Flat Coat population analysis:

some background,

& a guide to the report.

THE KENNEL CLUB
Making a difference for dogs

The University of Nottingham

We all have

2 parents

4 grand parents

8 great grand parents

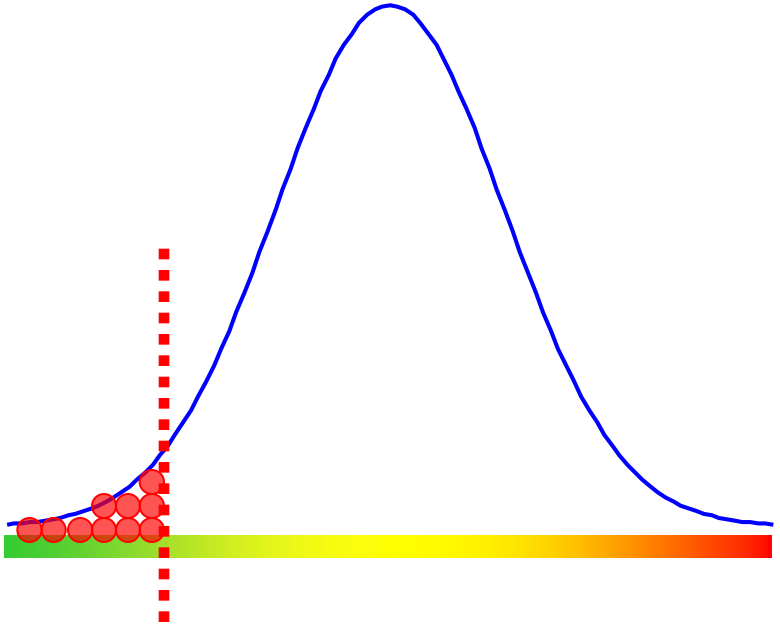
16 great great grand parents

etc…

2^n ancestors

where *n* = generations back

Furthermore, the resemblance of relatives...

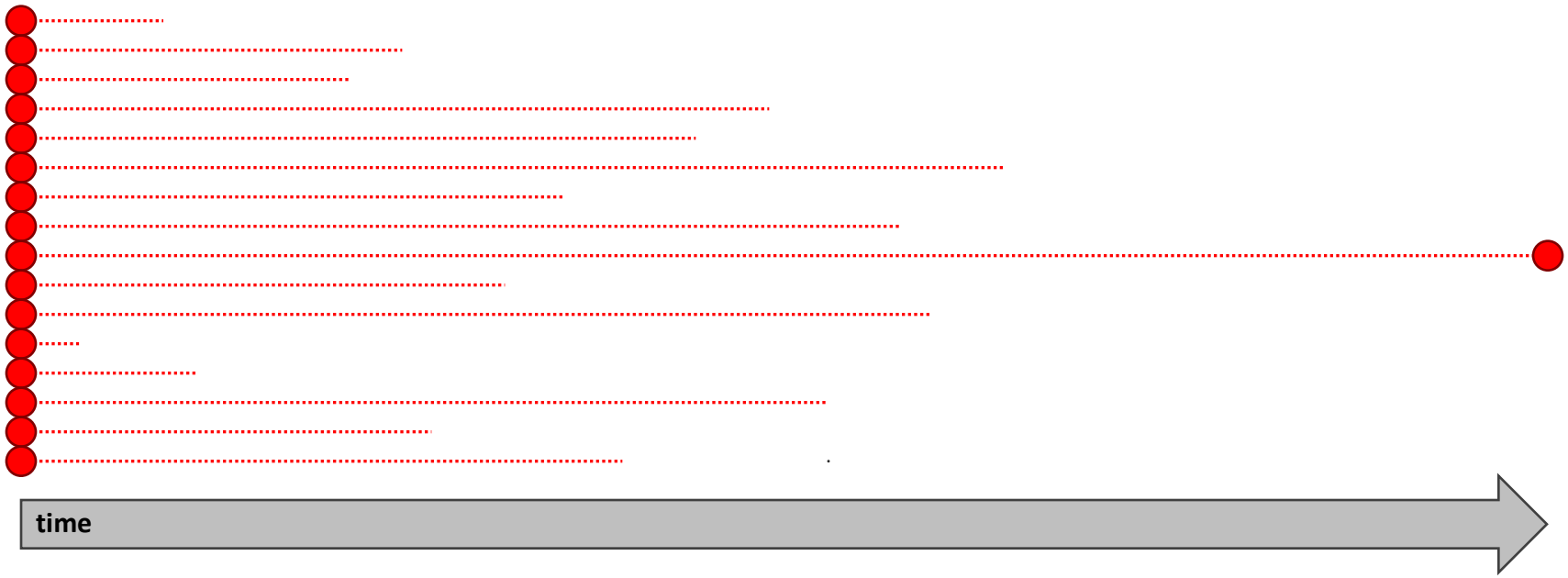


means selection will result in the mating of individuals more closely related than average

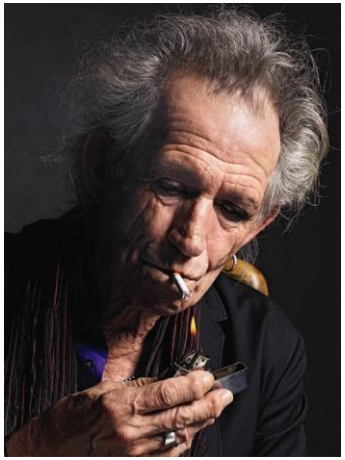
BUT - natural selection acts

against the detrimental

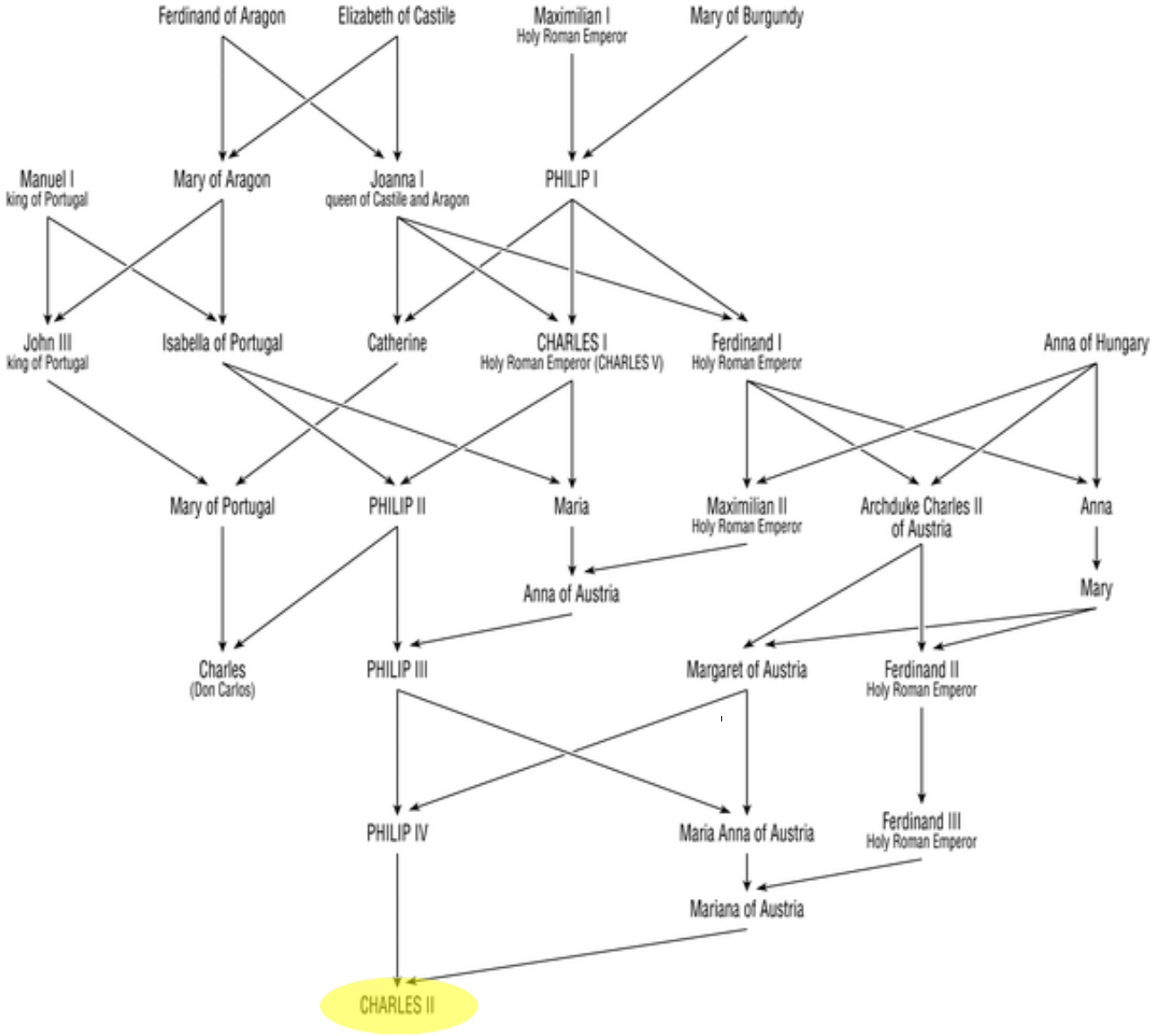
consequences of inbreeding…



It’s all about *risk*…



What are the risks associated with inbreeding?



