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September 2015

Population analysis of the *Bulldog* breed

Genetic analysis of the Kennel Club pedigree records of the UK ***Bulldog*** population has been carried out with the aim of estimating the rate of loss of genetic diversity within the breed and providing information to guide a future sustainable breeding strategy. The population statistics summarised provide a picture of trends in census size, the number of animals used for breeding, the rate of inbreeding and the estimated effective population size. The rate of inbreeding and estimated effective population size indicate the rate at which genetic diversity is being lost within the breed. The analysis also calculates the average relationship (kinship) among all individuals of the breed born per year and is used to determine the level of inbreeding that might be expected if matings were made among randomly selected dogs from the population (the expected rate of inbreeding).

Summary of results

The analysis utilises the complete computerised pedigree records for the current UK Kennel Club registered ***Bulldog*** population, and statistics were calculated for the period 1980-2014.



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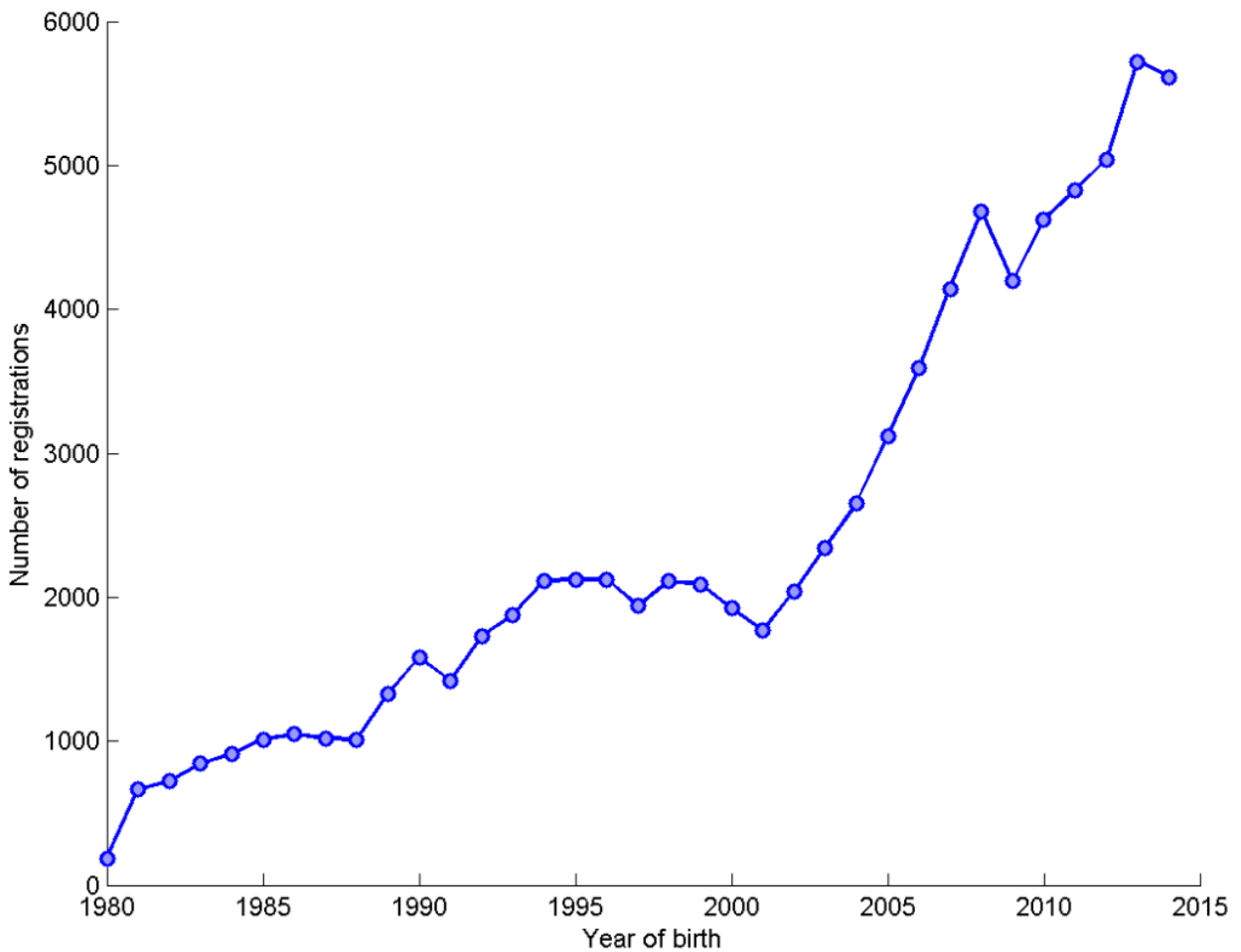
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Figure 1: a plot of number of registrations by year of birth, indicative of any changing trend in popularity of the breed, followed by the yearly trend in number of animals registered (and 95% confidence interval).

