INTERBEEF ACROSS-COUNTRY VARIANCE COMPONENTS ESTIMATION FOR LIMOUSINE WEANING WEIGHT

1. Summary - Conclusion

Across country genetic correlations were estimated across 8 countries for the Limousin breeds using data and pedigree extracted from the IDEA database in June 2013.

Series of 2-country analysis were done successively for direct effect of weaning weight, direct effect of weaning weight after accounting for maternal permanent environment, and finally direct and maternal effects of weaning weight after accounting for maternal permanent environment. The resulting correlation matrices were bended in order to get them positive definite, and used to compute a final correlation matrix for direct and maternal weaning weight.

The across-country InterBeef correlation matrix for direct and maternal weaning weight using the within country correlations between direct and maternal weaning weight was then created.

A final step consisted in building the genetic and residual (co)variances InterBeef matrix using national estimates for genetic and residual variances.

2. Data

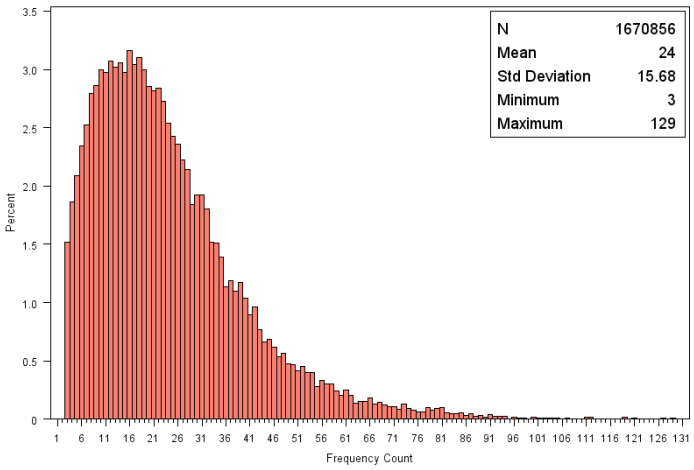
1 pedigree file and 8 performance files (FRA, IRL, GBR, ESP, CZE, SWE, DNK & FIN) were received from InterBeef at the end June 2013 (Table1).

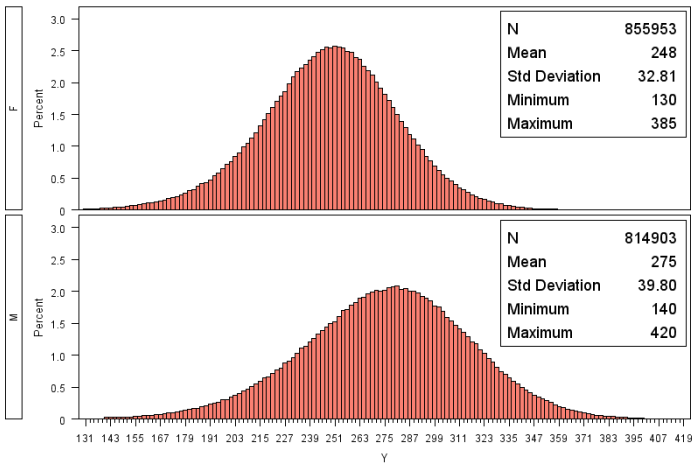
Table 1. Data received			
Type	Country of origin	N	
Pedigree	All countries	2,623,917	
Performance	**FRA**	**2,083,518**	89%
	GBR	**117,056**	5%
	DNK	**40,737**	2%
	ESP	**33,259**	1%
	IRL	**19,512**	1%
	SWE	**18,201**	1%
	FIN	**13,035**	1%
	CZE	**5,791**	0%

Minimum edits on performance files included the exclusion of embryo transplant animals (**ET**) calves and a minimum size for contemporary groups (**CG**).

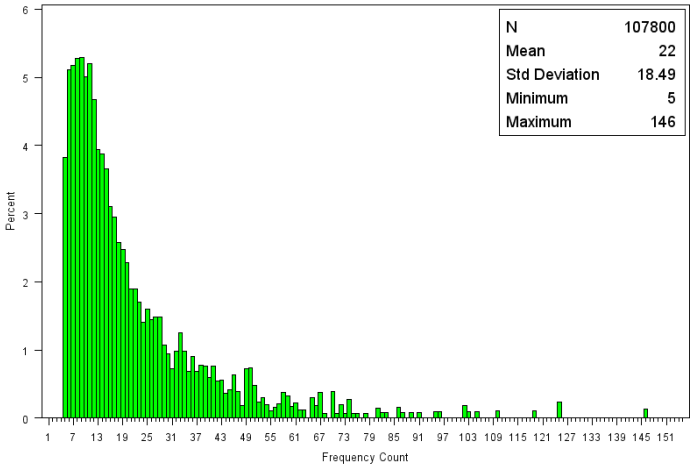
Table 2. Animals successively edited*				
Countries	**1. ET**	**2. No sire or/and MGS**	**3. CG (min CG size)**	**4. Remaining animals**
FRA	0	386,115	26,547 (3)	**1,670,856**
GBR	5,886	2,121	1,249 (5)	**107,800**
DNK	423	2,222	3,748 (4)	**34,444**
ESP	0	1,725	61 (3)	**31,473**
IRL	1,102	2,916	647 (3)	**14,847**
SWE	0	1,810	871 (4)	**15,520**
FIN	72	1,408	237 (3)	**11,318**
CZE	431	224	214 (3)	**4,922**

