



IRISH CATTLE BREEDING FEDERATION

Across-country correlations Interbeef WG - May2014



ICBF genetic team / InterBeef



Background : presentation of r_g

- Oct 2013 - TC Prague : across-country r_g
 - 6 countries for CHA
 - 8 countries for LIM
- Mar 2014 - TC Uppsala: across-country r_g
 - 8 countries for CHA
 - 10 countries for LIM
- May 2014 TC Berlin: across-country r_g
 - 8 countries for CHA – corrected for DEU
 - 10 countries for LIM – corrected for DEU

Data edits: LIM

Table 1. Summary of Interbeef data and basic edits.

	N	E.T.	UNK. PARENT	C.G. < 3	N SIRE/CG < 2	EDITED DATA
Pedigree	2,978,596					2,978,596
FRA	2,322,277		439,923	28,080	342,682	1,511,592
GBR	123,974	6,261	2,683	233	29,461	85,336
IRL	16,189	669	1,891	382	2,773	10,474
DNK	42,165	428	1,929	2,507	6,017	31,284
ESP	33,259		2,482	71	5,229	25,477
SWE	21,124		1,465	687	3,554	15,418
FIN	13,036	72	1,436	237	1,067	10,224
CZE	7,531	559	210	256	582	5,924
DEU	67,710		3,674	2,245	11,115	50,676
CHE	24,978		4,333	455	3,150	17,040
NOR*						56,926

*NOR = SWE + FIN + DNK

Data edits: CHA

Table 1. Summary of Interbeef data and basic edits.

	N	E.T.	UNK. PARENT	C.G. < 3	N SIRE/CG < 2	EDITED DATA
Pedigree	4,965,053					4,965,053
FRA	3,945,951		652144	35916	328805	2,929,086
IRL	18,791	479	2706	428	2535	12,643
DNK	15,881	520	650	1032	1877	11,802
SWE	114,501		4114	3727	17120	89,540
FIN	17,185	142	2586	345	1469	12,643
CZE	28,261	1466	1678	755	2337	22,025
DEU	75,522		4586	3063	12101	55,772
CHE	8,292		1212	98	557	6,425
NOR*						113,985

*NOR = SWE + FIN + DNK

Method

- Create VCE files with max. connection
 - ~ max 100,000 animals with records
 - 5 generations of pedigree
- Series of 2 x 2 country analysis
 - Using 603 defined models
 - Using S/MGS model in DMU