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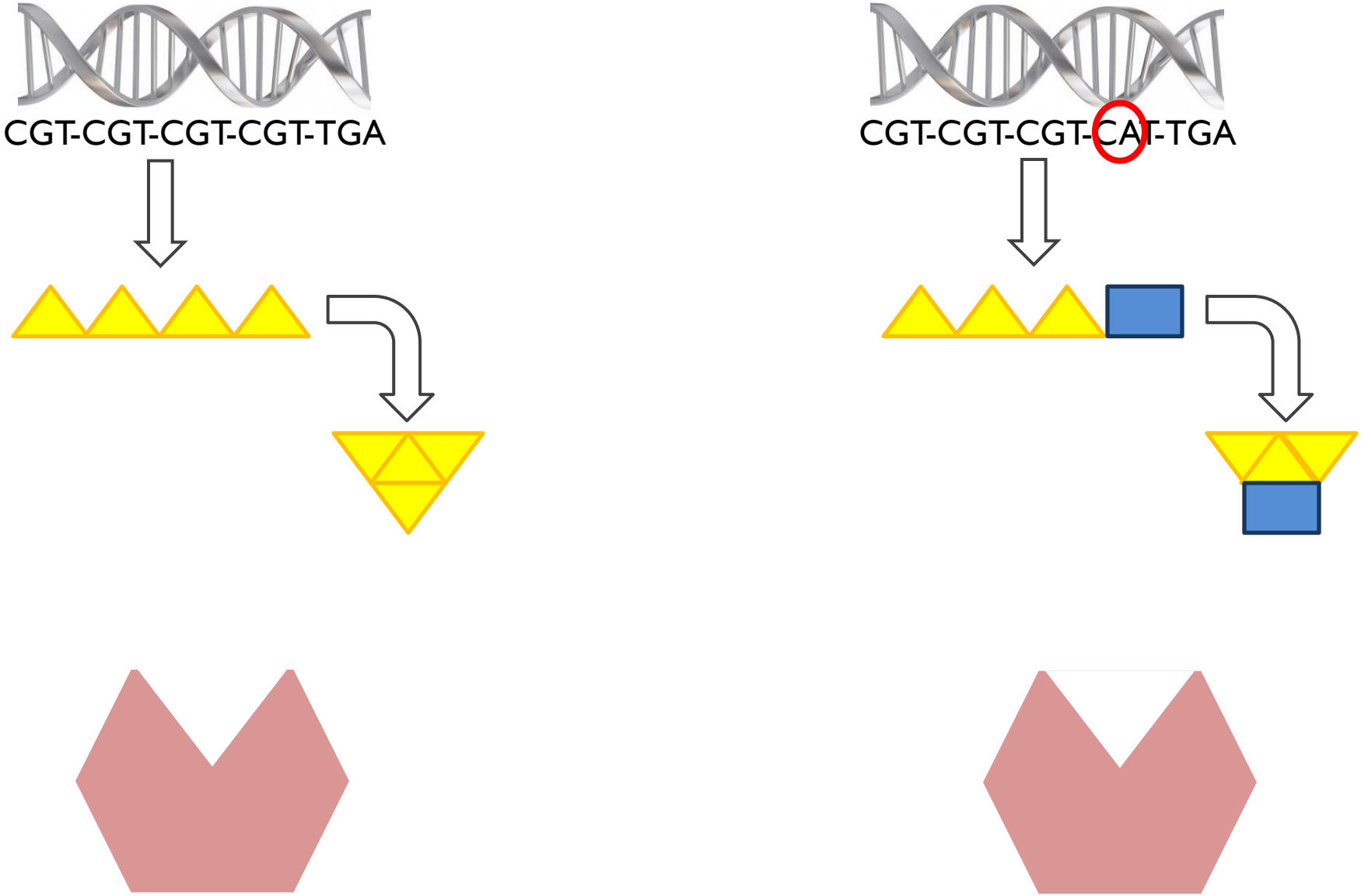
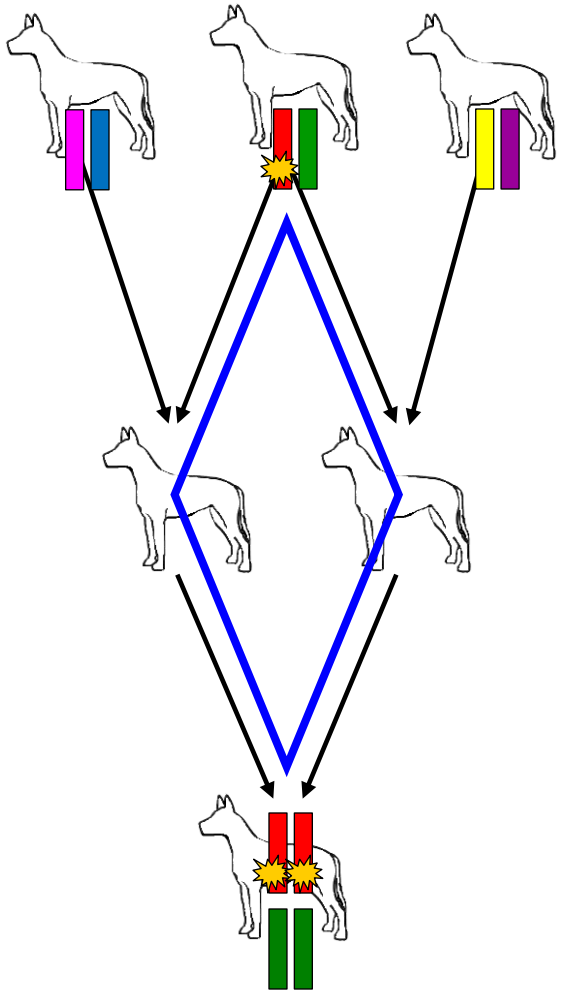
Why does inbreeding cause these problems?

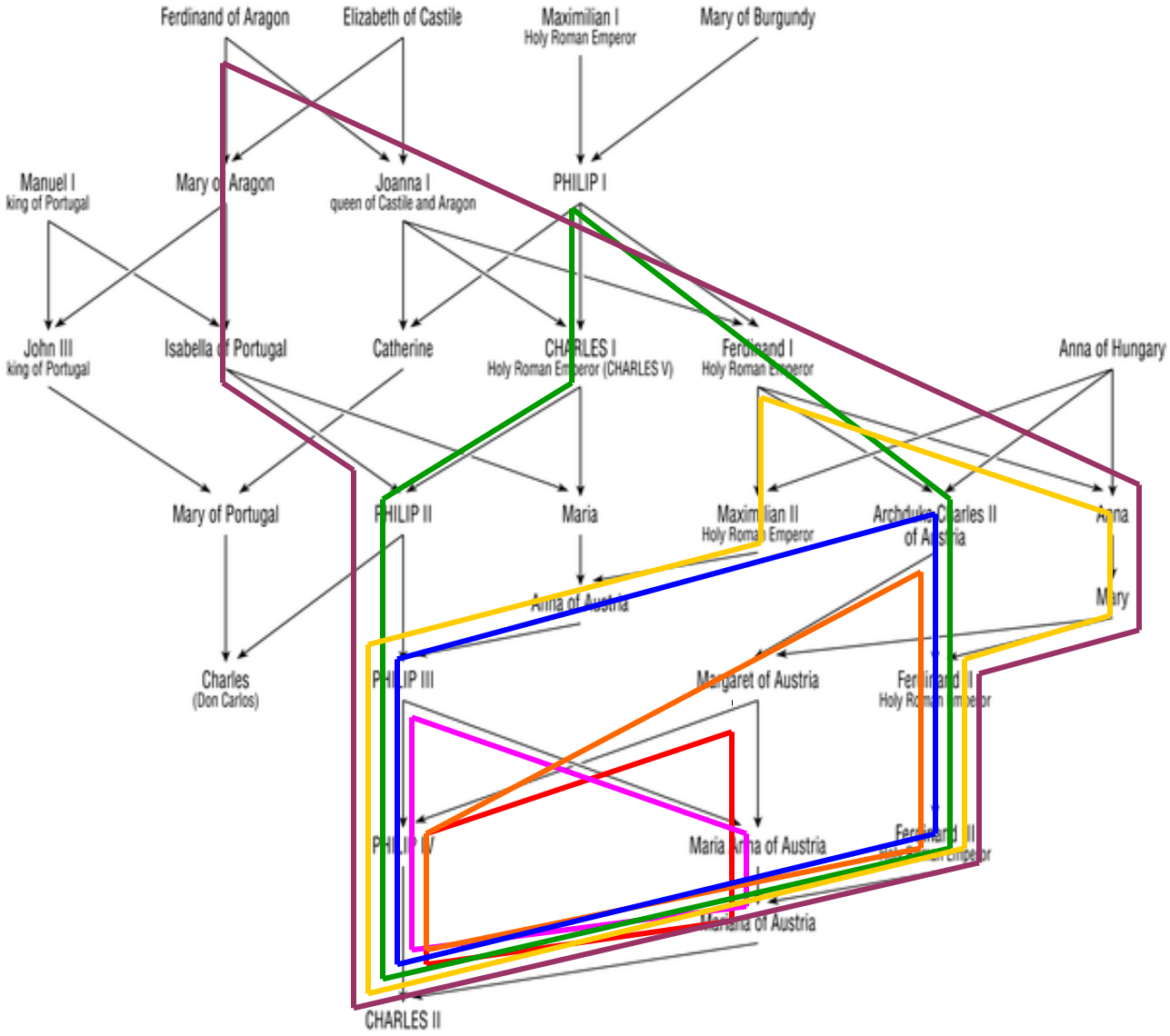


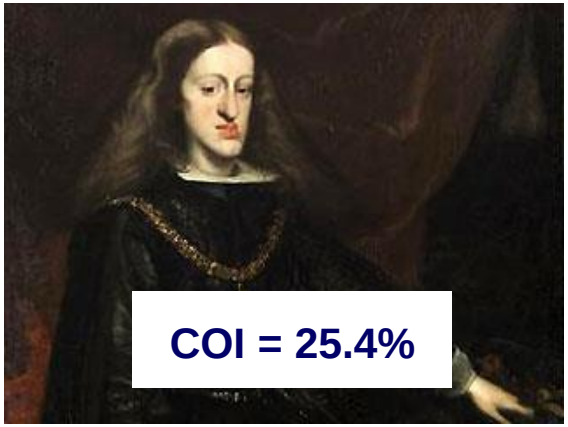
Coefficient of inbreeding (COI)



COI is the probability that the 2 copies of a gene are *Identical By Descent* (IBD)

- ***25%*** *for offspring of a full sib mating or a parent/offspring mating*
- ***12.5%*** *for offspring of a half sib mating*
- ***6.25%*** *for offspring of 1st cousins*