Breed: Bulldog

Figure 1: Number of registrations by year of birth



Trend of registrations over year of birth (1980-2014) = 140.71 per year (with a 95% confidence interval of 122.19 to 159.22).



Table 1: census statistics by year, including sire use statistics.

Table 1: by year (1980-2014), the number of registered puppies born, by the number of unique dams and sires; maximum, median, mode, mean and standard deviation of number of puppies per sire; and the percentage of all puppies born to the most prolific 50%, 25%, 10% and 5% of sires.

year	#born	#dams	#sires	puppies per sire					%puppies sired by most prolific sires			
				max	median	mode	mean	sd	50% sires	25% sires	10% sires	5% sires
1980	185	128	64	14	2	1	2.89	2.78	80	58.38	31.35	20
1981	670	235	118	57	4	1	5.68	7.02	82.69	60.75	38.81	25.67
1982	721	227	105	41	5	1	6.87	6.78	82.8	57.28	33.56	19.97
1983	844	236	98	109	5	3	8.61	12.91	83.65	64.45	42.89	29.86
1984	909	256	101	83	5	2	9	11.81	84.71	66.01	42.13	25.96
1985	1011	272	105	77	5	1	9.63	12.35	85.76	63.4	42.33	26.61
1986	1050	299	102	62	6	2	10.29	11.78	83.81	64.86	38.38	23.14
1987	1019	281	101	76	6	2	10.09	11.24	83.61	60.55	36.31	23.06
1988	1011	286	104	59	6	1	9.72	11.24	84.97	63.8	37.78	23.44
1989	1332	323	125	89	7	1	10.66	12.51	85.44	62.16	38.74	22.97
1990	1583	386	137	77	7	1	11.55	13.51	86.04	63.36	39.23	25.02
1991	1422	368	156	60	6	3	9.12	9.73	81.79	59.14	35.72	23.35
1992	1732	428	167	59	6	2	10.37	11.74	85.05	62.82	38.28	23.73
1993	1877	470	168	122	6	3	11.17	15.28	85.3	66.22	42.57	27.12
1994	2114	500	175	113	7	6	12.08	15.54	85.15	66.13	42.34	26.82
1995	2123	519	165	78	7	6	12.87	14.32	84.08	62.46	37.49	23.17
1996	2124	483	181	117	6	6	11.73	16.02	85.64	66.81	42.33	28.48
1997	1942	464	186	105	6	5	10.44	12.97	84.71	63.59	39.13	25.18
1998	2112	517	222	71	5	4	9.51	11.16	83.85	63.87	38.68	24.76
1999	2091	459	194	58	7.5	5	10.78	10.36	82.59	58.73	31.9	20.37
2000	1924	438	205	73	6	2	9.39	10.97	83.37	62.06	38.57	24.48
2001	1769	422	189	76	6	1	9.36	10.7	85.02	61.5	36.74	22.5
2002	2042	482	215	79	6	1	9.5	10.69	84.92	62.68	37.32	23.36
2003	2342	535	232	68	6	1	10.09	11.66	85.78	63.88	37.96	24.89
2004	2652	606	222	97	7	1	11.95	14.04	85.97	64.93	38.46	23.6
2005	3117	714	285	136	7	1	10.94	14.28	85.98	64.9	40.62	25.02
2006	3589	829	317	144	6	1	11.32	15.57	86.88	67.54	43.72	28.42
2007	4142	937	368	178	6	1	11.26	15.44	85.8	65.02	40.42	26.07
2008	4677	1100	427	133	6	1	10.95	13.5	84.56	64.29	39.53	25.06
2009	4196	1039	434	99	5	1	9.67	12.57	86.42	65.92	40.87	27.76
2010	4622	1087	454	113	6	1	10.18	12.65	83.9	62.92	39.53	26.78
2011	4830	1126	497	77	6	1	9.72	11.2	84.66	63.35	38.53	24.29
2012	5043	1181	557	95	5	1	9.05	11.29	85.78	64.72	40.27	25.82
2013	5720	1303	553	94	6	1	10.34	13.61	86.24	66.24	42.06	27.73
2014	5615	1214	497	118	7	6	11.3	13.52	82.97	61.37	38.5	26.09