**From Table 1, delete successively 1. then 2. then 3.*

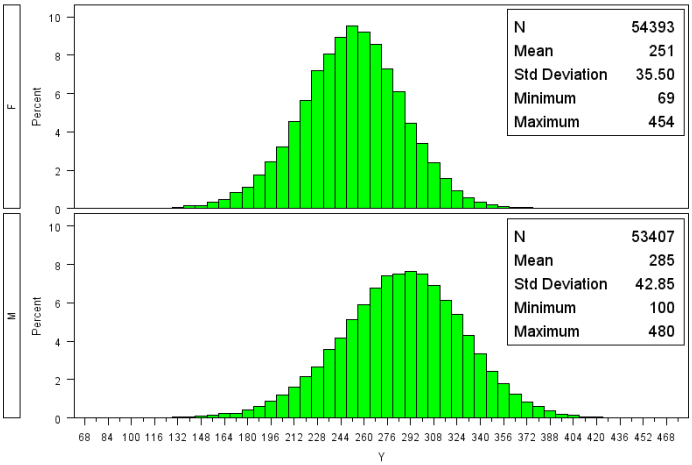




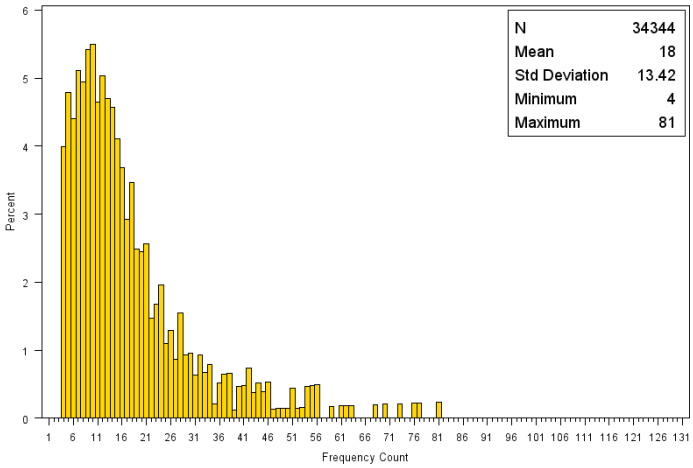
DISTRIBUTION OF SIZE OF C. GROUPS — GBR



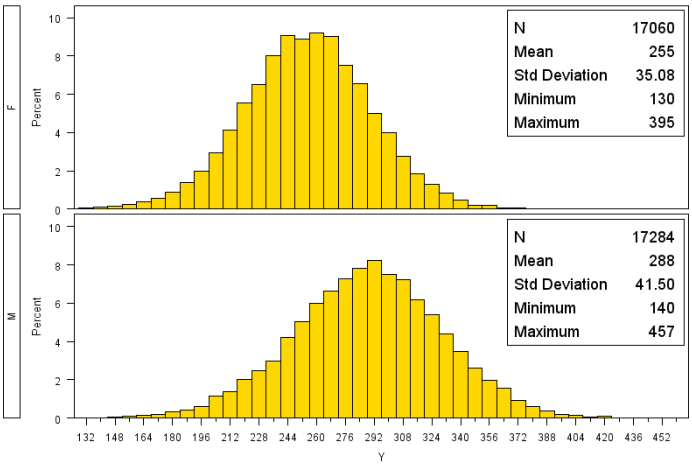
DISTRIBUTION OF WEANING WEIGHTS — GBR



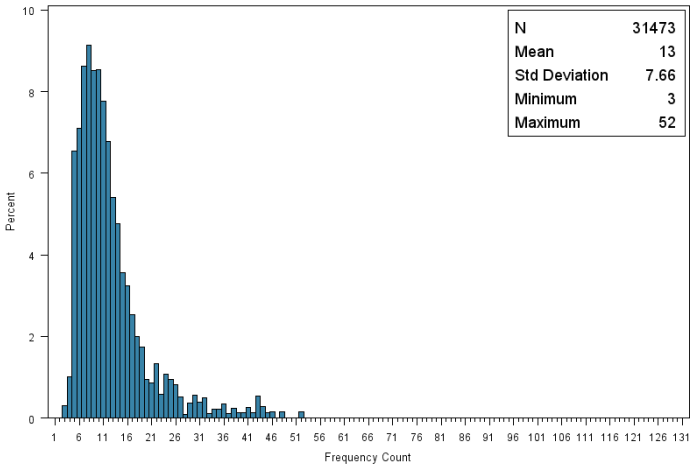
DISTRIBUTION OF SIZE OF C. GROUPS — DNK



DISTRIBUTION OF WEANING WEIGHTS — DNK



DISTRIBUTION OF SIZE OF C. GROUPS — ESP



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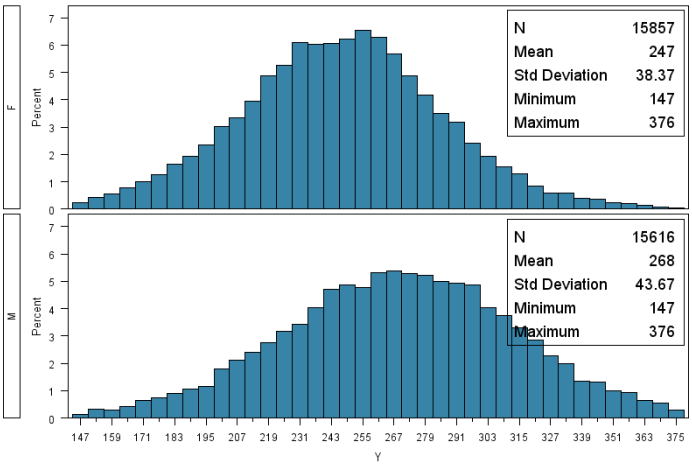
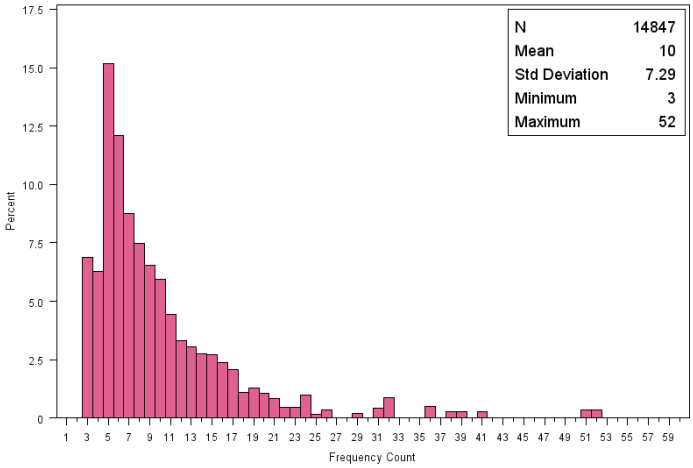
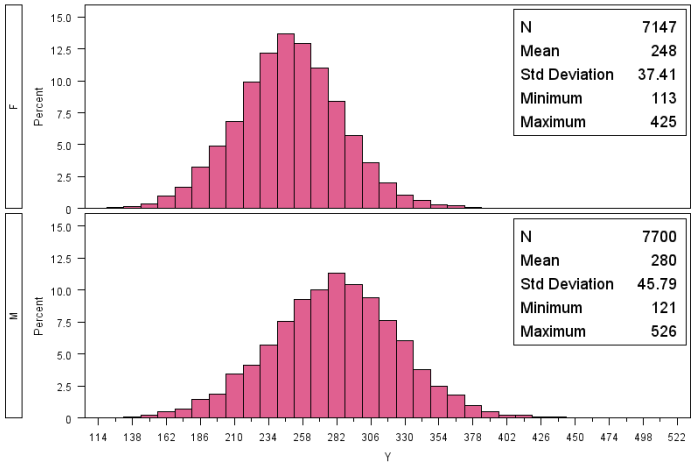