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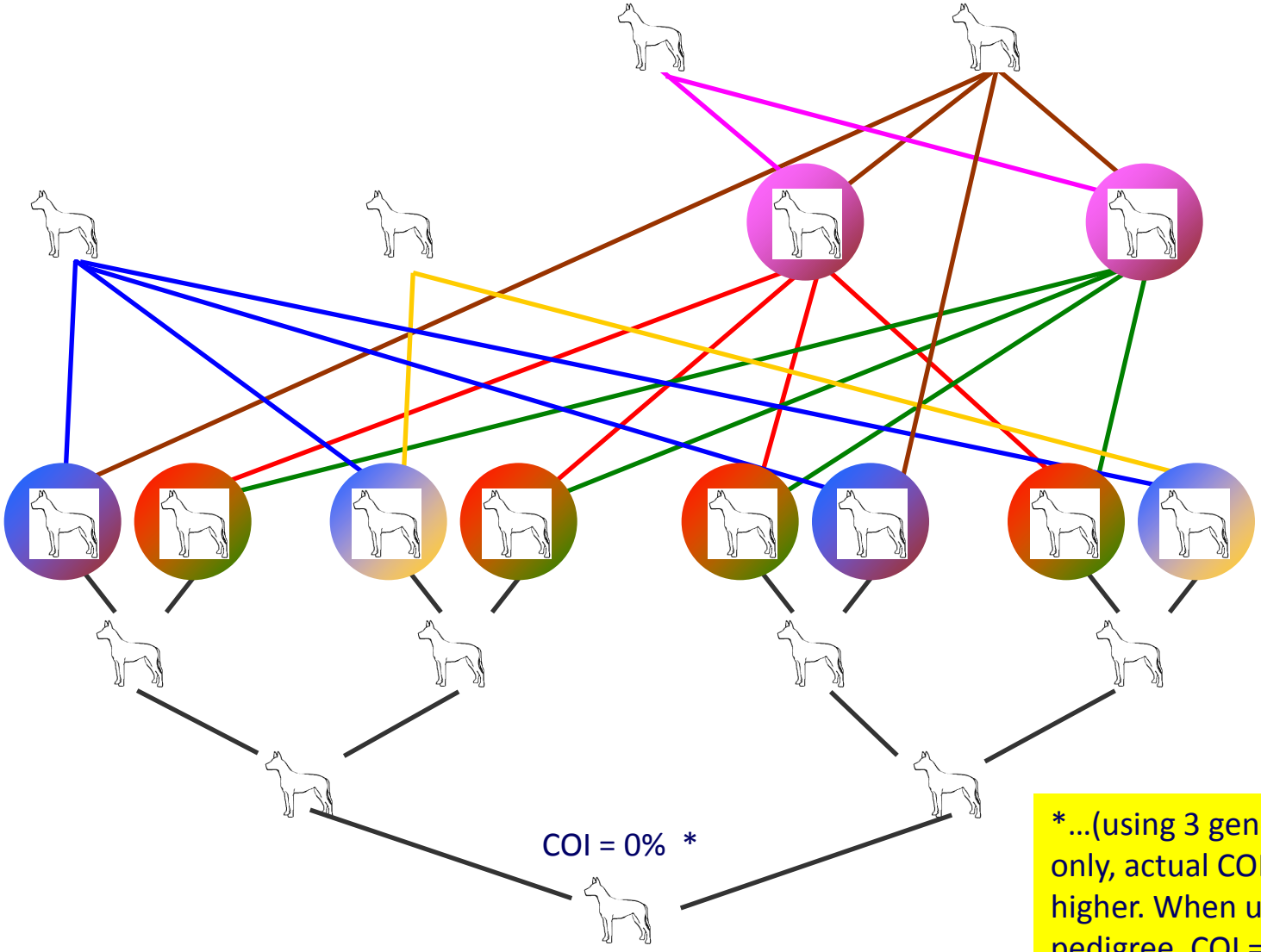
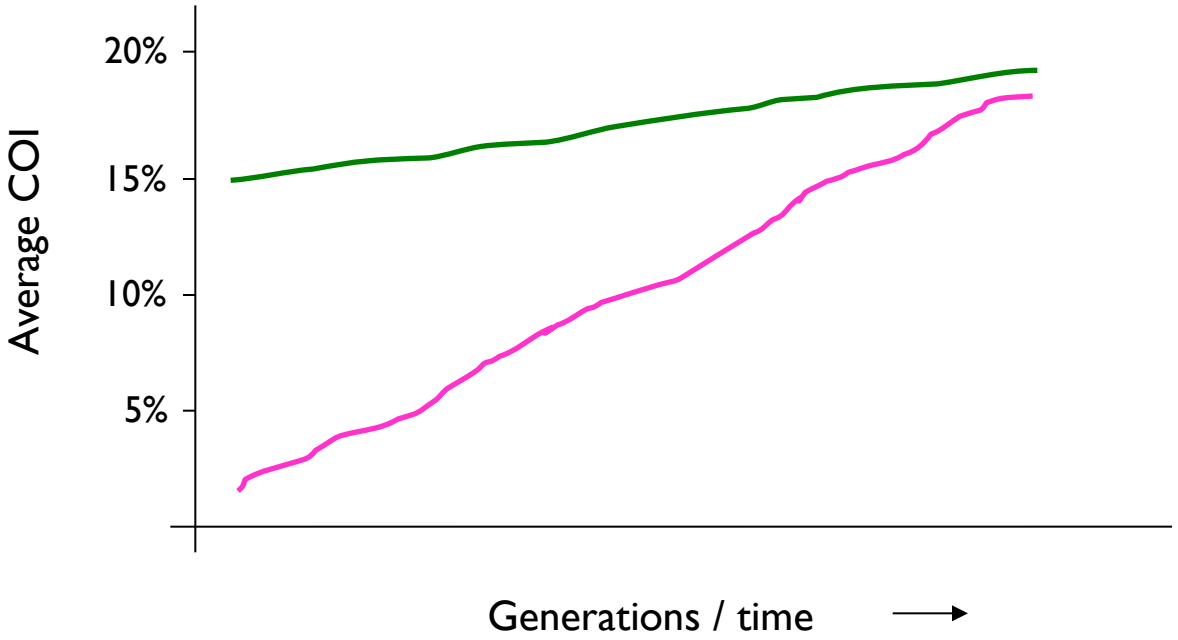
Number of generations is all important



*…(using 3 generations of pedigree only, actual COI may be considerably higher. When using 5 generations of pedigree, COI = 17%)

Rate of inbreeding (ΔF)



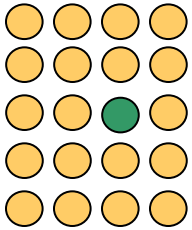
rate of inbreeding (ΔF) = **change** in average COI **over time** (or generations)

Usually quoted as the **Effective population size (Ne)**

Genetic drift

f(g) = 0.05

(1 in 20 green)

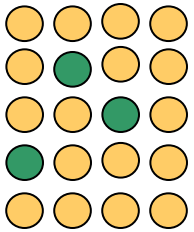


Pr = 0.06

(6/100)

f(g) = 0.15

(3 in 20 green)

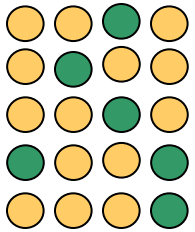


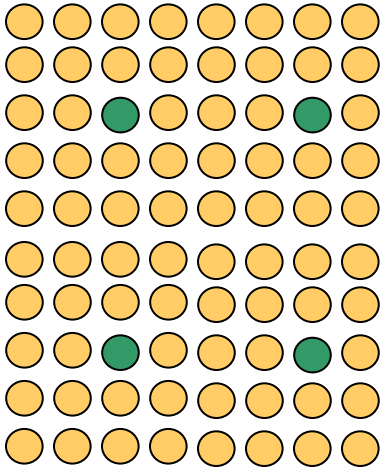
Pr = 0.045

(45/1,000)

f(g) = 0.30

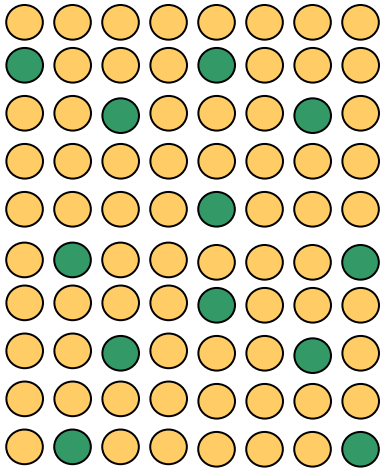
(6 in 20 green)





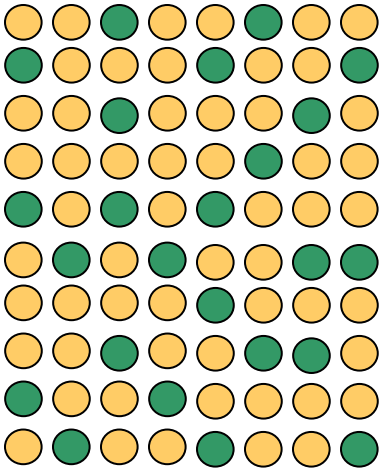
Pr = 0.0004

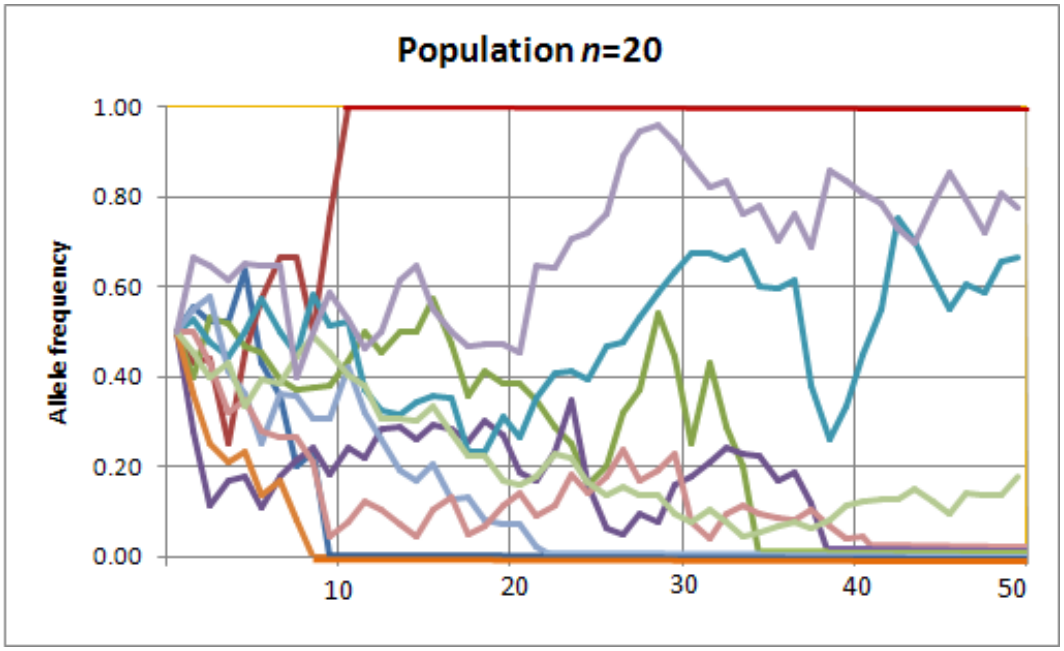
(4/10,000)