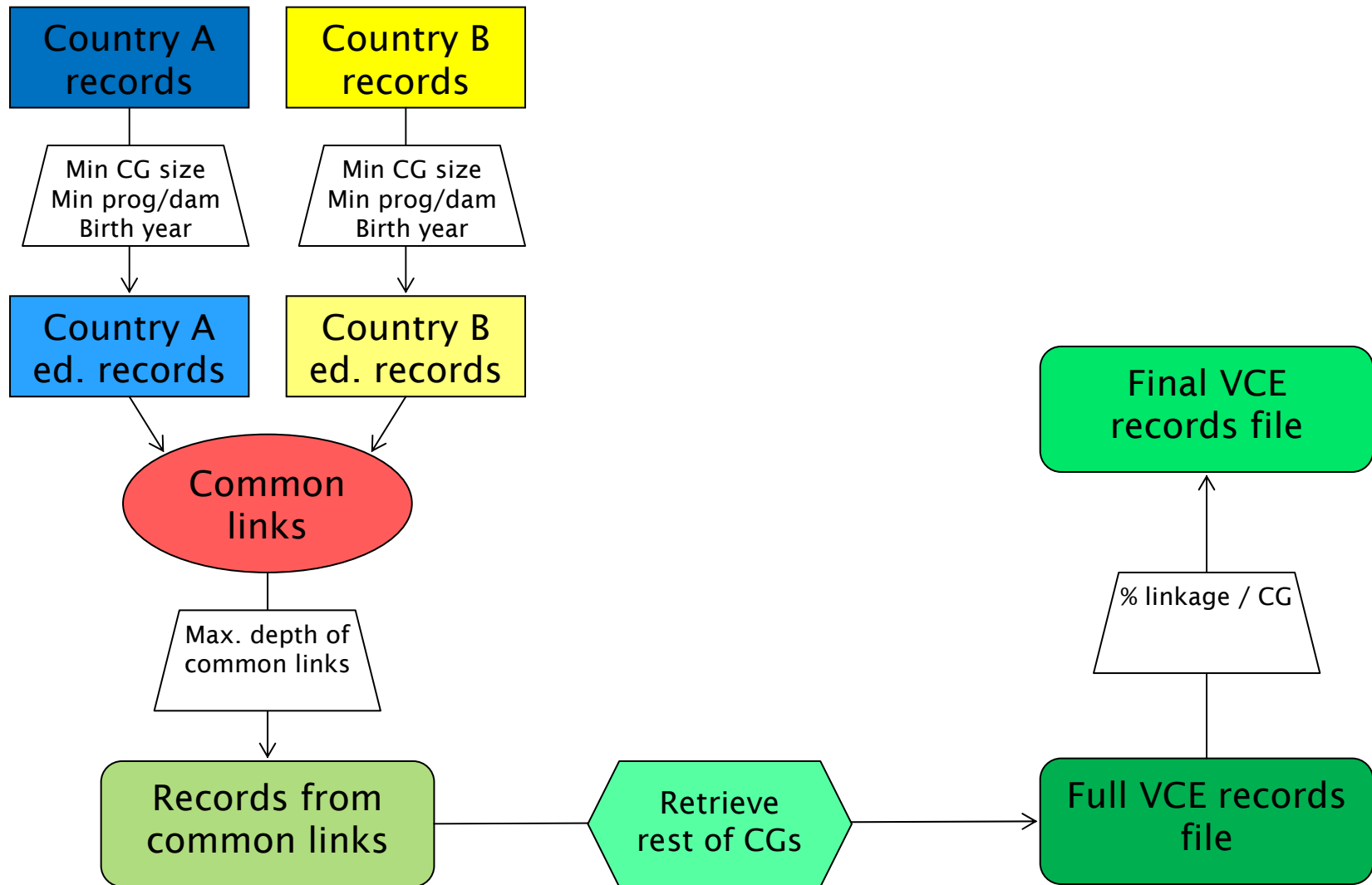
Table 3. Structure of covariance matrix in correlation models.

			country1		country2	
			dir1	mat1	dir2	mat2
country1	dir1	VARdir1				
	mat1	-0.20 (F)*		VARmat1		
country2	dir2	COV(dir1,dir2)		0 (F)**	VARdir2	
	mat2	0 (F)**		COV(mat1,mat2)	-0.20 (F)*	VARmat2

*Correlation fixed to approx. -0.20 (-0.10 to -0.30) except for CHE (0).

**Correlation fixed to 0.

Building perf. files



LIM raw r_g

		Maternal effect									
Direct effect		FRA	GBR	IRL	DNK	ESP	SWE	FIN	CZE	DEU	CHE
	FRA		0.87	0.82	0.70				0.85	0.56	0.76
	GBR	0.84		0.71		0.70			0.80	0.55	
	IRL	0.96	0.93		0.79	0.83					
	DNK	0.91		0.93			0.91		0.62		0.60
	ESP		0.96							0.71	0.50
	SWE				0.73			0.70			0.68
	FIN						0.79				
	CZE	0.59	0.71		0.71						0.74
	DEU	0.65	0.80			0.79	0.77				0.67
	CHE	0.72			0.73	0.80	0.66		0.89	0.71	