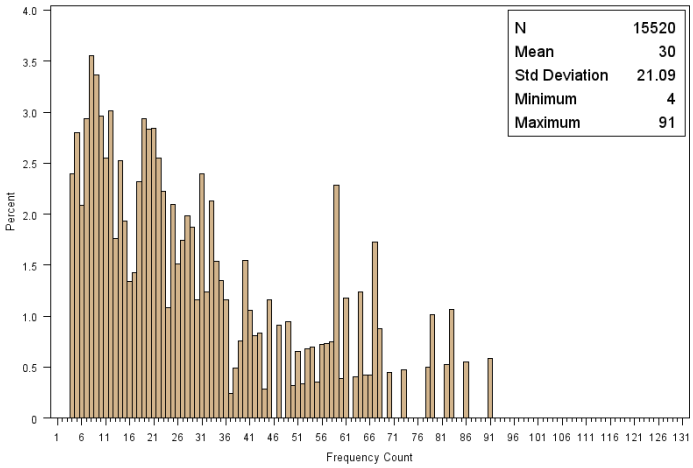
DISTRIBUTION OF SIZE OF C. GROUPS — IRL



DISTRIBUTION OF WEANING WEIGHTS — IRL



DISTRIBUTION OF SIZE OF C. GROUPS — SWE



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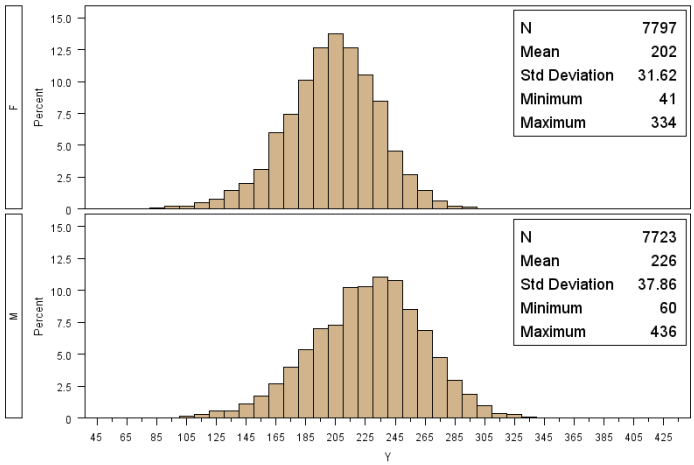
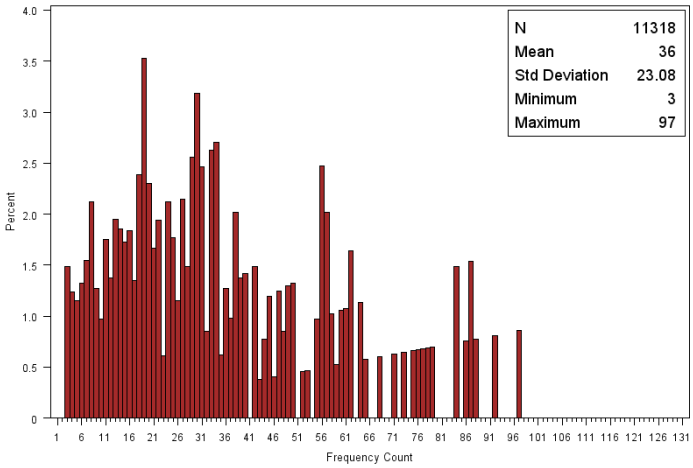


DISTRIBUTION OF SIZE OF C. GROUPS — FIN



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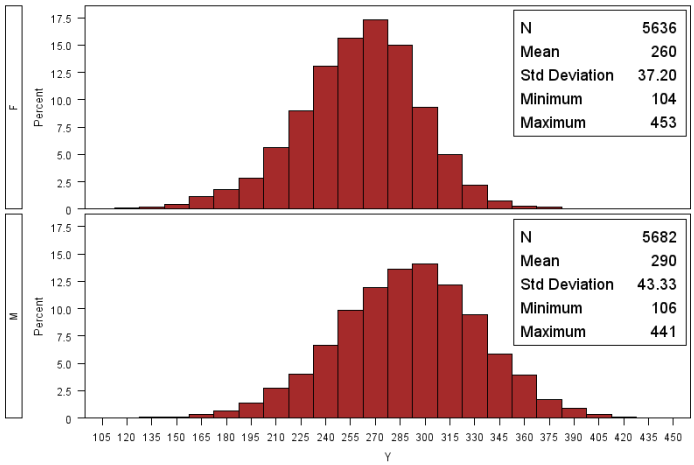
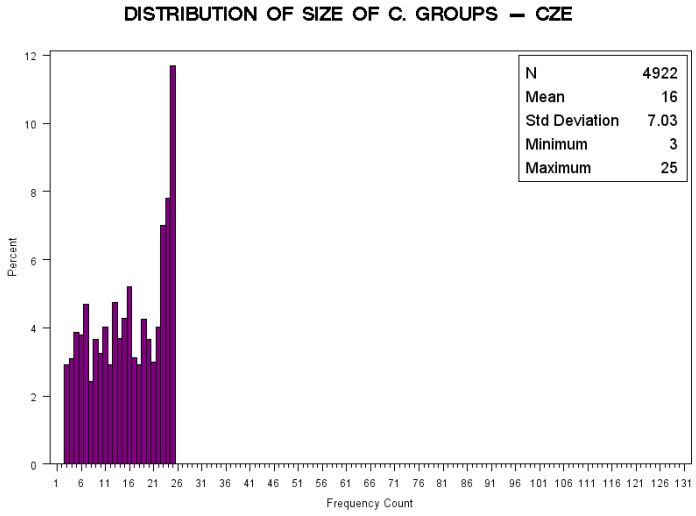
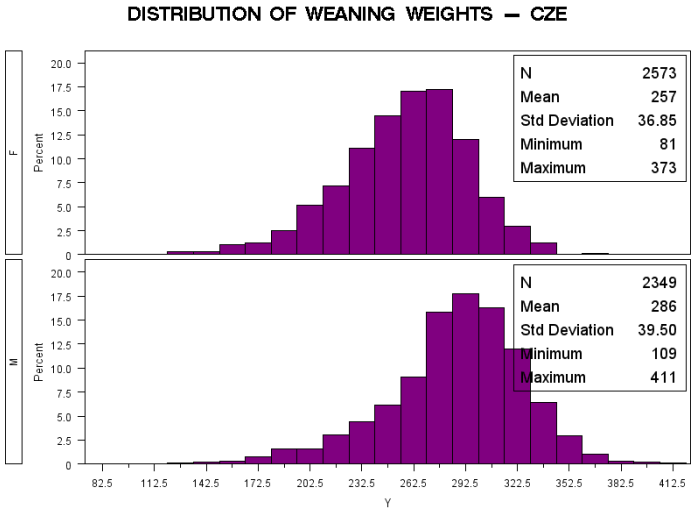






3. Overview of across-country connection

3.1. Where sires come from?

Table 3.: Origin of sires across InterBeef countries

		Country of 1st reg. of sire										
		CZE	DNK	ESP	FIN	FRA	GBR	IRL	SWE	Other	% national	%FRA
Country of 1st reg. of animal with perf.	CZE	2423	65	3		2251	1		1	178	49%	46%
	DNK		25204			7850	173		110	1007	73%	23%
	ESP			12655		18818				0	40%	60%
	FIN		1147		8776	870	195		240	90	78%	8%
	FRA		285	101		1668080	393	97	6	1862	100%	100%
	GBR					24982	81842	976		0	76%	23%
	IRL		10			8243	1079	5515		0	37%	56%
	SWE		1143		156	630			13339	252	86%	4%

3.2. Where maternal grand-sire come from?

Table 4.: Origin of maternal grand-sires across InterBeef countries

		Country of 1st reg. of maternal grand-sire										
		CZE	DNK	ESP	FIN	FRA	GBR	IRL	SWE	Other	% national	%FRA
Country of 1st reg. of animal with perf.	CZE	1318	13			3409				182	27%	69%
	DNK		23099			9335	426	3	348	1133	67%	27%
	ESP			11894		19562	3			14	38%	62%
	FIN		1383		7926	1006	611		261	131	70%	9%
	FRA		95	27		1669290	401	9		1034	100%	100%
	GBR					35074	72628	94		4	67%	33%
	IRL		7			10950	305	3577		8	24%	74%
	SWE		1573		124	1031			12236	556	79%	7%

4. Building the VC files

Objective: Maximising genetic connection for direct and maternal traits.