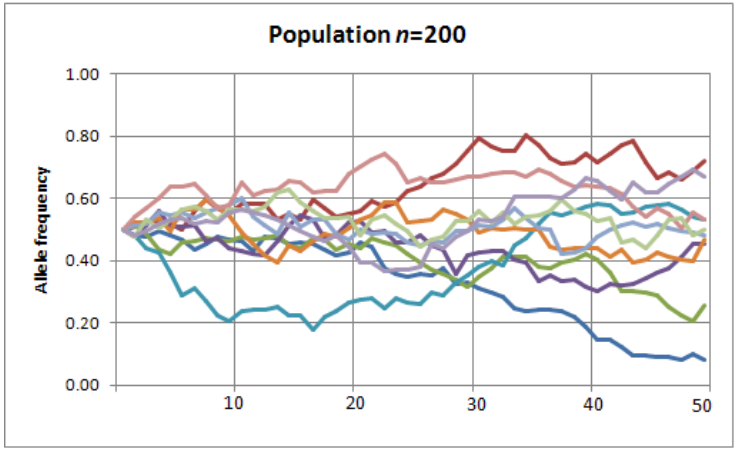


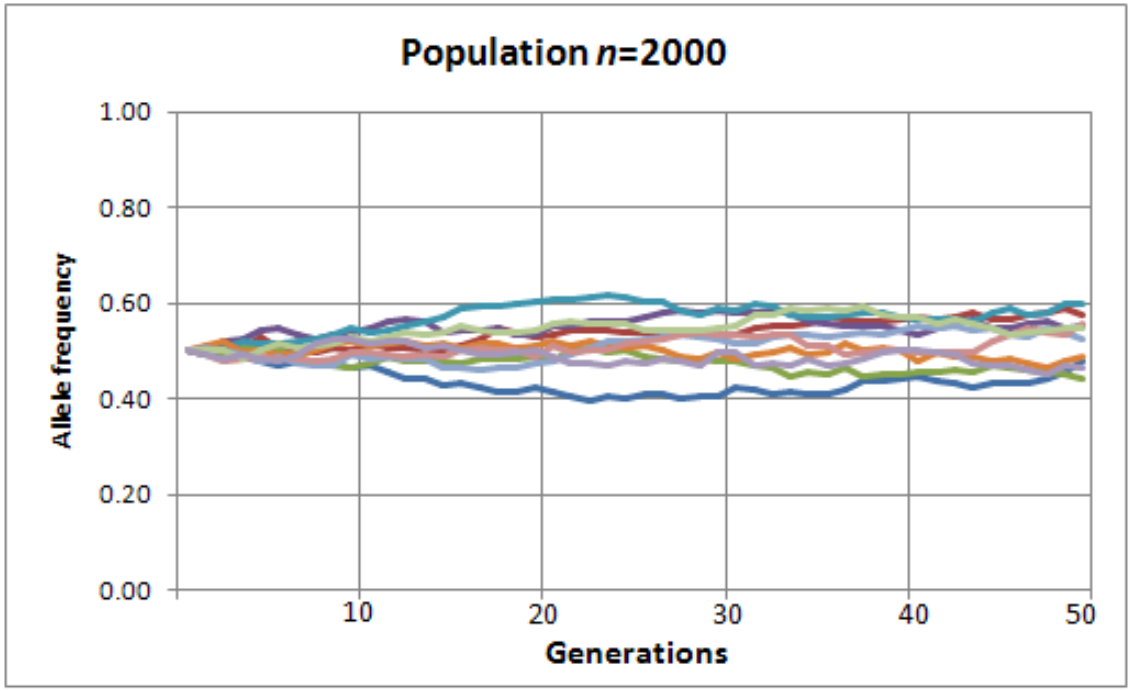
Pr = 0.0003

(3/10,000)




Population n=20
Allele frequency
1.00
0.80
0.60
0.40
0.20
0.00
10
20
30
40
50


Population n=200
Allele frequency
1.00
0.80
0.60
0.40
0.20
0.00
10
20
30
40
50


Population n=2000
Allele frequency
1.00
0.80
0.60
0.40
0.20
0.00
10
20
30
40
50
Generations

Inbreeding/drift summary

Inbreeding unavoidable in the long term

COI describes the probability of IBD, and so risk

Rate of inbreeding the important measure for breed/population

Inbreeding and drift act on allele frequencies

Paper detailing results available:

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Canine Genetics and Epidemiology

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Featured article: Trends in genetic diversity for all Kennel Club registered pedigree dog breeds

Nick Ridley / The Kennel Club

Inbreeding is widely viewed as being harmful to the well-being of individuals and populations. In populations of a limited size, complete avoidance of breeding between individuals with a shared ancestry quickly becomes impossible. Furthermore, selection within dog breeds for desirable traits will inevitably result in the breeding of individuals that resemble each other with respect to the traits under selection. This study reports the general trends in the rate of inbreeding observed through population analyses of all 215 pedigree dog breeds currently recognised by the UK Kennel Club, over the period 1980 to 2014.

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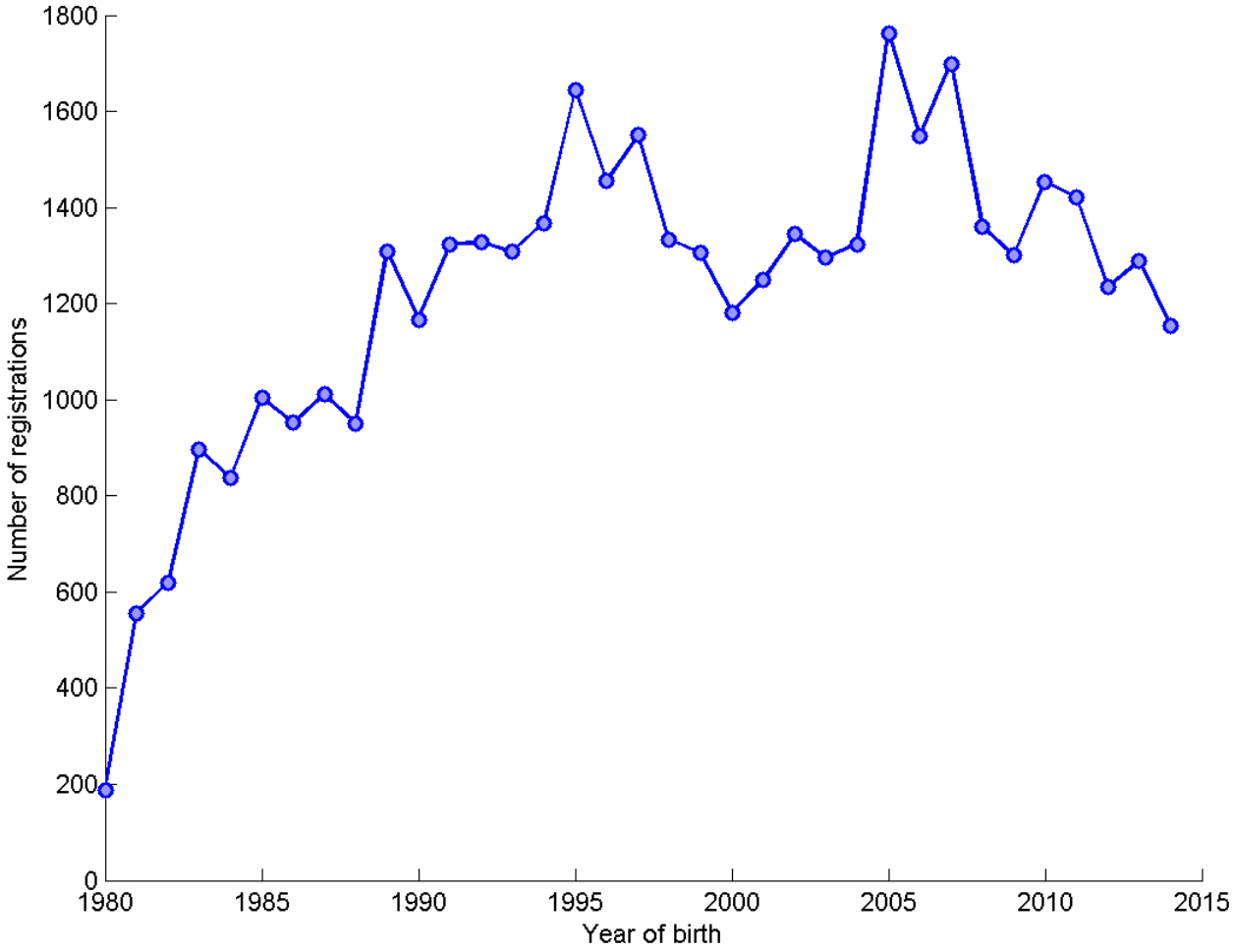
Figure 1: registrations by year of birth

