marsupial *Sarcophilus harrisii* (Tasmanian devil)

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Disease induced changes in gene flow patterns among Tasmanian devil populations

Anna Brüniche-Olsen[a,*], Christopher P. Burridge[a], Jeremy J. Austin[b,c], Menna E. Jones[a]

Life-history change in disease-ravaged Tasmanian devil populations

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Changes in life history are expected when new sources of extrinsic

MHC gene copy number variation in Tasmanian devils: implications for the spread of a contagious cancer

Hannah V. Siddle[1,†], Jolanta Marzec[1,†], Yuanyuan Cheng[1], Menna Jones[2] and Katherine Belov[1,*]

Evaluation of Selective Culling of Infected Individuals to Control Tasmanian Devil Facial Tumor Disease

SHELLY LACHISH,*†† HAMISH McCALLUM,†§ DYDEE MANN,‡ CHRISSY E. PUKK,‡ AND MENNA E. JONES†‡

Conservation biology

Low major histocompatibility complex diversity in the Tasmanian devil predates European settlement and may explain susceptibility to disease epidemics

Katrina Morris[1], Jeremy J. Austin[2] and Katherine Belov[1]

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Research questions

- Has the population size of devils changed through time?

- Is the low genetic diversity a recent phenomena?

- Does different regions differ in demographic histories?

- Does summary statistics, full–likelihood and ABC give congruent results?

Last glacial maximum 20k YBP

Arid and semi-arid ☐ Pleistocene sand dunes
☐ Temperate ☐ Rainforest ☐ Steppe
☐ Dry woodland and savanna
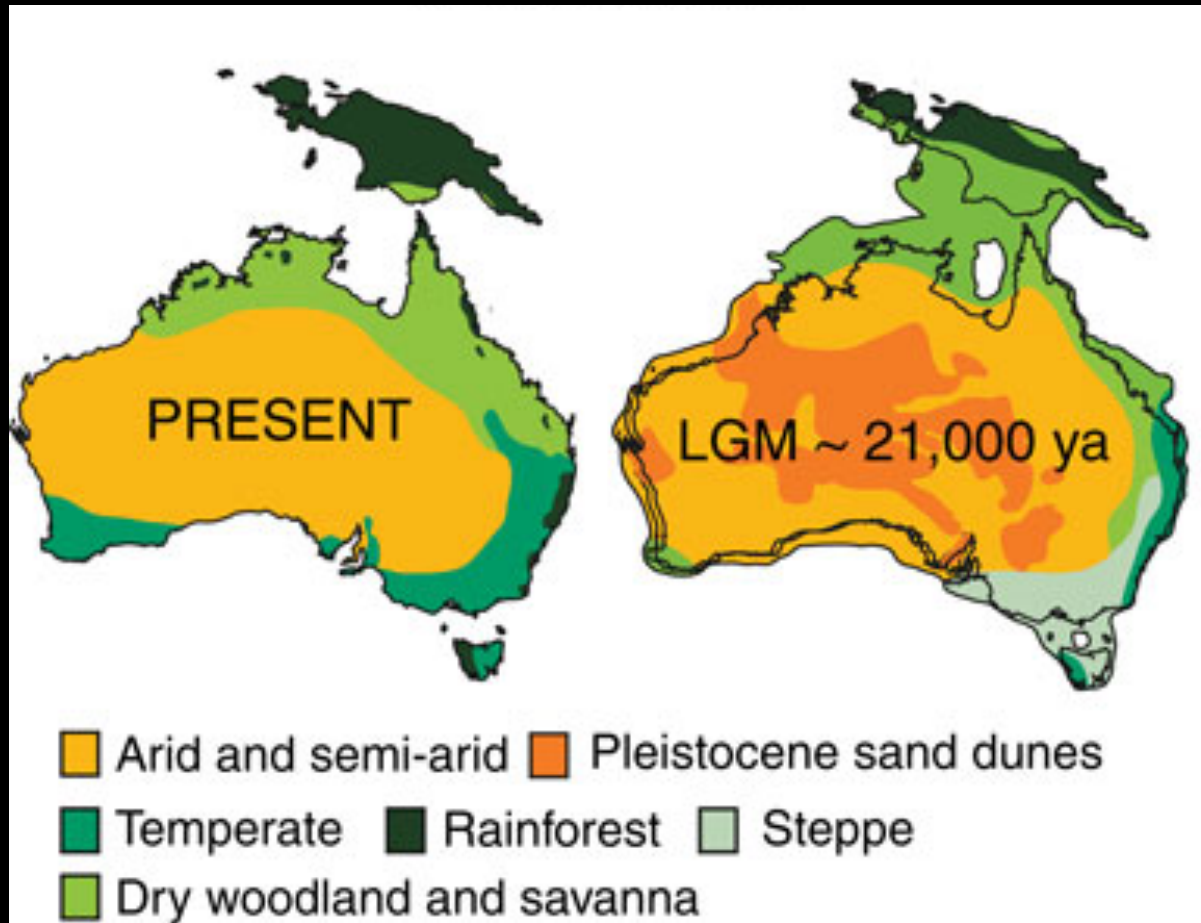
El Niño–Southern Oscillation activity 3–5k YBP