Method: identifying ancestors common across countries, retrieve animals with performances attached to the common genetic materials, retrieve full CG for animals with performances identified, build pedigree, run VCE.

Models: using series of 2-country analysis ; starting with a sire model (**S**), moving to S + permanent environment of dam (**pe**) model, concluding by S + maternal grand-sire (**MGS**) + pe model.

Software: Models were ran in DMU (Madsen et al, 2012). Some tests were conducted with ASreml (Gilmour et al, 2002) or MiX99 (Lindauer et al, 2011). Wombat (Meyer, 2007) has not been tested thoroughly.

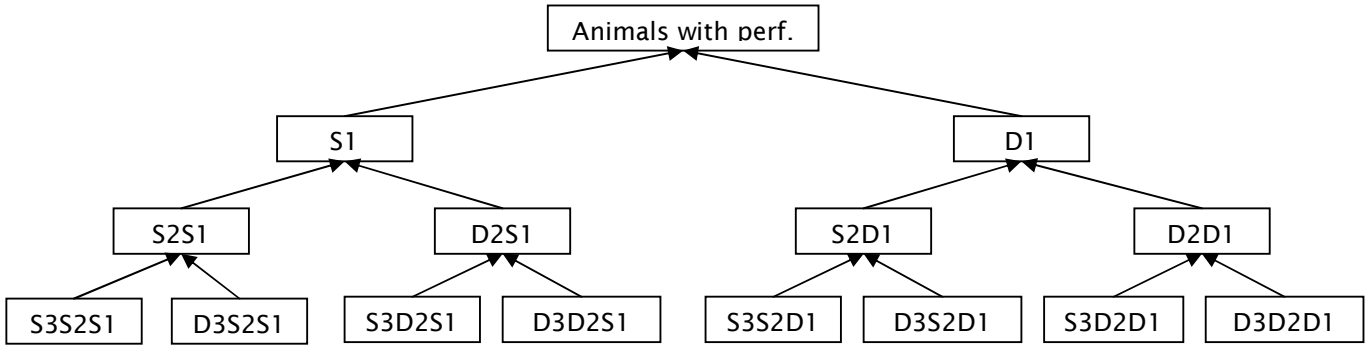
Constraint: See Appendix A ; after n trials and errors, in an animal model, 2 countries, direct, maternal and maternal permanent environment effects, the perf. file can't exceed ~100,000 lines, and the pedigree file, ~200,000 lines.

Process:

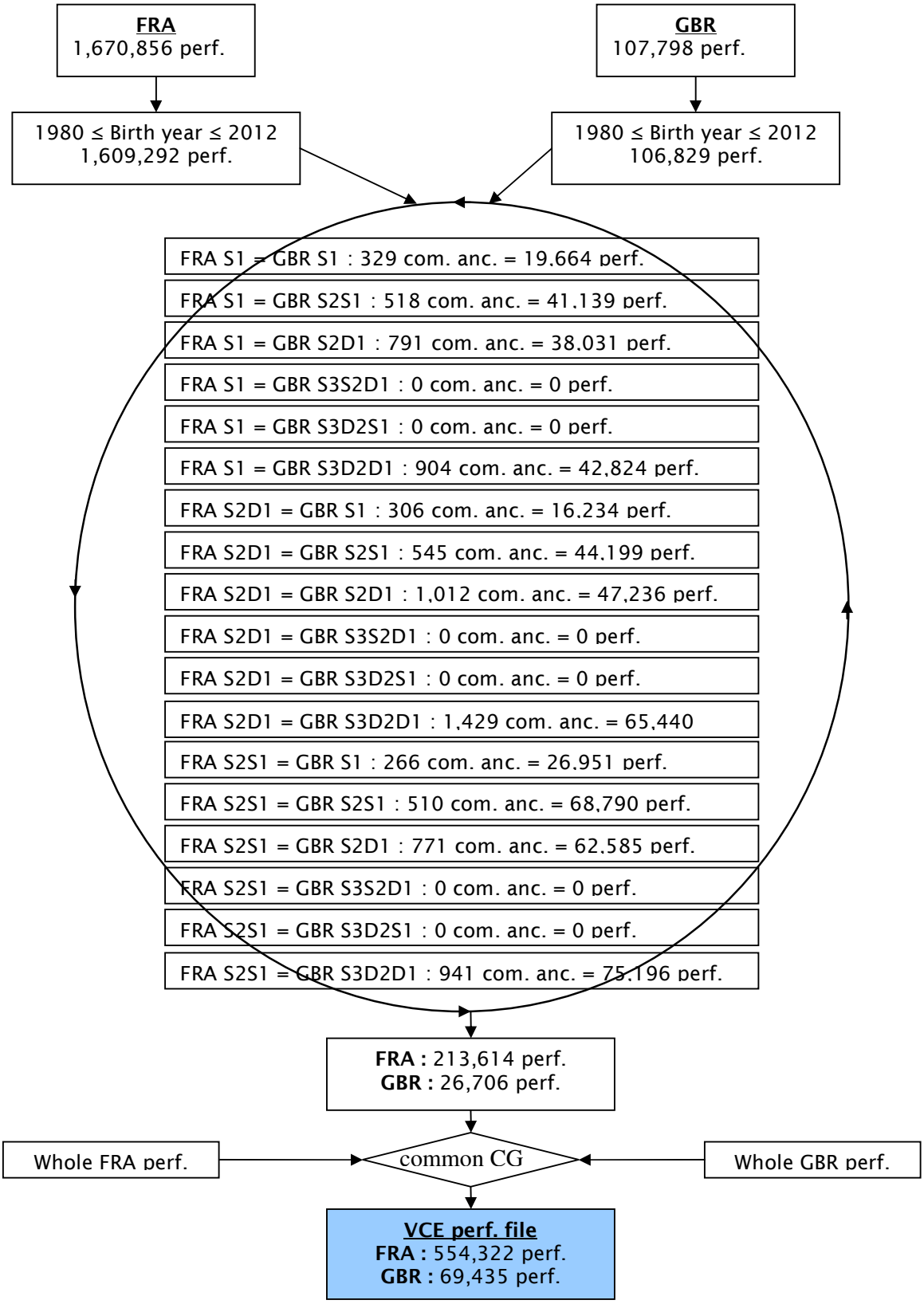
1. find common ancestors to the 2 countries
2. retrieve animals with performances linked to common ancestors in each of the country performance files
3. If necessary, for each country, reduce performance file size
   - using (average) year of CG and keeping CG created in the last *x* years (*x* to be define for each analysis)

   and / or
   - keeping the largest CG
4. repeat 1., 2., and 3. in order to increase connection between countries :
   - S country1 = S country2
   - MGS country1 = MGS country2
   - S country1 = MGS country2
   - MGS country1 = S country2
   - S of S country1 = Sire country2
   - S of S country1 = MGS country2
   - ...etc...
5. Build file of animals with performances issued from common ancestors in both countries (Append all animal files)
6. Retrieve additional animals with performances present in the selected CG.
7. Build and ranked pedigree file (5 generations)
8. Run VCE