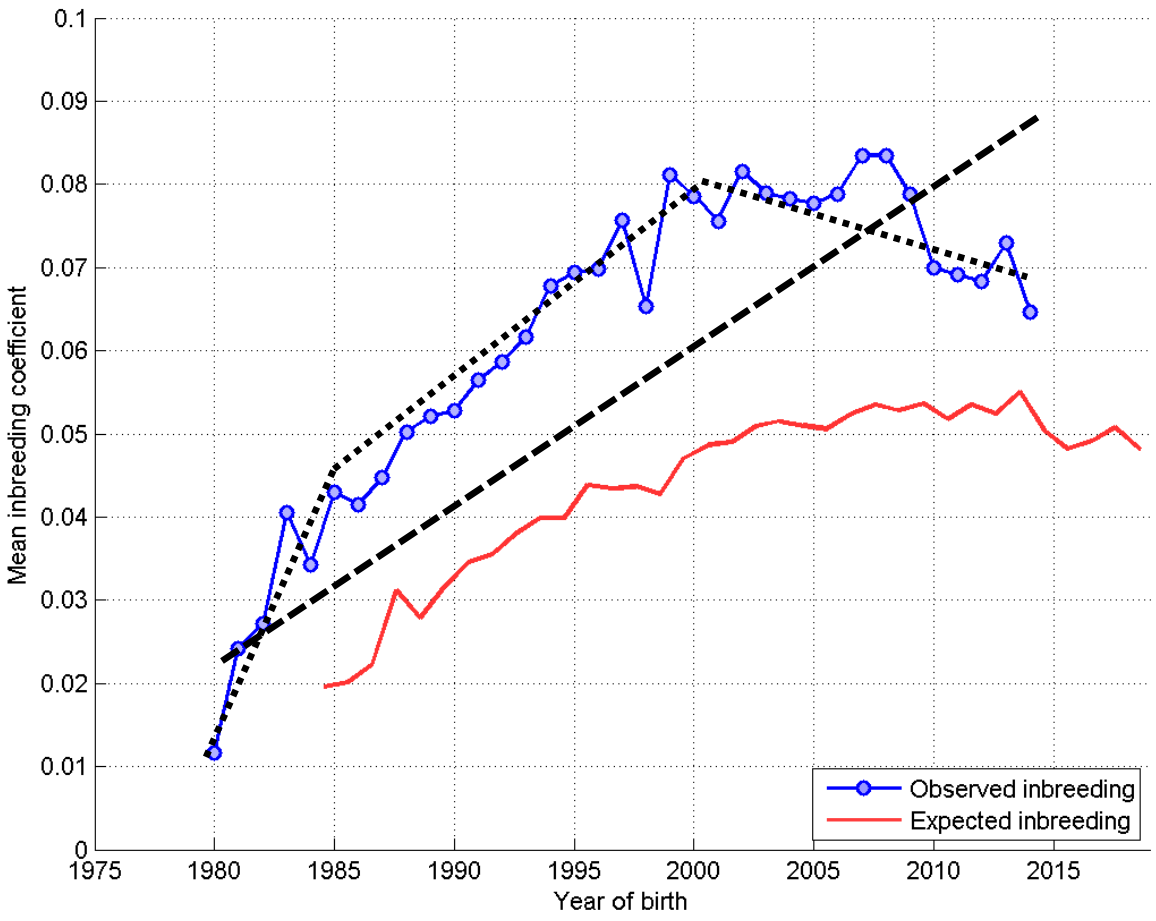


Trend of registrations over year of birth (1980-2014) = 21.3 per year
(with a 95% confidence interval of 13.01 to 29.59)

Table 1: sire statistics per year

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	187	85	57	21	2	1	3.28	3.8	85.03	63.1	38.5	25.13
1981	556	121	77	44	5	3	7.22	7.83	81.83	58.81	37.41	23.92
1982	620	111	67	36	8	1	9.25	7.53	79.19	52.74	29.84	15.81
1983	897	167	86	65	7	4	10.43	10.57	81.49	59.75	35.12	19.51
1984	837	145	83	44	8	8	10.08	8.18	78.73	53.88	27.96	16.01
1985	1003	179	98	49	7	4	10.23	9.53	78.27	56.53	34.1	20.64
1986	953	179	99	86	6	4	9.63	11.35	81.64	60.55	37.57	24.45
1987	1011	176	96	60	7.5	6	10.53	9.68	80.32	55.79	30.86	19.29
1988	950	169	90	59	7	3	10.56	11.14	82.42	62	35.89	23.68
1989	1309	195	111	73	8	7	11.79	11.43	78.76	56.76	33.23	22.31
1990	1167	178	119	52	8	10	9.81	8.78	76.69	52.78	32.31	20.22
1991	1322	183	110	71	8	7	12.02	11.77	76.4	56.81	34.11	23.45
1992	1328	183	108	79	9	9	12.3	12.9	75.6	55.87	37.05	22.89
1993	1309	178	96	70	10	9	13.64	12.14	77.31	54.09	31.86	20.7
1994	1368	195	109	50	10	6	12.55	9.91	78.36	51.83	28.22	15.72
1995	1644	221	118	66	9	9	13.93	12.58	77.25	57.73	32.06	18.49
1996	1455	192	110	102	9	6	13.23	13.94	77.53	57.46	35.53	23.99
1997	1550	212	127	79	9	9	12.2	11.7	78.19	56.77	33.03	19.42
1998	1333	185	109	58	9	1	12.23	11.9	80.65	58.21	35.11	18.3
1999	1305	187	113	43	9	9	11.55	8.89	77.24	52.87	26.36	15.94
2000	1181	161	105	51	9	9	11.25	8.85	74.51	51.48	29.64	17.02
2001	1249	180	108	54	8	1	11.56	12	82.55	60.45	37.07	20.26

Figure 2: rate of inbreeding



Estimated effective population size= 67.9

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

Table 2: trends within 1980-2014

years	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014
mean #registrations	619.4	1045.2	1298.8	1457.4	1278.6	1534.2	1309.8
Total #sires	214	295	317	327	343	389	357
Max #progeny	188	228	209	202	245	187	230
Mean #progeny	14.416	17.712	20.467	22.281	18.627	19.717	18.331
Median #progeny	7	9	10	10	10	10	9
Mode #progeny	1	4	10	1	1	1	1
SD #progeny	21.186	26.088	28.019	30.854	27.284	26.194	27.565
Skew #progeny	3.7632	3.9644	3.3338	2.738	3.8687	2.841	3.6907
Total #dams	492	699	693	783	731	846	765
Max #progeny	37	35	40	38	38	45	31
Mean #progeny	6.2703	7.4678	9.3694	9.3052	8.7442	9.0662	8.5542
Median #progeny	5	6	8	8	8	8	8
Mode #progeny	1	6	9	9	8	1	1
SD #progeny	5.0422	5.0861	5.842	5.7055	5.7146	6.2725	5.6867
Skew #progeny	1.8215	1.5296	1.3072	1.3508	1.33	1.3705	0.90344
Rate of inbreeding	0.026309	0.012895	0.017143	0.010074	0.001502	0.003463	-0.00317
Generation interval	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
Effective pop size	19.005	38.774	29.167	49.634	332.93	144.39	n/a

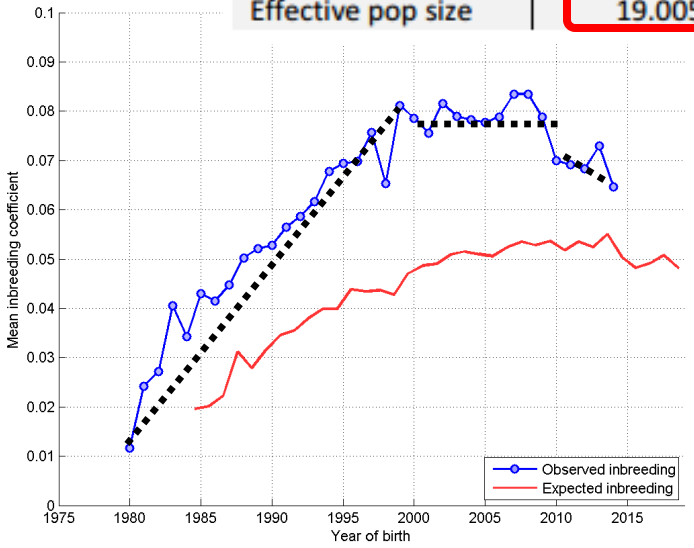
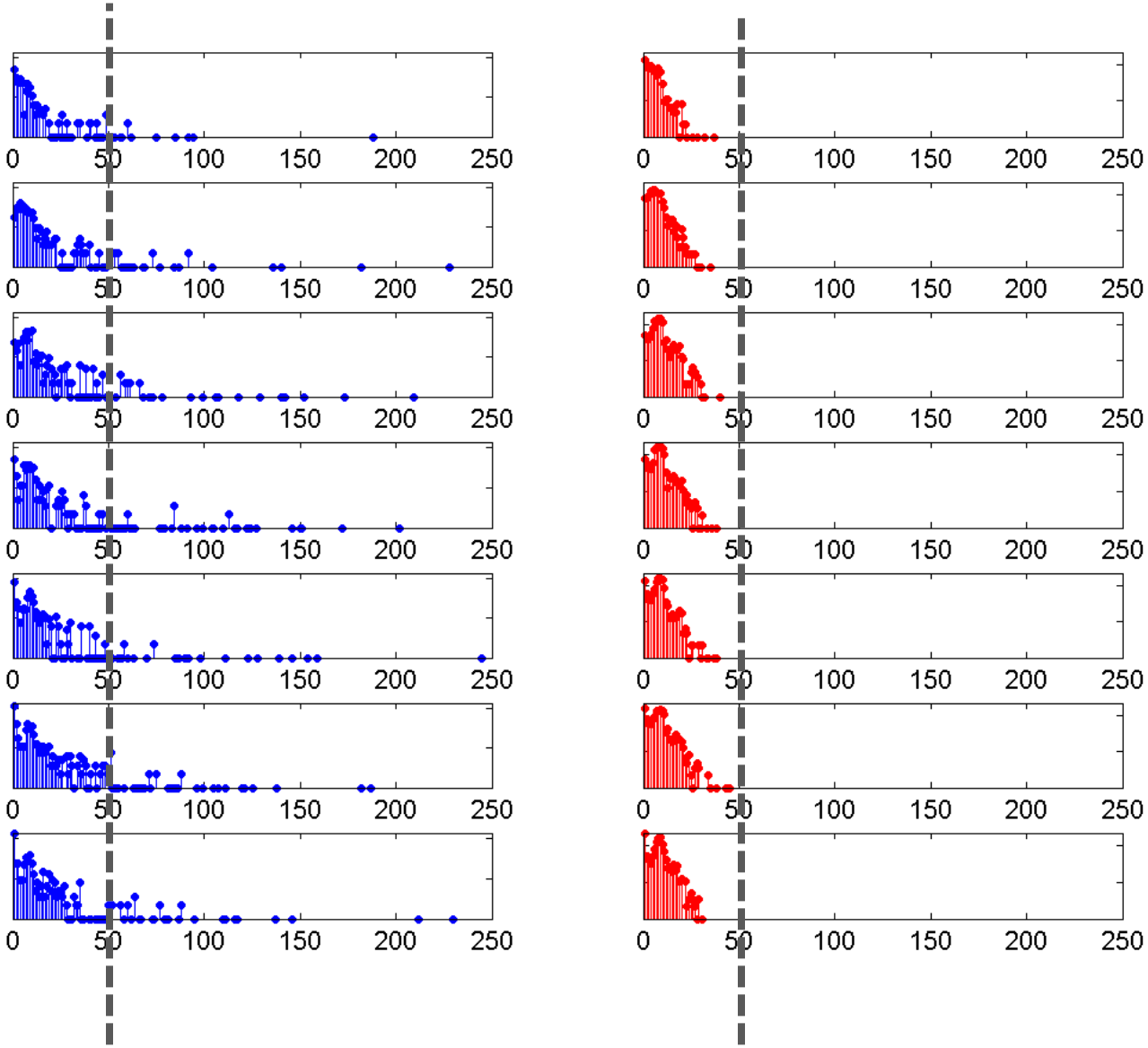
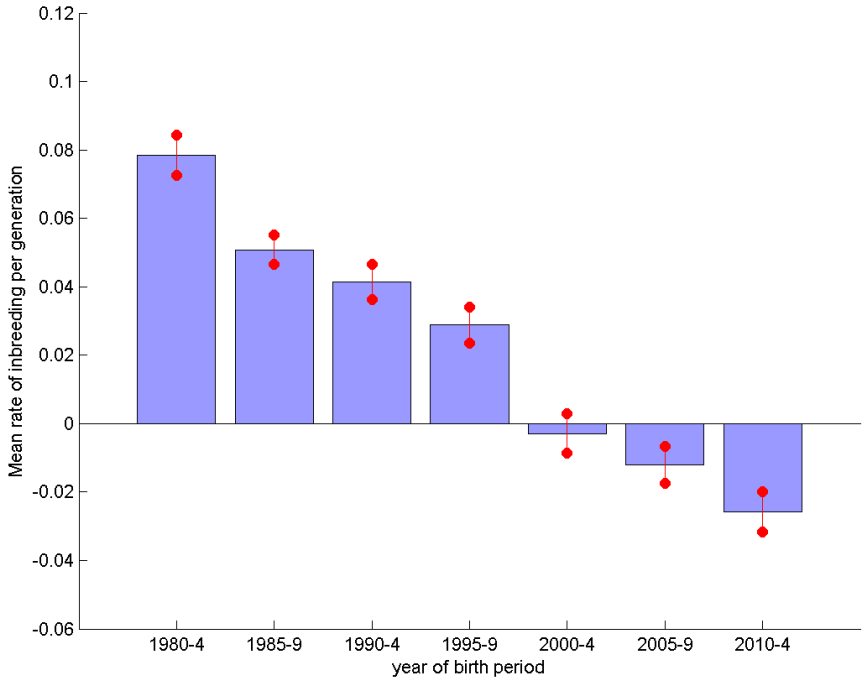