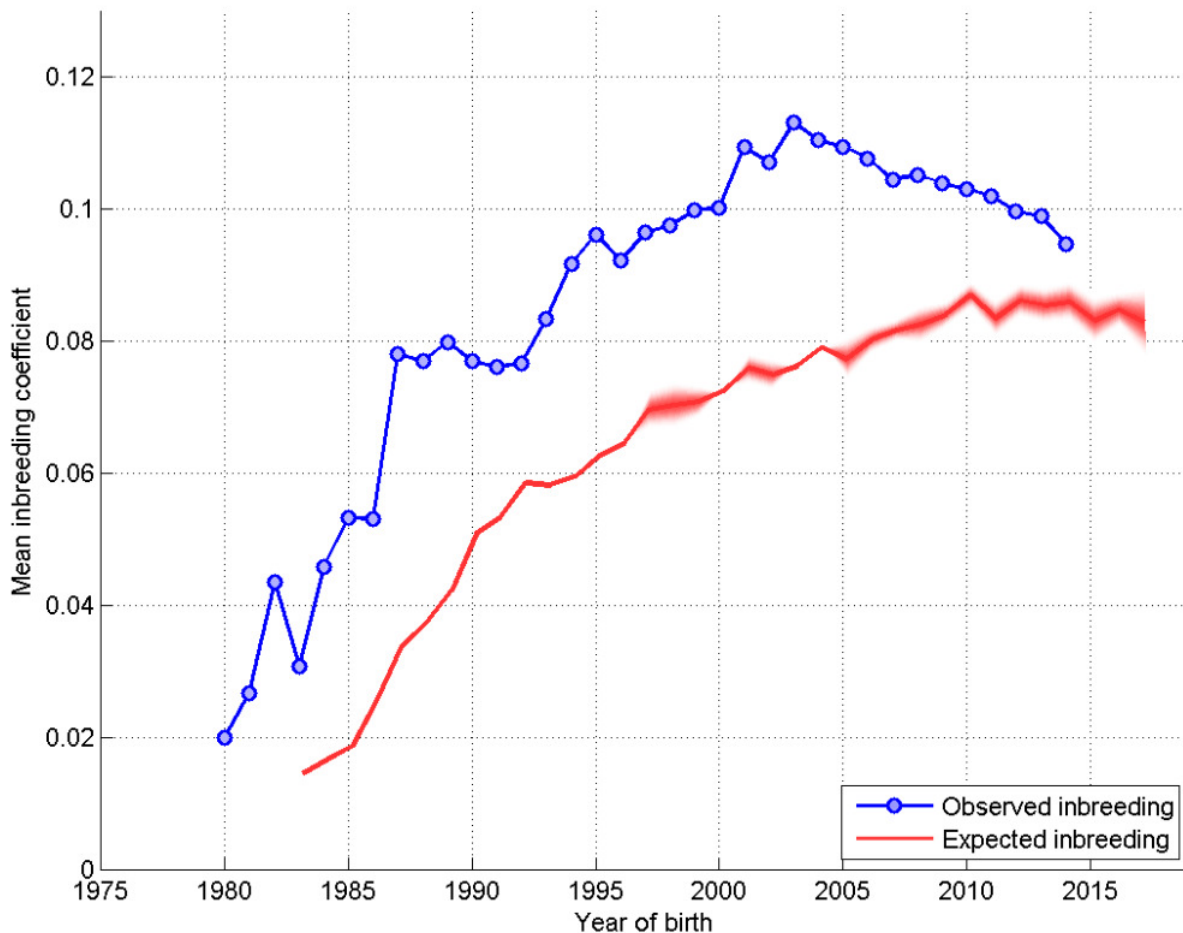


Generation interval: the mean average age (in years) of parents at the birth of offspring which themselves go on to reproduce.