Pedigree labels

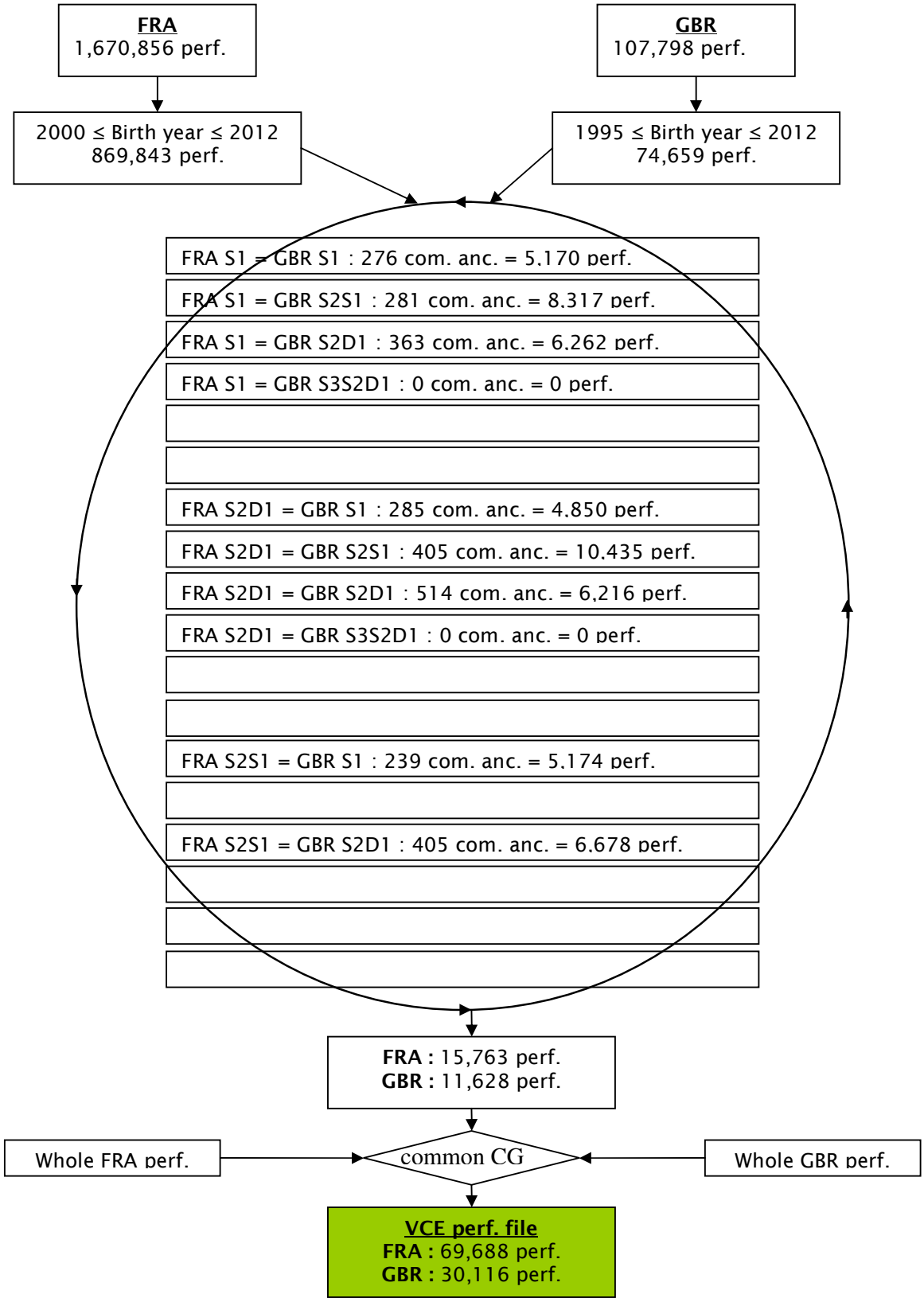


No restrictions on birth year or CG



{Sires} and [MGS] used in FRA and GBR - Common {Sires} and [MGS] off diagonal		
	FRA	GBR
FRA	{22,394}[22,984]	[1,012]
GBR	{329}	{3,469}[3,162]

Restrictions on birth year or CG



{Sires} and [MGS] used in FRA and GBR - Common {Sires} and [MGS] off diagonal		
	FRA	GBR
FRA	{4,580}[6,719]	[469]
GBR	{229}	{1,787}[2,269]

5. Results

5.1. The VCE files

In the following tables, number of sires are between { }, and number of MGS between [ ].

	Ped : 248,074	
	FRA perf. : 69,688	GBR perf. : 30,116
FRA	{4,580}[6,719]	[469]
GBR	{229}	{1,787}[2,269]

	Ped : 222,301	
	FRA perf. : 70,641	DNK perf. : 20,372
FRA	{5,404} [8,552]	[166]
DNK	{93}	{1,107} [1,274]

	Ped : 229,307	
	FRA perf. : 58,507	ESP perf. : 21,504
FRA	{4,309}[6,514]	[604]
ESP	{211}	{829 }[1,103]

	Ped : 219,643	
	FRA perf. : 71,334	IRL perf. : 11,071
FRA	{5,889} [8,727]	[395]
IRL	{148}	{821} [871]

	Ped : 165,428	
	FRA perf. : 47,385	SWE perf. : 15,520
FRA	{3,613}[5,872]	[35]
SWE	{38}	{691}[595]

	Ped : 164,769	
	FRA perf. : 48,313	FIN perf. : 11,318
FRA	{3,651} [5,774]	[29]
FIN	{39}	{522} [539]

	Ped : 188,667	
	FRA perf. : 71,875	CZE perf. : 4,042
FRA	{4,327}[6,211]	[302]
CZE	{95}	{138}[112]

	Ped : 113,902	
	GBR perf. : 43,593	DNK perf. : 20,483
GBR	{2,790} [3,462]	[92]
DNK	{68}	{1,159} [1,369]

	Ped : 128,286	
	GBR perf. : 44,742	ESP perf. : 21,375
GBR	{2,812}[3,452]	[178]
ESP	{93}	{965}[1,537]

	Ped : 141,575	
	GBR perf. : 69,893	IRL perf. : 13,040
GBR	{3,526} [3,909]	[267]
IRL	{174}	{909} [1,081]

	Ped : 68,322	
	GBR perf. : 17,889	SWE perf. : 15,520
GBR	{1,546}[2,237]	[26]
SWE	{27}	{702}[604]

	Ped : 88,885	
	GBR perf. : 33,248	FIN perf. : 11,318
GBR	{2,349} [3,066]	[37]
FIN	{37}	{524} [531]

	Ped : 75,953	
	GBR perf. : 27,612	CZE perf. : 4,932
GBR	{2,149}[2,862]	[57]
CZE	{33}	{239}[382]

	Ped : 106,566	
	DNK perf. : 34,344	ESP perf. : 31,473
DNK	{1,811} [1,834]	[71]
ESP	{62}	{1,103} [1,741]

	Ped : 85,396	
	DNK perf. : 34,344	IRL perf. : 14,847
DNK	{1,819}[1,831]	[74]
IRL	{54}	{1,174}[1,400]

	Ped : 66,054	
	DNK perf. : 34,344	SWE perf. : 15,520
DNK	{1,810} [1,827]	[78]
SWE	{63}	{666} [552]