# European settlement 200 YBP

Devil facial tumour disease 10 YBP

Approach
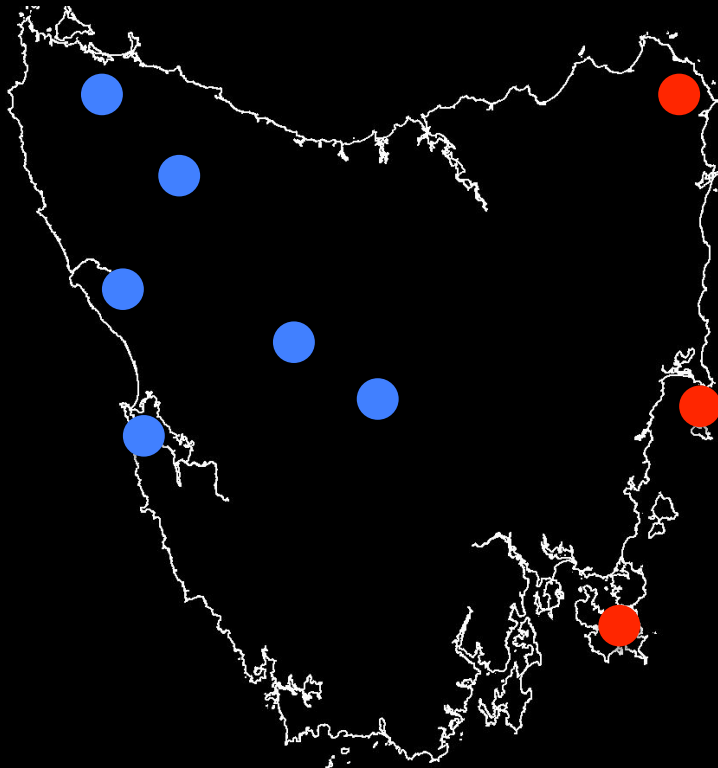
- 330 devils

- 10 microsatellite loci

- 3 DFTD populations

- 6 non–DFTD populations

- Sampled in 1964 and 2004–2005

Population structure
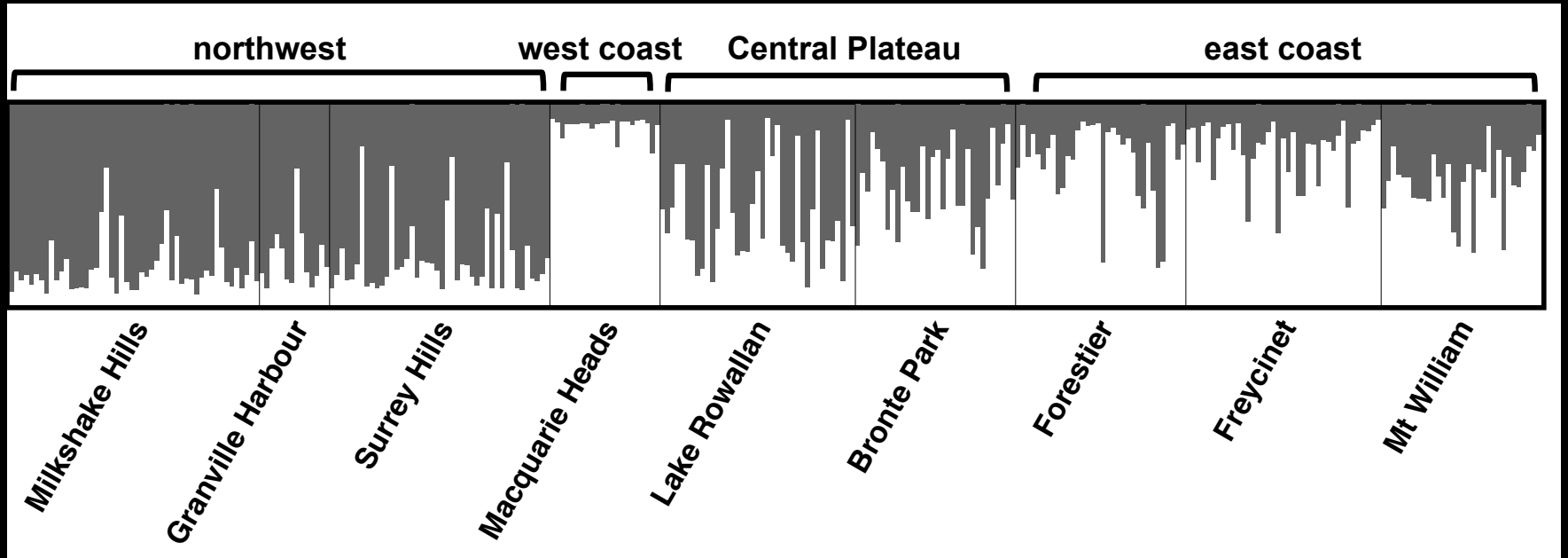
Genetic diversity

| Region	Year	n	A_O	A_E	H_O	H_E	f
northwest	2004	108	3.1	1.9	0.394	0.411	0.043
west coast	2004	22	2.3	1.4	0.24	0.230	-0.023
Central Plateau	2004	71	3.5	1.8	0.439	0.444	0.009
east coast	2005	105	3.4	1.8	0.402	0.409	0.018
east coast	1964	24	2.4	1.7	0.36	0.340	-0.051
Pooled	2004-2005	306	3.9	1.9	0.396	0.444	**0.108**

P-values <0.05 are indicated with bold.

Bottleneck tests

Loci	Region	Mutation model	Loci with excess of heterozygotes	Wilcoxon test P-value	mode–shift test
All repeats	northwest	IAM	8	**0.007**	L
		TPM70	7	0.097	L
		SMM	5	0.577	L
	west coast	IAM	4	0.715	L
		TPM70	4	0.850	L
		SMM	4	0.898	L
	Central Plateau	IAM	8	**0.003**	L
		TPM70	6	0.278	L
		SMM	3	0.947	L
	east coast	IAM	7	**0.042**	L
		TPM70	6	0.348	L
		SMM	4	0.935	L
	east coast (1964)	IAM	5	**0.027**	L
		TPM70	5	0.156	L
		SMM	5	0.419	L
	Pooled	IAM	9	**0.002**	L
		TPM70	8	0.116	L
		SMM	1	0.988	L