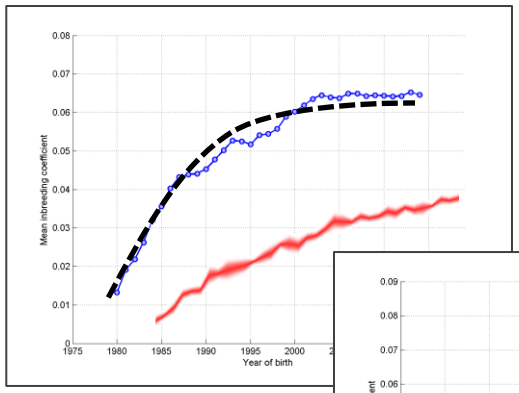
Figure 3: distribution of progeny per sire/dam

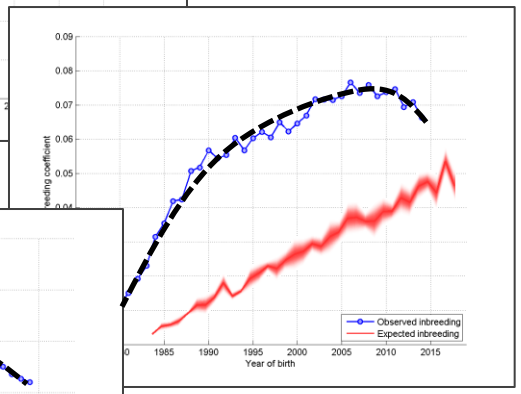


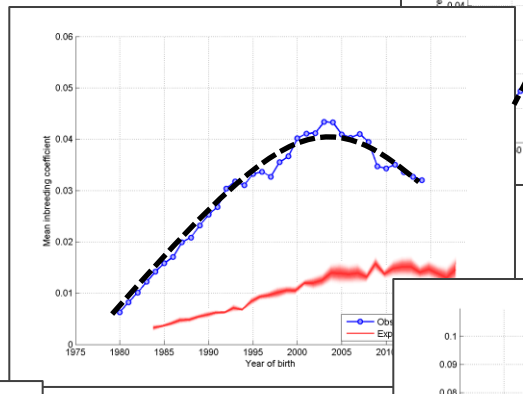
Broad trends and interesting examples…

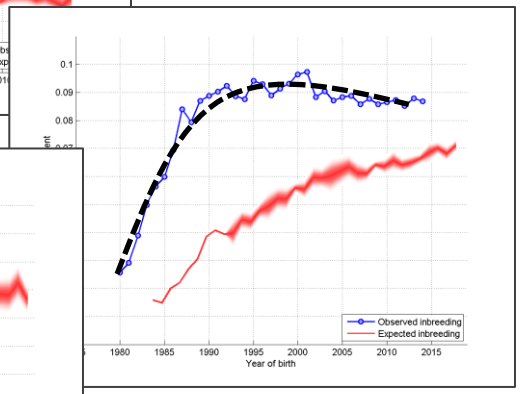
The rate of inbreeding is (generally) slowing…