	Ped : 64,744	
	DNK perf. : 34,344	FIN perf. : 11,318
DNK	{1,817}[1,833]	[74]
FIN	{56}	{505}[494]

	Ped : 61,330	
	DNK perf. : 34,344	CZE perf. : 4,922
DNK	{1,838} [1,870]	[35]
CZE	{35}	{237} [404]

	Ped : 96,854	
	ESP perf. : 31,473	IRL perf. : 14,847
ESP	{1,092}[1,662]	[150]
IRL	{73}	{1,155}[1,324]

	Ped : 81,636	
	ESP perf. : 31,473	SWE perf. : 15,520
ESP	{1,134} [1,786]	[26]
SWE	{31}	{698} [624]

	Ped : 80,388	
	ESP perf. : 31,473	FIN perf. : 11,318
ESP	{1,140}[1,791]	[21]
FIN	{25}	{536}[547]

	Ped : 73,311	
	ESP perf. : 31,473	CZE perf. : 4,922
ESP	{1,123} [1,736]	[76]
CZE	{42}	{230} [363]

	Ped : 60,153	
	IRL perf. : 14,847	SWE perf. : 15,520
IRL	{1,208}[1,053]	[21]
SWE	{20}	{709}[609]

	Ped : 73,311	
	IRL perf. : 14,847	FIN perf. : 11,318
IRL	{1,203} [1,452]	[22]
FIN	{25}	{536} [546]

	Ped : 53,321	
	IRL perf. : 14,847	CZE perf. : 4,922
IRL	{1,200}[1,417]	[57]
CZE	{28}	{244}[382]

	Ped : 37,870	
	SWE perf. : 15,520	FIN perf. : 11,318
SWE	{693} [597]	[33]
FIN	{36}	{525} [535]

	Ped : 35,731	
	SWE perf. : 15,520	CZE perf. : 11,318
SWE	{708}[609]	[21]
CZE	{21}	{252}[418]

	Ped : 34,539	
	FIN perf. : 11,318	CZE perf. : 4,922
FIN	{542} [421]	[18]
CZE	{19}	{253} [421]

5.2. Traits & models tested

Table 5. Effects (except genetic effect) accounted for in the models*#

FRA	GBR	IRL	DNK	ESP	SWE	FIN	CZE
	Sex	Sex	Sex	Sex	Sex	Sex	Sex Twin
Twin	Twin	Twin	Twin	Twin	Twin	Twin	
Parity x Age		Parity					
Season			Season		Season	Season	
Ind. situation							
CG	CG	CG	CG	CG	CG	CG	CG*
	B. month						
	Age#	Age #	Age	Age	Age	Age	Age
	Age^2 #						
							B. year

** treated as random*

#treated as fixed regression

Random genetic effects of Sire, Sire + pe, Sire + MGS + pe were included in 3 successive models for each of the 2-country analysis.

5.3. Direct weaning weight using sire models

In these models, all residual correlations were set to zero.

Table 6. Across-country genetic correlation (standard error) for direct weaning weight								
	FRA	**GBR**	**DNK**	**ESP**	**IRL**	**SWE**	**FIN**	**CZE**
FRA								
GBR	0.88 (0.077)							
DNK	0.88 (0.064)	nc						
ESP	0.96 (0.043)	0.96 (0.081)	nc					
IRL	0.97 (0.065)	0.94 (0.067)	0.80 (0.135)	0.85 (0.124)				
SWE	0.90 (0.109)	0.82 (0.214)	0.64 (0.164)	0.93 (0.161)	0.81 (0.211)			
FIN	nc	nc	0.91 (0.09)	nc	nc	0.76 (0.178)		
CZE	0.56 (0.174)	0.57 (0.259)	0.09 (0.322)	0.75 (0.216)	0.80 (0.187)	0.63 (0.263)	nc	

Table 7. InterBeef and national variances									
		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
ITBF	variance DIR	304	259	288	278	163	312	436	324
	variance MAT								
	variance PE								
	variance RES	704	778	679	898	872	651	890	748
	h2 DIR	**30%**	**25%**	**30%**	**24%**	**16%**	**32%**	**33%**	**30%**
	h2 MAT								
	h2 PE								
NATIONAL	variance DIR	240	268		136	450	170	257	310
	variance MAT	96	55		68	194	120	144	197
	variance PE	106	63		43	45	80	102	81
	variance RES	586	421		294	647	500	693	374
	h2 DIR	**26%**	**36%**		**27%**	**35%**	**22%**	**23%**	**35%**
	h2 MAT	10%	7%		14%	15%	15%	13%	22%
	h2 PE	15%	13%		13%	7%	14%	13%	18%

5.4. Direct weaning weight and maternal p.e. using sire models

In these models, all residual correlations were set to zero.

Table 8. Across-country genetic correlation (standard error) for direct weaning weight accounting for p.e.								
	FRA	**GBR**	**DNK**	**ESP**	**IRL**	**SWE**	**FIN**	**CZE**
FRA								
GBR	0.85 (0.083)							
DNK	0.91 (0.057)	nc						
ESP	nc	0.96 (0.085)	nc					
IRL	0.97 (0.068)	0.94 (0.068)	0.81 (0.134)	0.85 (0.128)				
SWE	0.94 (0.100)	nc	0.71 (0.148)	0.97 (0.140)	0.95 (0.162)			
FIN	nc	nc	0.92 (0.09)	nc	nc	0.79 (0.173)		
CZE	0.58 (0.174)	0.70 (0.234)	0.18 (0.326)	0.85 (0.197)	0.89 (0.162)	0.82 (0.210)	nc	

Table 9. InterBeef and national variances									
		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
ITBF	variance DIR	286	251	276	241	155	265	394	295
	variance MAT								
	variance PE	147	164	111	176	169	160	233	205
	variance RES	556	622	574	730	707	500	671	560
	h2 DIR	**29%**	**24%**	**29%**	**21%**	**15%**	**29%**	**30%**	**28%**
	h2 MAT								
	h2 PE	**15%**	**16%**	**12%**	**15%**	**16%**	**17%**	**18%**	**19%**
NATIONAL	variance DIR	240	268		136	450	170	257	310
	variance MAT	96	55		68	194	120	144	197
	variance PE	106	63		43	45	80	102	81
	variance RES	586	421		294	647	500	693	374
	h2 DIR	**26%**	**36%**		**27%**	**35%**	**22%**	**23%**	**35%**
	h2 MAT	10%	7%		14%	15%	15%	13%	22%
	h2 PE	**15%**	**13%**		**13%**	**7%**	**14%**	**13%**	**18%**

5.5. Direct, maternal weaning weight and maternal p.e. using sire-MGS models

In these models, all residual correlations were set to zero and all direct - maternal correlations were maintain to zero.

Table 10. Across-country genetic correlation (standard error) for direct (below diagonal) and maternal (above diagonal) weaning weight accounting for p.e.