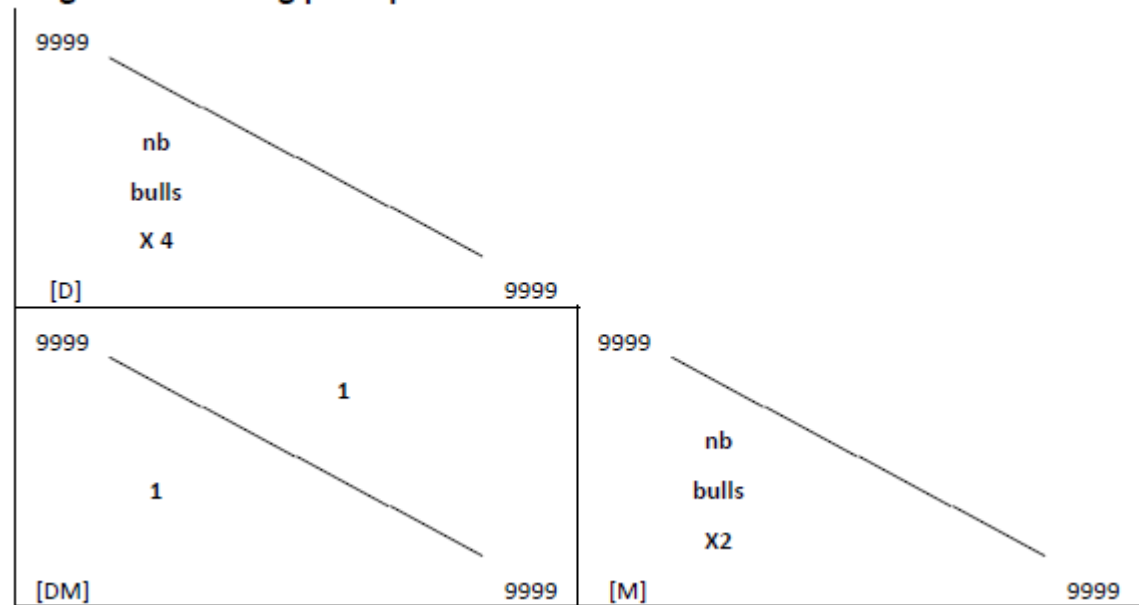
CHA raw r_g

		Maternal effect							
		FRA	IRL	DNK	SWE	FIN	CZE	DEU	CHE
Direct effect	FRA		0.70		0.67			0.60	
	IRL	0.77							
	DNK				0.70	0.64			
	SWE	0.90		0.59		0.87	0.81	0.50	0.70
	FIN			0.90	0.68		0.93		
	CZE				0.79	0.83		0.78	
	DEU	0.78			0.78		0.78		
	CHE				0.70				

Bending procedure

- Jorjani et al. (2003) weighted bending procedure was used
- r_g were weighted by number of common bulls

Figure 1. Bending principle.