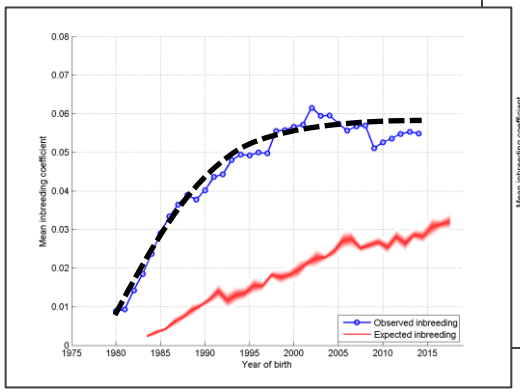


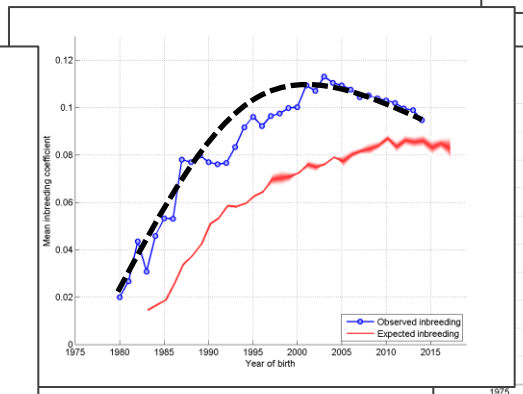


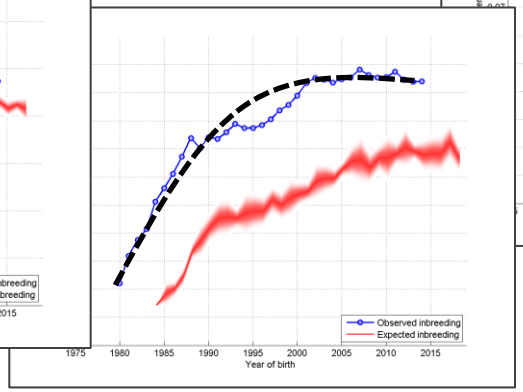




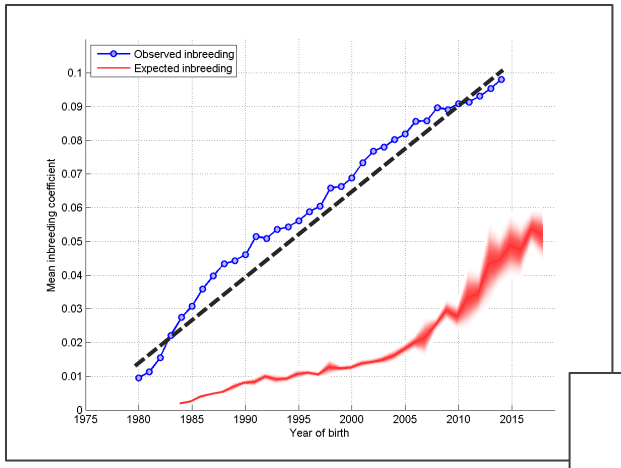


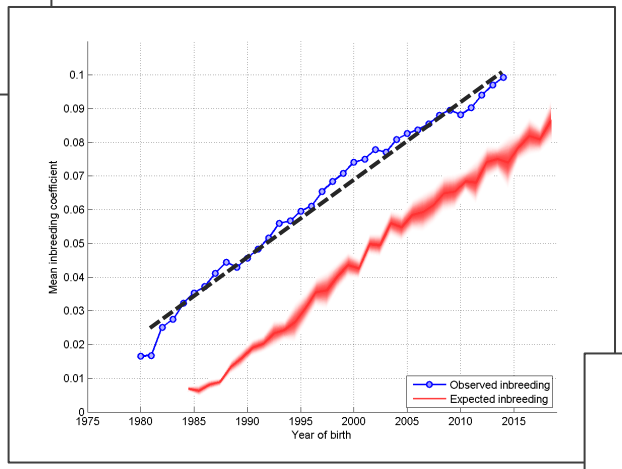


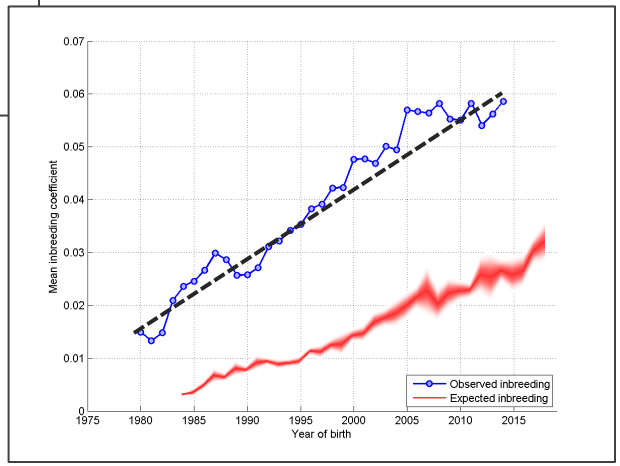




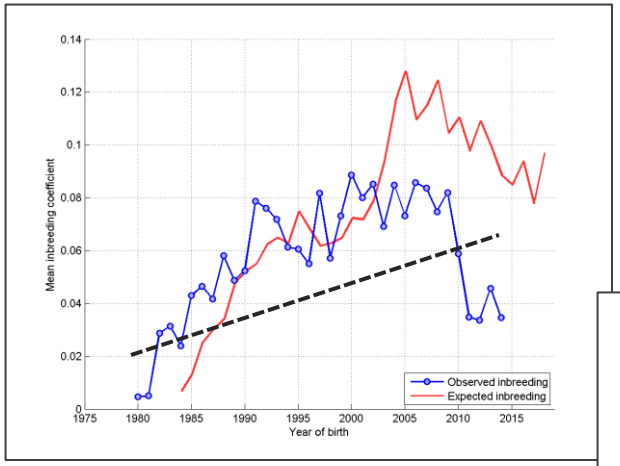
…although, not in <u>all</u> breeds…

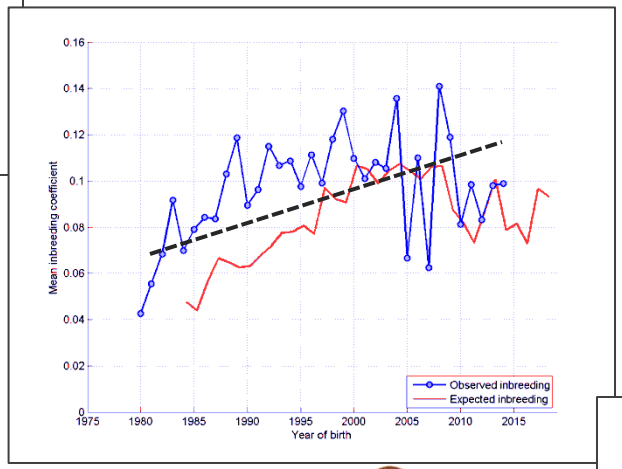


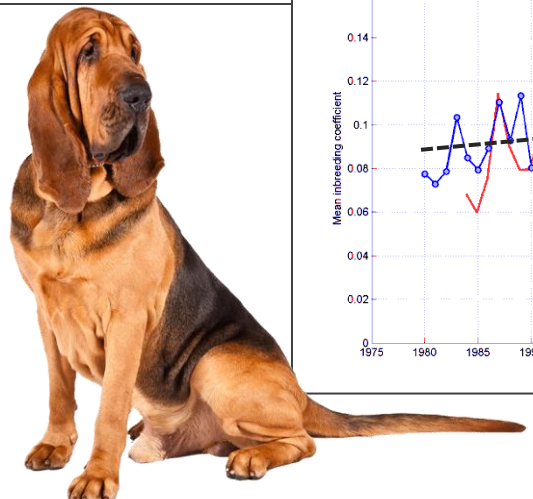


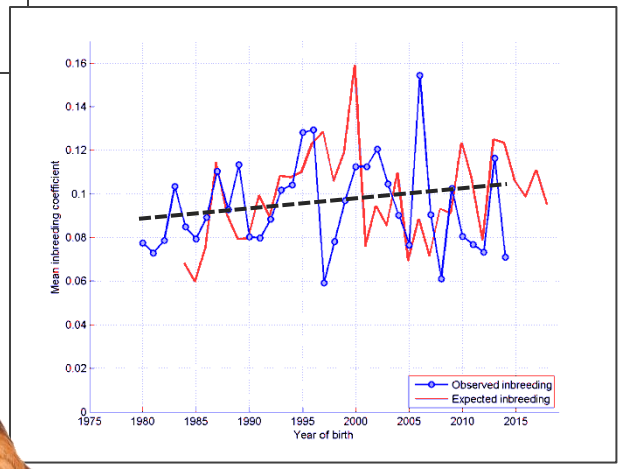


Some rarer breeds are conserving diversity…

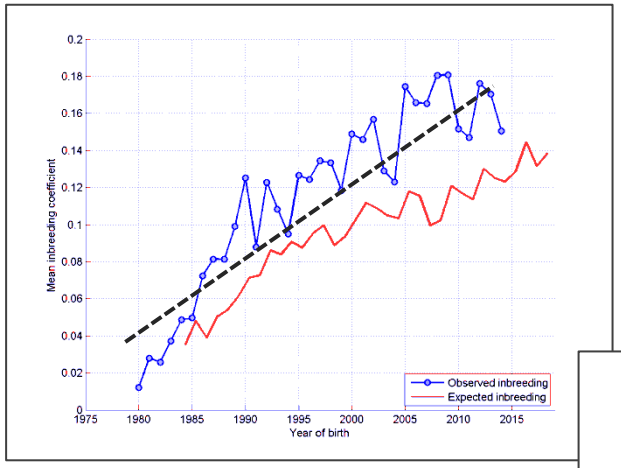


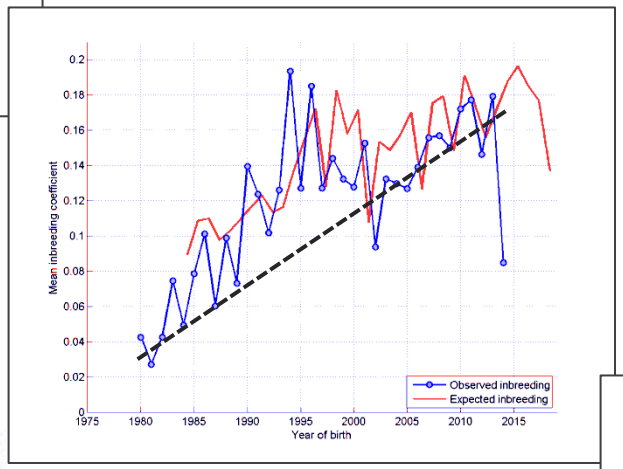


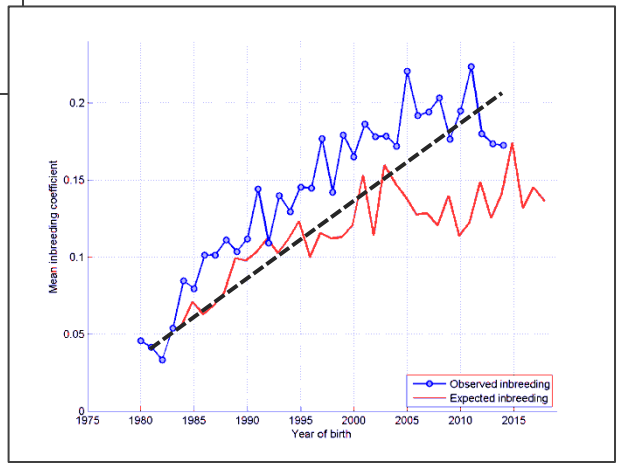




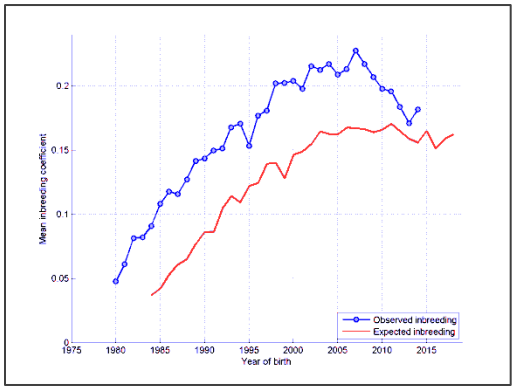
…but others are really struggling…

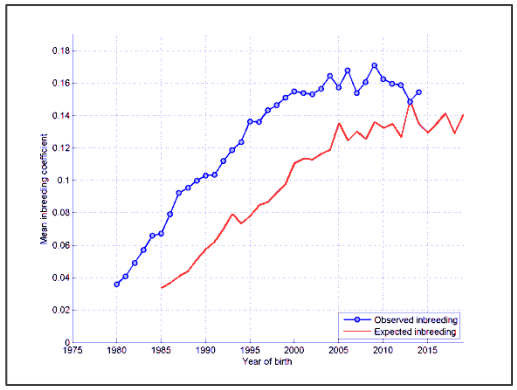


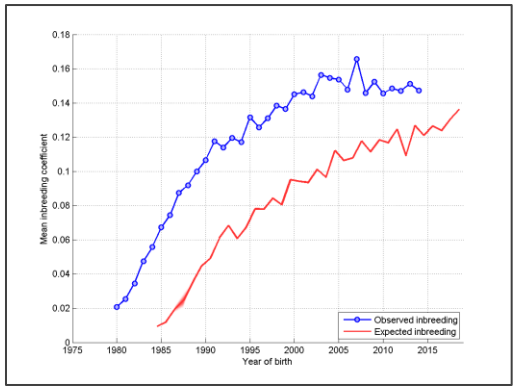


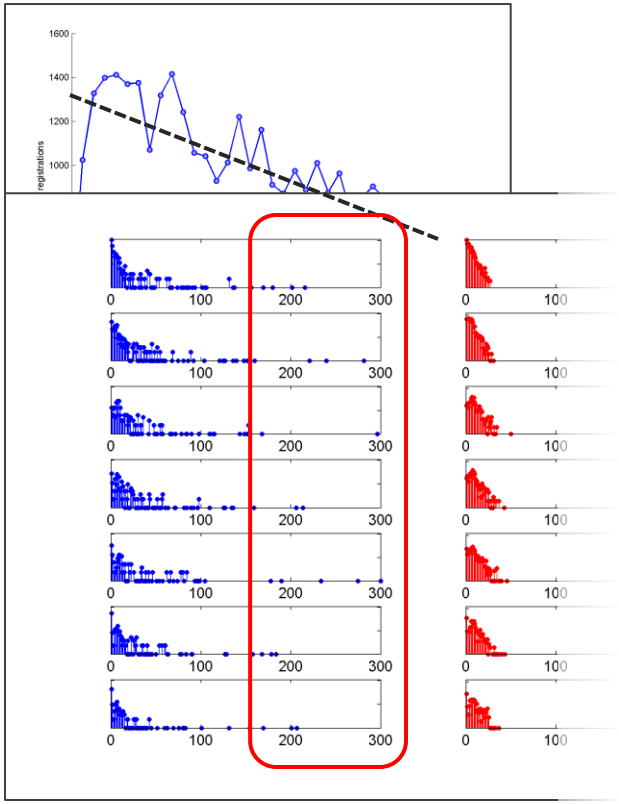


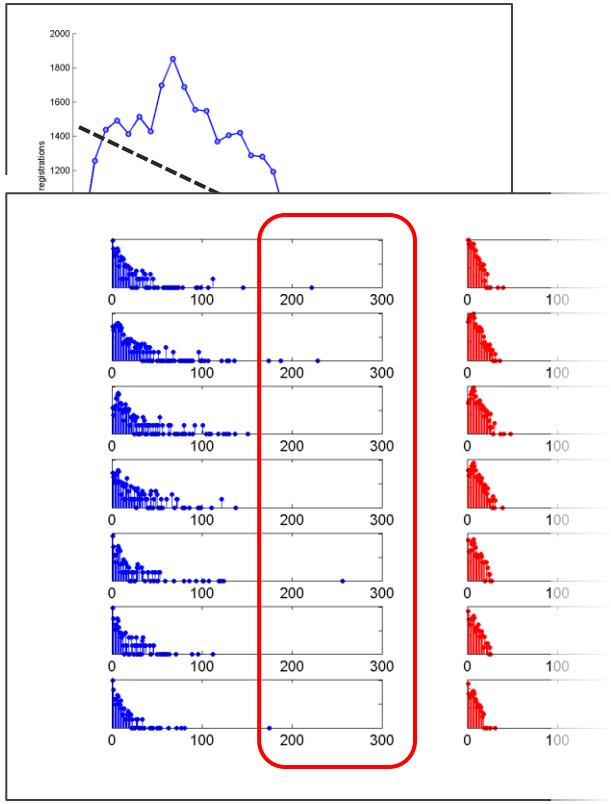
Drastic loss of genetic diversity in some breeds