Population size changes
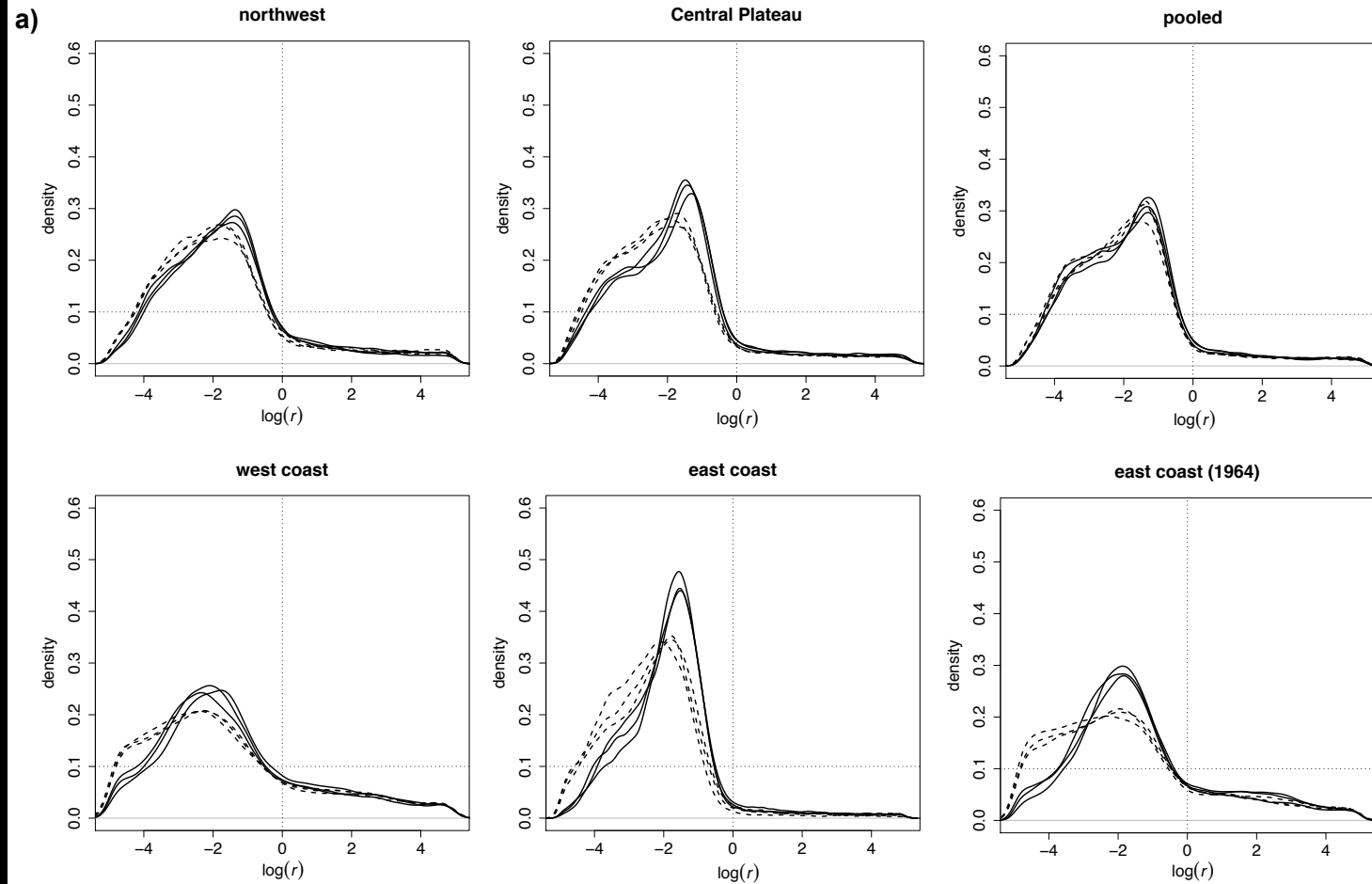
Population size changes

Region	Model Parameter	Exponential 90% HPD lower	Mean	Median	90% HPD upper	BF ($N_0 < N_1$)	Linear 90% HPD lower	Mean	Median	90% HPD upper	BF ($N_0 < N_1$)
northwest	$\log_{10}(r)$	-4.61	-1.59	-1.77	0.99	6.5	-5.00	-1.75	-2.04	0.94	6.4
	$\log_{10}(t_f)$	-2.22	0.26	0.13	5.00		-1.30	1.31	1.39	5.00	
	$\log_{10}(\theta)$	-4.17	-1.94	-1.80	0.05		-4.14	-1.88	-1.67	0.03	
west coast	$\log_{10}(r)$	-5.00	-1.41	-1.83	1.91	3.8	-5.00	-1.62	-2.11	2.15	3.7
	$\log_{10}(t_f)$	-2.40	0.90	0.96	5.00		-1.89	1.92	2.37	5.00	
	$\log_{10}(\theta)$	-3.59	-1.24	-1.02	0.39		-3.44	-1.25	-1.10	0.33	
Central Plateau	$\log_{10}(r)$	-4.82	-1.76	-1.83	0.24	8.6	-5.00	-2.03	-2.22	-0.19	9.8