	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
FRA		0.97 (0.109)	0.90 (0.152)	nc	0.95 (0.104)	nc	nc	0.85 (0.138)
GBR	0.84 (0.086)		nc	0.98 (0.138)	0.71 (0.211)	nc	nc	0.93 (0.299)
DNK	0.91 (0.057)	nc		nc	0.79 (0.140)	0.91 (0.186)	nc	0.62 (0.391)
ESP	nc	0.96 (0.086)	nc		0.83 (0.133)	nc	nc	nc
IRL	0.96 (0.070)	0.93 (0.067)	0.93 (0.204)	0.97 (0.101)		nc	nc	0.77 (0.220)
SWE	nc	nc	0.73 (0.142)	nc	nc		0.20 (0.447)	nc
FIN	nc	nc	nc	nc	nc	0.79 (0.177)		nc
CZE	0.56 (0.177)	0.71 (0.236)	0.12 (0.332)	nc	0.92 0.153)	nc	nc	

Table 11 InterBeef and national variances

		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
ITBF	variance DIR	287	248	272	228	159	261	359	263
	variance MAT	83	87	68	126	83	126	231	270
	variance PE	130	145	98	150	150	139	203	157
	variance RES	558	618	573	735	709	499	668	561
	h2 DIR	**27%**	**23%**	**27%**	**18%**	**14%**	**25%**	**25%**	**21%**
	h2 MAT	**8%**	**8%**	**7%**	**10%**	**8%**	**12%**	**16%**	**22%**
	h2 PE	**12%**	**13%**	**10%**	**12%**	**14%**	**14%**	**14%**	**13%**
NATIONAL	variance DIR	240	268		136	450	170	257	310
	variance MAT	96	55		68	194	120	144	197
	variance PE	106	63		43	45	80	102	81
	variance RES	586	421		294	647	500	693	374
	h2 DIR	**26%**	**36%**		**27%**	**35%**	**22%**	**23%**	**35%**
	h2 MAT	**10%**	**7%**		**14%**	**15%**	**15%**	**13%**	**22%**
	h2 PE	**15%**	**13%**		**13%**	**7%**	**14%**	**13%**	**18%**

6. The InterBeef weaning weight correlation matrix

6.1. Bending the direct and the maternal matrices

Jorjani et al. (2003) weighted bending was used to compute the InterBeef co-variance matrix in 4 steps:

i) matrix of correlations for direct weaning weight using a sire model (Table 4) was first bended ; all non-converged correlations (and correlations < 0.15) were set to 0.80 with a standard error of 0.322 (largest s.e. in the table).

ii) matrix of correlations for direct weaning weight using a sire model corrected for maternal pe (Table 8) was then bended ; all correlations non converged in i) were set to their bended value ; all remaining non-converged correlations were set to 0.80 with a standard error of 0.326 (largest s.e. in the table).

iii) matrix of correlations for direct weaning weight using a sire-MGS model corrected for maternal pe (Table 10) was then bended ; all correlations non converged in ii) were set to their bended value ; all remaining non-converged correlations (and correlations < 0.15) were set to 0.90 with a standard error of 0.332 (largest s.e. in the table).

iv) matrix of correlations for maternal weaning weight using a sire-MGS model corrected for maternal pe (Table 10) was then bended ; all correlations non converged correlations (and correlations < 0.25) were set to 0.62 with a standard error of 0.391 (largest s.e. in the table).

Table 12. Across-country before bending* genetic correlation (standard error) for direct (below diagonal) and maternal (above diagonal) weaning weight accounting for p.e.

	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
FRA		0.97 (0.109)	0.90 (0.152)	0.62 (0.391)	0.95 (0.104)	0.62 (0.391)	0.62 (0.391)	0.85 (0.138)
GBR	0.84 (0.086)		0.62 (0.391)	0.98 (0.138)	0.71 (0.211)	0.62 (0.391)	0.62 (0.391)	0.93 (0.299)
DNK	0.91 (0.057)	0.85 (0.332)		0.62 (0.391)	0.79 (0.140)	0.91 (0.186)	0.62 (0.391)	0.62 (0.391)
ESP	0.94 (0.332)	0.96 (0.086)	0.74 (0.332)		0.83 (0.133)	0.62 (0.391)	0.62 (0.391)	0.62 (0.391)
IRL	0.96 (0.070)	0.93 (0.067)	0.93 (0.204)	0.97 (0.101)		0.62 (0.391)	0.62 (0.391)	0.77 (0.220)
SWE	0.91 (0.332)	0.90 (0.332)	0.73 (0.142)	0.94 (0.332)	0.90 (0.332)		0.62 (0.447)	0.62 (0.391)
FIN	0.92 (0.332)	0.94 (0.332)	0.83 (0.332)	0.87 (0.332)	0.93 (0.332)	0.79 (0.177)		0.62 (0.391)
CZE	0.56 (0.177)	0.71 (0.236)	0.12 (0.332)	0.72 (0.332)	0.92 (0.153)	0.71 (0.332)	0.63 (0.332)	

*Coloured cells indicate an initial guess in i) for correlation between direct traits (0.90), and in iv) for correlations between maternal traits (0.62).

Table 13. Across-country bended genetic correlation (standard error) for direct (below diagonal) and maternal (above diagonal) weaning weight accounting for p.e.

	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
FRA		0.87	0.82	0.71	0.87	0.57	0.53	0.82
GBR	0.83		0.57	0.85	0.77	0.53	0.54	0.80
DNK	0.89	0.69		0.56	0.83	0.82	0.54	0.57
ESP	0.76	0.94	0.70		0.88	0.52	0.53	0.59
IRL	0.91	0.91	0.79	0.83		0.58	0.55	0.67
SWE	0.81	0.73	0.72	0.82	0.83		0.54	0.52
FIN	0.71	0.68	0.83	0.74	0.73	0.76		0.54
CZE	0.59	0.70	0.59	0.71	0.84	0.70	0.70	

6.2. Computing the full InterBeef matrix

Pre-bending genetic correlation and weight matrices

CORRELATIONS		DIRECT WEANING WEIGHT								MATERNAL WEANING WEIGHT							
		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
DIRECT	FRA	1.00															
	GBR	0.83	1.00														
	DNK	0.89	0.69	1.00													
	ESP	0.76	0.94	0.70	1.00												
	IRL	0.91	0.91	0.79	0.83	1.00											
	SWE	0.81	0.73	0.72	0.82	0.83	1.00										
	FIN	0.71	0.68	0.83	0.74	0.73	0.76	1.00									
	CZE	0.59	0.70	0.59	0.71	0.84	0.70	0.70	1.00								
MATERNAL	FRA	**-0.39**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	1.00							
	GBR	**0**	**-0.15**	**0**	**0**	**0**	**0**	**0**	**0**	0.87	1.00						
	DNK	**0**	**0**	**-0.16**	**0**	**0**	**0**	**0**	**0**	0.82	0.57	1.00					
	ESP	**0**	**0**	**0**	**-0.24**	**0**	**0**	**0**	**0**	0.71	0.85	0.56	1.00				
	IRL	**0**	**0**	**0**	**0**	**-0.21**	**0**	**0**	**0**	0.87	0.77	0.83	0.88	1.00			
	SWE	**0**	**0**	**0**	**0**	**0**	**-0.14**	**0**	**0**	0.57	0.53	0.82	0.52	0.58	1.00		
	FIN	**0**	**0**	**0**	**0**	**0**	**0**	**-0.26**	**0**	0.53	0.54	0.54	0.53	0.55	0.54	1.00	
	CZE	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**-0.18**	0.82	0.80	0.57	0.59	0.67	0.52	0.54	1.00