Mean generation interval (years) = 3.16

Figure 2: a plot of the annual mean observed inbreeding coefficient (showing loss of genetic diversity), and mean expected inbreeding coefficient (from 'random mating') over the period 1980-2014. 'Expected inbreeding' is staggered by the generation interval and, where >2000 animals are born in a single year, the 95% confidence interval is indicated.

Figure 2: Annual mean observed and expected inbreeding coefficients





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Estimated effective population size: the rate of inbreeding (slope or steepness of the observed inbreeding in Figure 2) is used to estimate the effective population size of the breed. The effective population size is the number of breeding animals in an idealised, hypothetical population that would be expected to show the same rate of loss of genetic diversity (rate of inbreeding) as the breed in question. It may be thought of as the size of the 'gene pool' of the breed.

Below an effective population size of 100 (inbreeding rate of 0.50% per generation) the rate of loss of genetic diversity in a breed/population increases dramatically (Food & Agriculture Organisation of the United Nations, "Monitoring animal genetic resources and criteria for prioritization of breeds", 1992). An effective population size of below 50 (inbreeding rate of 1.0% per generation) indicates the future of the breed may be considered to be at risk (Food & Agriculture Organisation of the United Nations, "Breeding strategies for sustainable management of animal genetic resources", 2010).

Where the rate of inbreeding is negative (implying *increasing* genetic diversity in the breed), effective population size is denoted 'n/a'.

Estimated effective population size = 67.9

NB - this estimate is made using the rate of inbreeding over the whole period 1980-2014



Table 2: a breakdown of census statistics, sire and dam usage and indicators of the rate of loss of genetic diversity over 5 year periods (1980-4, 1985-9, 1990-4, 1995-9, 2000-4, 2005-9, 2010-14). Rate of inbreeding and estimated effective population size for each 5-year block can be compared with the trend in observed inbreeding in Figure 2.

Table 2: by 5-year blocks, the mean number of registrations; for sires the total number used, maximum, mean, median, mode, standard deviation and skewness (indicative of the size of the 'tail' on the distribution) of number of progeny per sire; for dams the total number used, maximum, mean, median, mode, standard deviation and skewness of number of progeny per dam; rate of inbreeding per generation (as a decimal, multiply by 100 to obtain as a percentage); mean generation interval; and estimated effective population size.

years	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014
Mean #registrations	665.8	1084.6	1745.6	2078.4	2145.8	3944.2	5166
Total #sires	259	294	432	522	599	1052	1506
Max #progeny	239	193	273	358	273	355	273
Mean #progeny	12.842	18.432	20.201	19.904	17.91	18.745	17.147
Median #progeny	6	8	8	9	8	7	7
Mode #progeny	1	1	1	1	1	1	1
SD #progeny	21.831	30.229	32.282	32.186	27.483	32.01	29.003
Skew #progeny	5.8041	3.5463	3.7494	4.6873	3.5771	4.4243	4.2347
Total #dams	810	1082	1535	1841	1870	3403	4624
Max #progeny	20	25	30	34	32	27	30
Mean #progeny	4.1062	5.0111	5.6853	5.6437	5.7369	5.7949	5.5848
Median #progeny	3	4	5	5	5	5	5
Mode #progeny	1	1	4	4	1	1	1
SD #progeny	3.0628	3.7275	4.1312	3.9071	4.1299	4.0841	3.9183
Skew #progeny	1.4701	1.4483	1.5207	1.4594	1.4744	1.2448	1.4102
Rate of inbreeding	0.019137	0.026097	0.01257	0.004356	0.008621	-0.00451	-0.00708
Generation interval	3.3219	3.1698	3.1645	3.1129	3.1638	3.0042	3.215
Effective pop size	26.127	19.159	39.778	114.8	57.996	n/a	n/a