	$\log_{10}(t_f)$	-1.32	0.28	0.08	4.70		-0.37	1.43	1.39	4.95	
	$\log_{10}(\theta)$	-4.36	-2.09	-1.91	-0.07		-4.33	-2.05	-1.87	-0.10	
east coast	$\log_{10}(r)$	-4.09	-1.80	-1.75	-0.42	18.4	-4.59	-2.30	-2.29	-0.71	25.0
	$\log_{10}(t_f)$	-1.31	0.34	0.31	3.02		0.03	1.65	1.55	4.50	
	$\log_{10}(\theta)$	-4.05	-1.95	-1.79	-0.12		-3.93	-1.96	-1.79	-0.15	
east coast (1964)	$\log_{10}(r)$	-4.53	-1.23	-1.67	2.45	3.6	-5.00	-1.69	-2.07	1.80	4.2
	$\log_{10}(t_f)$	-2.67	0.87	0.96	5.00		-0.75	2.07	2.47	5.00	
	$\log_{10}(\theta)$	-3.24	-1.00	-0.86	0.46		-2.92	-1.09	-0.97	0.32	
Pooled	$\log_{10}(r)$	-4.67	-1.82	-1.89	0.02	9.8	-4.83	-1.91	-2.02	-0.14	10.3
	$\log_{10}(t_f)$	-1.52	0.13	-0.05	4.65		-0.64	1.23	1.16	4.93	
	$\log_{10}(\theta)$	-4.35	-2.16	-2.05	-0.06		-4.21	-1.99	-1.76	-0.04	