WEIGHTS		DIRECT WEANING WEIGHT								MATERNAL WEANING WEIGHT							
		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
DIRECT	FRA	100.0															
	GBR	100.0	100.0														
	DNK	100.0	100.0	100.0													
	ESP	100.0	100.0	100.0	100.0												
	IRL	100.0	100.0	100.0	100.0	100.0											
	SWE	100.0	100.0	100.0	100.0	100.0	100.0										
	FIN	100.0	100.0	100.0	100.0	100.0	100.0	100.0									
	CZE	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0								
MATERNAL	FRA	**50.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	100.0							
	GBR	**5.0**	**50.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	100.0	100.0						
	DNK	**5.0**	**5.0**	**50.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	100.0	100.0	100.0					
	ESP	**5.0**	**5.0**	**5.0**	**50.0**	**5.0**	**5.0**	**5.0**	**5.0**	100.0	100.0	100.0	100.0				
	IRL	**5.0**	**5.0**	**5.0**	**5.0**	**50.0**	**5.0**	**5.0**	**5.0**	100.0	100.0	100.0	100.0	100.0			
	SWE	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**50.0**	**5.0**	**5.0**	100.0	100.0	100.0	100.0	100.0	100.0		
	FIN	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**50.0**	**5.0**	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	CZE	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**5.0**	**50.0**	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

Post-bending InterBeef genetic matrix

CORRELATIONS		DIRECT WEANING WEIGHT								MATERNAL WEANING WEIGHT							
		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
DIRECT	FRA																
	GBR	0.81															
	DNK	0.88	0.88														
	ESP	0.87	0.68	0.78													
	IRL	0.74	0.92	0.82	0.70												
	SWE	0.80	0.73	0.82	0.71	0.81											
	FIN	0.70	0.67	0.72	0.83	0.73	0.76										
	CZE	0.58	0.70	0.83	0.59	0.70	0.70	0.70									
MATERNAL	FRA	-0.32	-0.09	-0.15	-0.15	-0.03	-0.04	-0.01	0.02								
	GBR	-0.11	-0.13	-0.03	0.04	-0.10	0.04	0.01	0.02	0.85							
	DNK	-0.13	-0.03	-0.17	-0.03	-0.06	0.00	0.03	-0.07	0.85	0.76						
	ESP	-0.14	0.04	-0.07	-0.15	0.05	0.01	-0.01	0.03	0.80	0.57	0.81					
	IRL	-0.02	-0.09	-0.05	0.04	-0.22	-0.02	-0.02	0.01	0.69	0.84	0.86	0.56				
	SWE	0.01	0.01	0.02	-0.01	-0.03	-0.14	0.00	-0.01	0.57	0.53	0.58	0.81	0.51			
	FIN	0.00	0.00	0.01	-0.01	-0.01	0.00	-0.26	0.00	0.53	0.54	0.54	0.53	0.53	0.54		
	CZE	-0.08	0.01	-0.02	0.04	0.03	0.01	0.00	-0.18	0.80	0.80	0.67	0.57	0.59	0.52	0.54	

VAR. (on diag) COVARIANCES (below diag.)		DIRECT WEANING WEIGHT								MATERNAL WEANING WEIGHT							
		FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
DIRECT	FRA	**240.00**															
	GBR	206.34	**268.00**														
	DNK	229.14	190.24	**289.00**													
	ESP	134.32	175.11	138.29	**136.00**												
	IRL	290.12	306.74	279.91	202.99	**450.00**											
	SWE	160.69	155.48	158.38	123.48	227.01	**170.00**										
	FIN	174.82	176.47	225.96	137.29	245.74	158.74	**257.00**									
	CZE	158.70	200.99	176.79	143.93	308.55	160.77	197.45	**310.00**								
MATERNAL	FRA	-49.23	-14.10	-24.96	-3.11	-30.67	-5.74	-2.02	3.98	**96.00**							
	GBR	-12.90	-16.13	5.36	-8.90	-4.42	3.86	1.10	2.22	61.52	**55.00**						
	DNK	-23.80	8.15	-28.56	7.00	-17.33	1.30	-0.98	5.06	88.55	47.48	**128.00**					
	ESP	-3.11	-11.57	5.61	-21.00	-9.26	-2.59	-2.20	1.30	56.05	51.44	52.71	**68.00**				
	IRL	-28.62	-7.81	-7.54	-9.29	-51.46	-0.11	5.63	-17.60	115.88	78.41	128.11	98.33	**194.00**			
	SWE	2.21	2.05	-2.56	-4.40	4.22	-19.59	-0.35	-1.17	60.74	42.69	100.52	46.30	87.98	**120.00**		
	FIN	-0.03	0.16	-1.38	-1.01	2.97	-0.33	-49.42	-0.70	61.90	48.31	72.48	52.27	90.57	70.93	**144.00**	
	CZE	-17.74	3.32	9.58	4.75	-4.70	1.36	-0.96	-43.78	110.00	82.91	90.25	68.31	130.29	79.76	90.23	**197.00**

Residual (co)variance InterBeef matrix

RESIDUAL	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
FRA	586							
GBR	0	421						
DNK	0	0	493					
ESP	0	0	0	294				
IRL	0	0	0	0	647			
SWE	0	0	0	0	0	500		
FIN	0	0	0	0	0	0	693	
CZE	0	0	0	0	0	0	0	374

Dam permanent environment (co)variance InterBeef matrix

RESIDUAL	FRA	GBR	DNK	ESP	IRL	SWE	FIN	CZE
FRA	61							
GBR	0	63						
DNK	0	0	85					
ESP	0	0	0	43.39				
IRL	0	0	0	0	45			
SWE	0	0	0	0	0	80		
FIN	0	0	0	0	0	0	63.4	
CZE	0	0	0	0	0	0	0	80.9

7. Appendix A : Dimension Constraint in DMU

From: Per Madsen [mailto:Per.Madsen@agrsci.dk]
Sent: 25 May 2009 16:30
To: Ross Evans
Subject: SV: DMU query

Dear Ross

The theoretical upper limit for number of traits that can be handled by DMU is 31. This is due to the way the pattern of missing values is handled.

The number of traits that can be handled is very data and model depended. If traits some of the traits are highly correlated this could give convergence problems if the data set is not large enough. Increasing the size of the data set will require more memory. DMUAI uses FSKAP for solving the MME and for obtaining elements of the inverse coefficient matrix. Part of the memory handling in FSPAK is by an integer work vector, different internal work vectors are than mapped into this global work vector. The size (number of 4 byte elements) needed for the global work vector is ~ NEQ*17 + NZU*7, where NEQ is the number of equations and NZU is the number of non-zero elements in the factored matrix. (NZU is number of non-zero elements in the coefficient matrix (NZE) + fillins). Both NZE and "fillins" are very model depended.

As the integer arithmetic in FAPAK is based on 4 byte integers, NEQ*17 + NZU*7 can not be larger than 2**(31) -1.

It will be the size of the global FSPAK work vector that sets the limit of the size of problems you can analyze.

One of the largest AI-REML analyses I have seen had ~1.700.000 equations and 62.000.000 NZE.

8. References

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