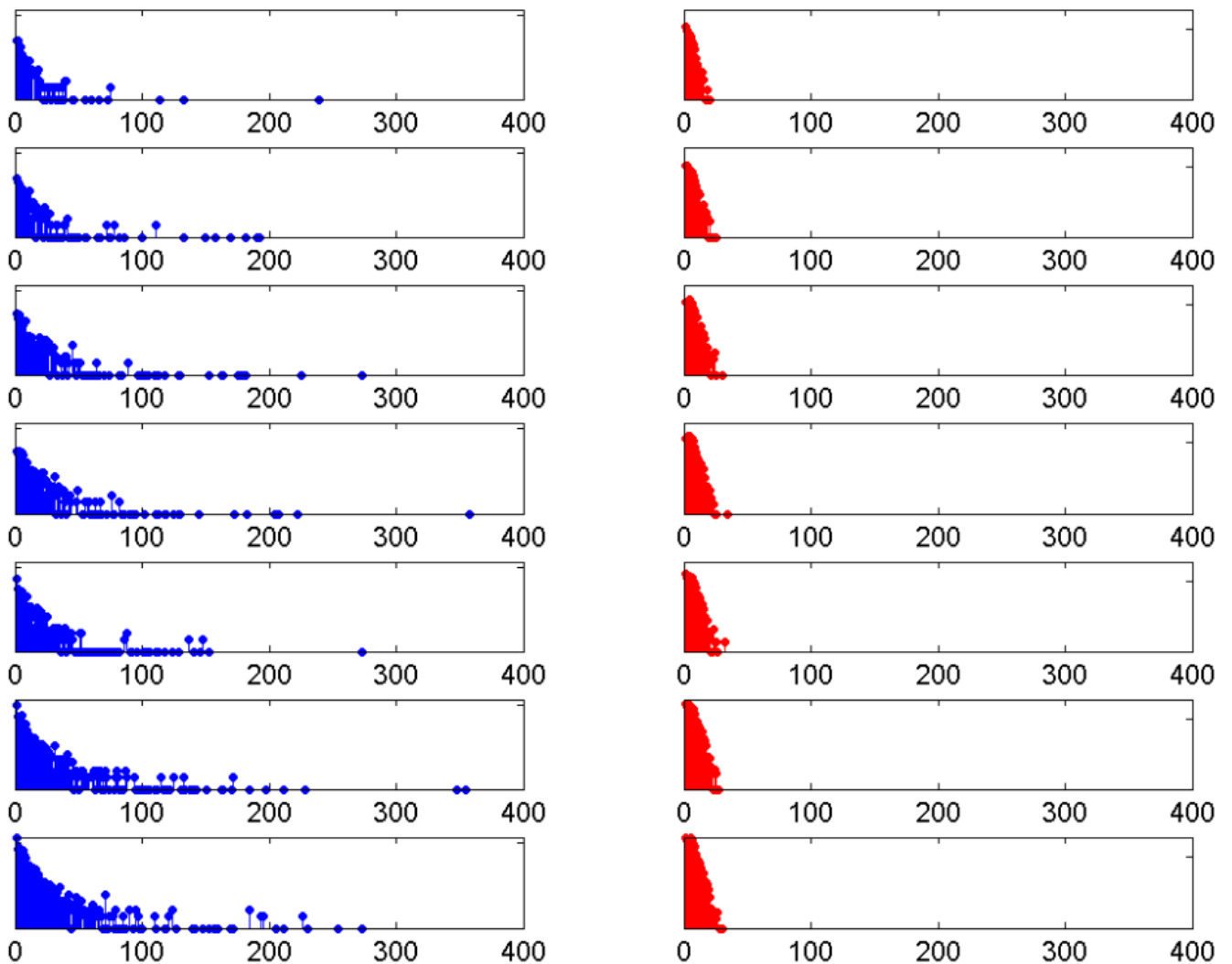
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Figure 3: a histogram ('tally' distribution) of number of progeny per sire and dam over each of the seven 5-year blocks above. A longer 'tail' on the distribution of progeny per sire is indicative of 'popular sires' (few sires with a very large number of offspring, known to be a major contributor to a high rate of inbreeding).

Figure 3: Distribution of progeny per sire (blue) and per dam (red) over 5-year blocks (1980-4 top, 2010-14 bottom). Vertical axis is a logarithmic scale.





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Comments

As with most breeds, the rate of inbreeding was at its highest in this breed in the 1980s and 1990s. This represents a 'genetic bottleneck', with genetic variation lost from the population. However, latterly the rate of inbreeding has declined and even been negative, implying a slowdown in the rate of loss, and modest replenishment, of genetic diversity (possibly through the use of imported animals).

It appears that the extensive use of popular dogs as sires has increased (the 'tail' of the blue distribution increasing in figure 3).

It should be noted that, while animals imported from overseas may appear completely unrelated, this is not always the case. Often the pedigree available to the Kennel Club is limited in the number of generations, hampering the ability to detect true, albeit distant, relationships.