Effective population sizes
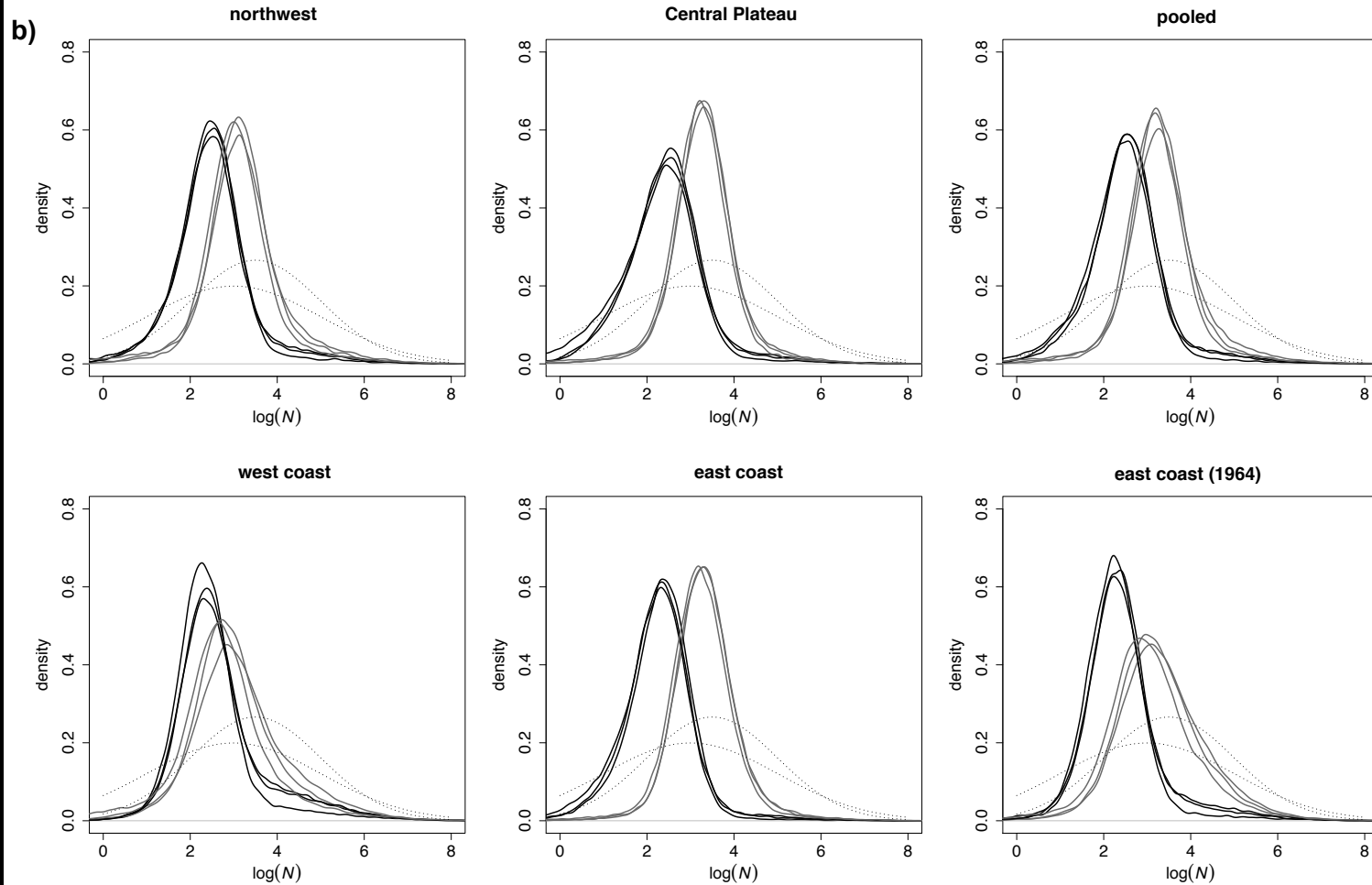
Effective population size