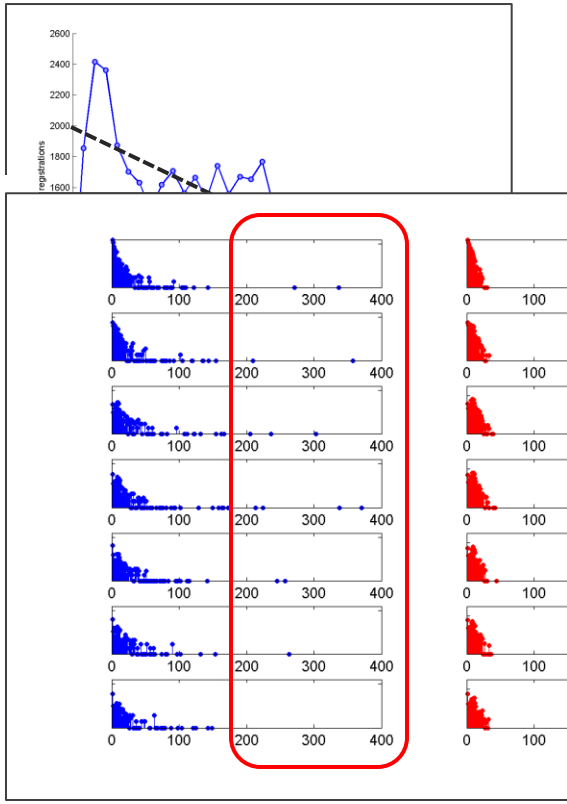




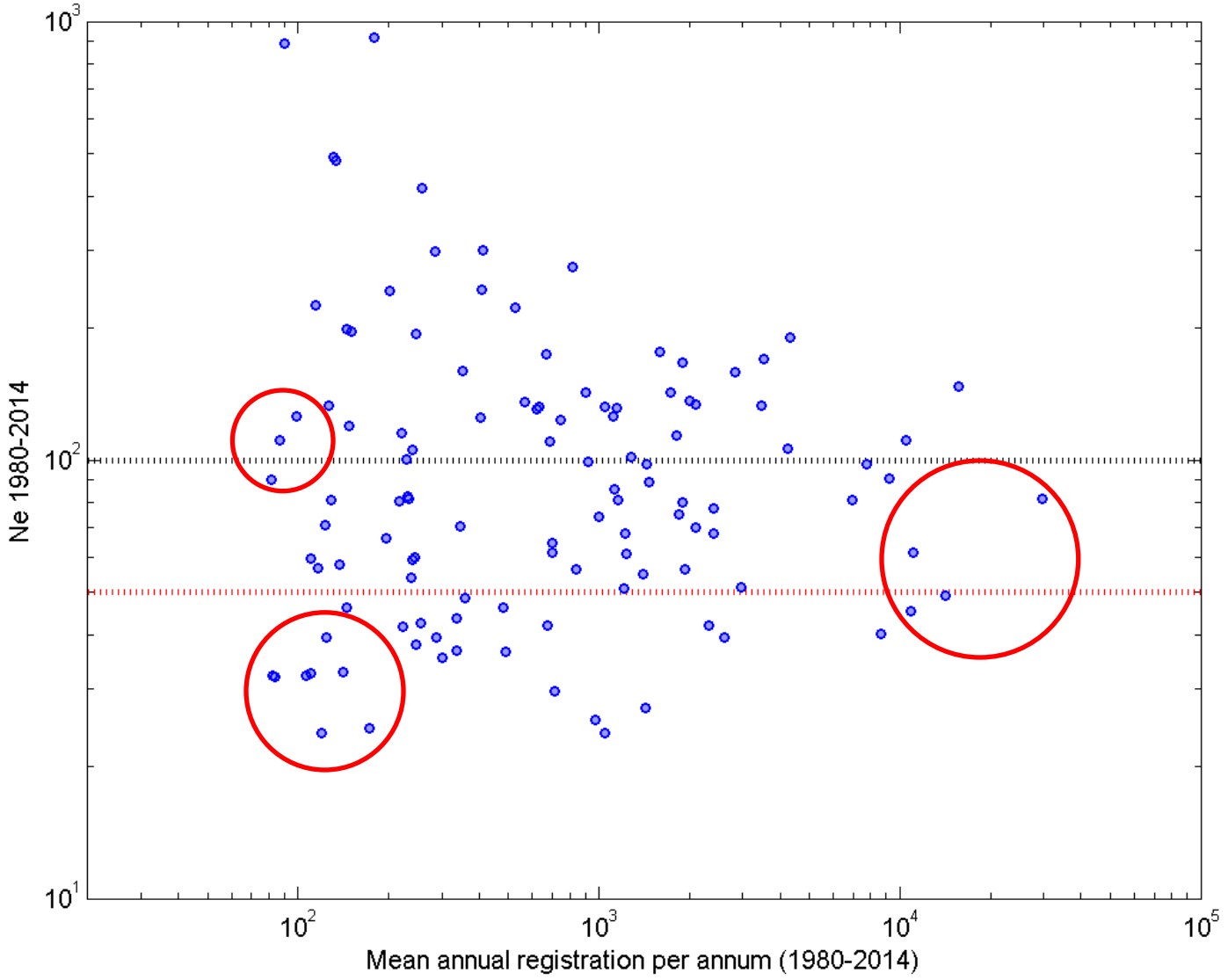




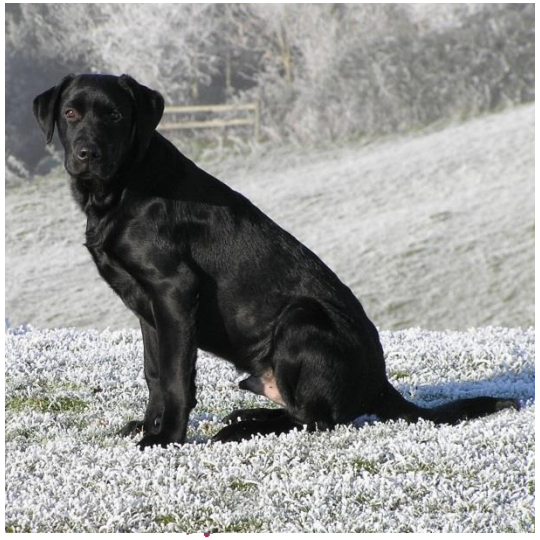


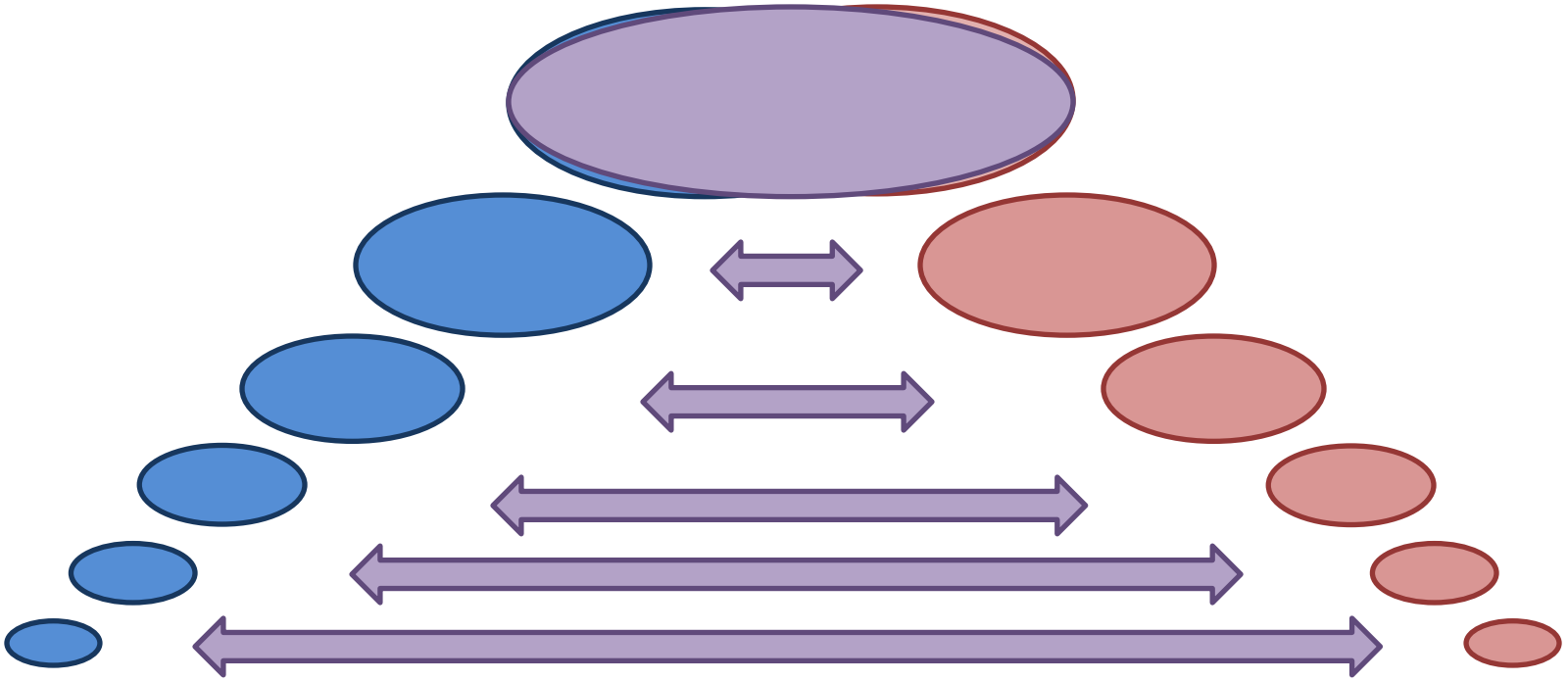


Effective and actual pop^{n} size appear unrelated



Possible effect of ‘sub’ populations…





Summary
Thank you – and any questions?

General trend across breeds is an easing in the rate of inbreeding

FCR rate of inbreeding is improving…

…but popular sires are still making large genetic contributions

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