LIM post-bending r_g

	Direct effect										Maternal effect									
	FRA	GBR	IRL	DNK	ESP	SWE	FIN	CZE	DEU	CHE	FRA	GBR	IRL	DNK	ESP	SWE	FIN	CZE	DEU	CHE
Direct effect	FRA																			
	GBR	0.84																		
	IRL	0.93	0.91																	
	DNK	0.88	0.88	0.87																
	ESP	0.89	0.93	0.90	0.87															
	SWE	0.81	0.83	0.85	0.73	0.86														
	FIN	0.85	0.86	0.80	0.88	0.83	0.76													
	CZE	0.61	0.74	0.75	0.70	0.82	0.78	0.70												
	DEU	0.64	0.78	0.67	0.85	0.79	0.73	0.83	0.84											
	CHE	0.71	0.71	0.72	0.70	0.79	0.65	0.82	0.81	0.71										
Maternal effect	FRA	-0.39	-0.12	-0.25	-0.17	-0.19	-0.13	-0.14	0.01	0.00	-0.04									
	GBR	-0.16	-0.15	-0.10	-0.03	-0.09	0.00	-0.05	0.06	0.04	0.02	0.86								
	IRL	-0.20	-0.06	-0.21	-0.07	-0.10	-0.01	0.01	-0.03	0.07	0.03	0.80	0.70							
	DNK	-0.11	-0.03	-0.06	-0.16	-0.03	0.05	-0.05	0.02	-0.08	0.04	0.67	0.66	0.74						
	ESP	-0.14	-0.09	-0.07	-0.03	-0.24	-0.03	0.00	-0.08	-0.03	-0.03	0.69	0.67	0.79	0.66					
	SWE	-0.06	0.02	0.00	0.01	-0.02	-0.14	0.00	-0.04	-0.05	0.05	0.65	0.63	0.61	0.86	0.62				
	FIN	-0.10	-0.03	0.01	-0.03	-0.01	0.02	-0.26	0.03	-0.06	-0.07	0.64	0.64	0.61	0.66	0.60	0.64			
	CZE	-0.09	0.07	-0.04	0.03	-0.07	-0.05	0.01	-0.18	-0.06	-0.07	0.82	0.74	0.64	0.57	0.65	0.65	0.59		
	DEU	0.01	0.01	0.07	-0.08	-0.04	-0.01	-0.06	-0.14	-0.30	0.04	0.55	0.53	0.67	0.67	0.69	0.64	0.64	0.66	
	CHE	-0.09	0.04	-0.02	-0.03	0.04	-0.05	0.07	0.09	-0.02	0.34	0.75	0.62	0.61	0.54	0.48	0.60	0.47	0.69	0.65

Average r_g
Direct = 0.80
Maternal = 0.66

CHA post-bending r_g

		Direct effect								Maternal effect							
		FRA	IRL	DNK	SWE	FIN	CZE	DEU	CHE	FRA	IRL	DNK	SWE	FIN	CZE	DEU	CHE
Direct effect	FRA																
	IRL	0.78															
	DNK	0.87	0.86														
	SWE	0.83	0.79	0.61													
	FIN	0.84	0.73	0.85	0.67												
	CZE	0.88	0.83	0.85	0.76	0.82											
	DEU	0.78	0.89	0.88	0.74	0.85	0.76										
	CHE	0.76	0.77	0.81	0.67	0.66	0.53	0.86									
Maternal effect	FRA	-0.40	-0.04	-0.16	-0.20	-0.15	-0.22	-0.07	-0.13								
	IRL	-0.07	-0.21	-0.05	-0.06	0.05	-0.07	-0.07	-0.04	0.68							
	DNK	-0.09	-0.03	-0.16	0.09	0.00	-0.05	-0.06	-0.05	0.68	0.66						
	SWE	-0.08	-0.04	0.04	-0.14	-0.01	0.00	0.02	0.01	0.63	0.61	0.66					
	FIN	-0.09	0.05	-0.01	0.00	-0.20	-0.04	-0.07	0.04	0.65	0.55	0.58	0.84				
	CZE	-0.09	-0.03	-0.04	-0.02	-0.05	-0.18	-0.07	0.11	0.69	0.65	0.66	0.75	0.86			
	DEU	-0.06	-0.10	-0.09	-0.04	-0.11	-0.06	-0.30	-0.15	0.59	0.67	0.67	0.47	0.65	0.76		
	CHE	-0.04	0.01	0.03	0.01	0.00	0.00	0.00	0.07	0.70	0.74	0.64	0.62	0.61	0.61	0.67	

Average r_g
Direct = 0.78
Maternal = 0.66

Summary

- Better convergence in LIM compared to CHA
- Average $r_{g(\text{direct})} \sim 0.79$ - $r_{g(\text{maternal})} \sim 0.66$
- Co-variance matrix was computed using national estimates
 - of variances (genetic & residual)
 - of within- country $\text{COV}_{(\text{dir}, \text{mat})}$
 - of perm. env. of dam variances
 - of other variances (e.g., CG)