Region	Parameter	90% HPD lower	Mean	Median	90% HPD upper	BF ($N_0 < N_1$)
northwest	N_0	8	308	290	6 319	3.4
	N_1	56	1 412	1291	48 966	
	T	2	2 722	1767	7 682 985	
west coast	N_0	12	414	276	15 350	1.8
	N_1	17	971	769	87 386	
	T	2	6394	30 463	15 908 784	
Central Plateau	N_0	4	225	243	5 043	5.2
	N_1	129	1 912	1880	28 184	
	T	2	1 209	617	24 199 114	
east coast	N_0	10	195	202	2 842	9.8
	N_1	140	2 023	1900	29 078	
	T	6	2 110	1702	1 094 806	
east coast (1964)	N_0	11	243	199	3 948	3.8
	N_1	45	1 709	1 416	91 738	
	T	3	7 021	9 622	5 996 999	
Pooled	N_0	9	318	318	6 457	4.6
	N_1	93	1 903	1 750	41 907	
	T	2	2 364	1 424	5 808 032	

Demographic scenarios
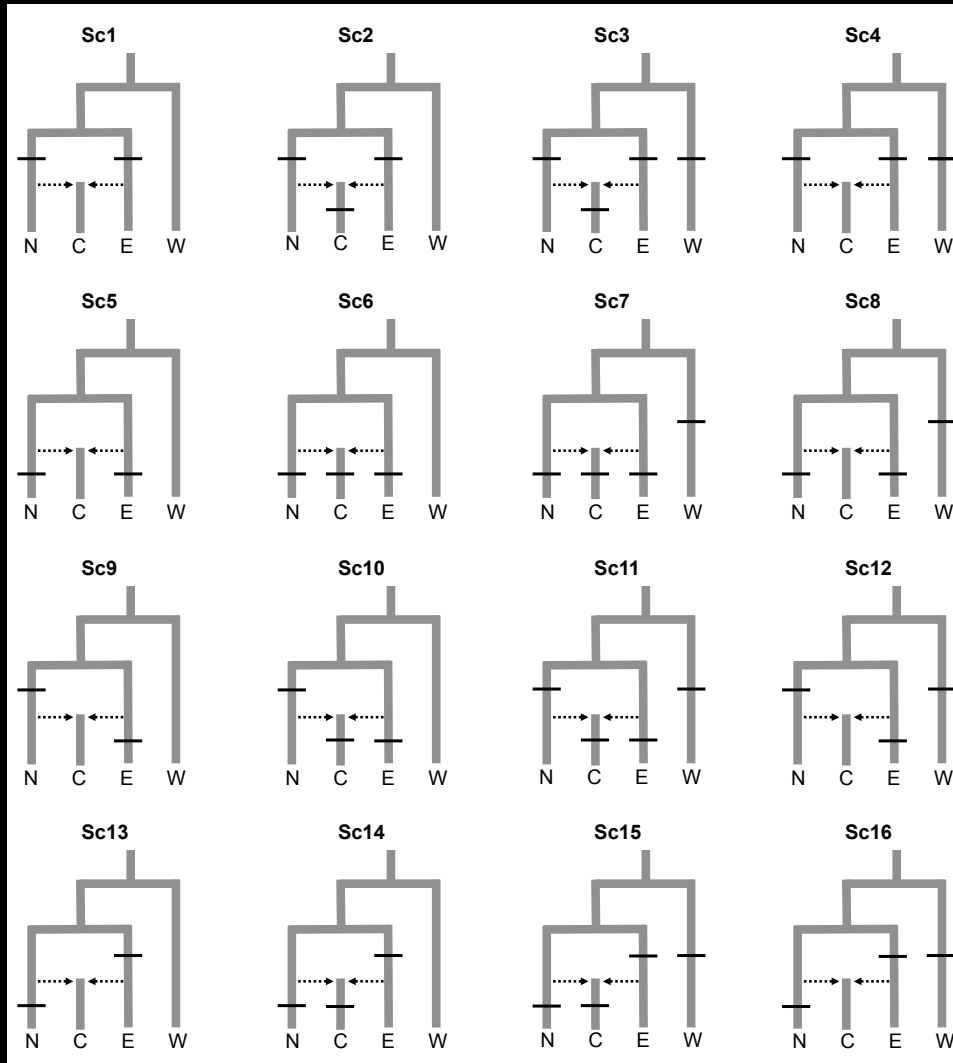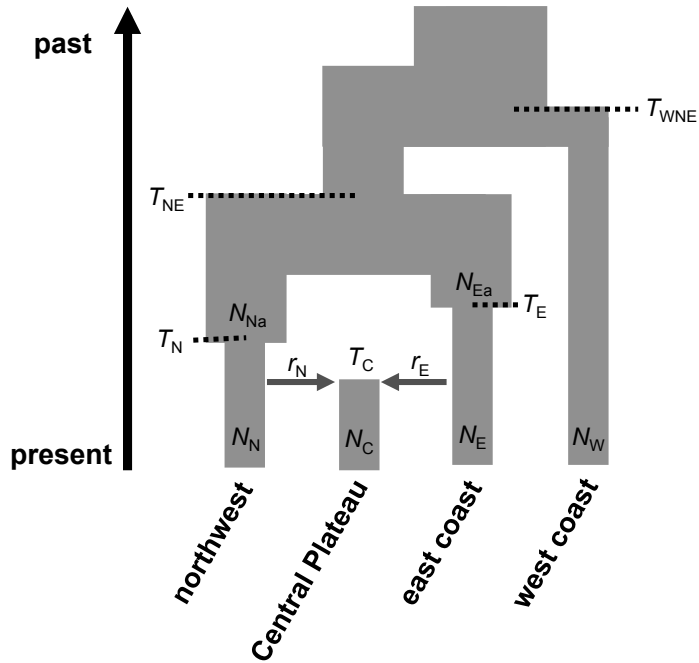
Parameter	90% HPD lower	Mean	Median	90% HPD upper	Prior
N_N	144	497	468	848	UN~[10; 1 000]
N_W	146	446	419	763	UN~[10; 1 000]
N_C	93	432	396	788	UN~[10; 1 000]
N_E	491	714	722	996	UN~[10; 1 000]
N_{Na}	1203	5213	5119	9377	UN~[10; 10 000]
N_{Ea}	2648	6418	6849	9999	UN~[10; 10 000]
T_C	21	117	100	202	UN~[20; 20 000]
T_N	40	578	402	1168	UN~[20; 20 000]
T_E	100	1140	836	2302	UN~[20; 20 000]
T_{NE}	2006	3060	2682	4312	UN~[20; 20 000]
T_{WNE}	2112	5180	3840	9640	UN~[20; 20 000]
r_N	0.08	0.40	0.40	0.70	UN~[0.001; 0.999]
r_E	0.30	0.60	0.60	0.92	UN~[0.001; 0.999]
μ	1×10^{-4}	3×10^{-4}	2×10^{-4}	4×10^{-4}	UN~[1×10^{-4}; 1×10^{-3}]
P	0.10	0.17	0.16	0.25	UN~[0.1; 0.3]
SNI	8×10^{-8}	7×10^{-7}	1×10^{-7}	2×10^{-6}	UN~[1×10^{-8}; 18×10^{-3}]

Summary of results

- ABC current N_e 432–714 individuals
- MSVAR ancestral N_e 1,000–2,000 individuals
- MSVAR current N_e 200–1,000 individuals

- BOTTLENECKs statewide   2–6k YBP

- MSVAR population declines   2–4k YBP
-                 29–48k YBP

- MSVAR population size decline   78–90%

Main findings

- Devils have had low genetic diversity for thousand of years

- Population declines coincides with climate changes during the LGM and increased ENSO activity

- European settlement and DFTD has not influenced genetic diversity

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Population genetics

Extensive population decline in the Tasmanian devil predates European settlement and devil facial tumour disease

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