

Snell score calving sire and parent

I have run a full model and a reduced model (same as used for interbull validation test3).

I have counted how many offspring each bull have in full and reduced.

A: Bull index full and parent index full

Bulls. AI. Nordic. Bull has >50 offspring in full model and zero offspring in reduced model.

Father has >50 offspring in full and MGS has >50 offspring in full.

Model1: own_index_full = mother_index_full + father_index_full

Model2: own_index_full = mgs_index_full + father_index_full

HOL current

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	206	0.62	0.47	0.59	206	0.24	0.41	0.33
dCE1	206	0.58	0.48	0.54	206	0.24	0.40	0.31
dCS1	173	0.69	0.40	0.49	173	0.22	0.33	0.15
dSB2	221	0.56	0.45	0.43	221	0.18	0.39	0.19
dCE2	215	0.52	0.38	0.38	215	0.25	0.33	0.19
dCS2	198	0.65	0.51	0.54	198	0.28	0.48	0.28

HOL current direct

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	206	0.57	0.46	0.57	206	0.21	0.43	0.32
dCE1	206	0.54	0.48	0.53	206	0.22	0.41	0.28
dCS1	173	0.65	0.40	0.48	173	0.22	0.32	0.15
dSB2	221	0.50	0.44	0.39	221	0.16	0.39	0.19
dCE2	215	0.46	0.37	0.35	215	0.27	0.35	0.20
dCS2	198	0.59	0.49	0.49	198	0.26	0.45	0.25

HOL snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	196	0.68	0.48	0.63	196	0.21	0.43	0.33
dCE1	195	0.61	0.46	0.53	195	0.24	0.38	0.26
dCS1	160	0.78	0.41	0.52	160	0.21	0.30	0.12
dSB2	209	0.77	0.48	0.59	209	0.27	0.43	0.28
dCE2	205	0.65	0.39	0.44	205	0.29	0.32	0.18
dCS2	189	0.71	0.52	0.56	189	0.28	0.48	0.26

RDC snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	123	0.82	0.33	0.55	123	0.15	0.25	0.07
dCE1	112	0.78	0.41	0.58	112	0.15	0.31	0.16
dCS1	42	0.65	0.55	0.50	42	0.13	0.53	0.25
dSB2	137	0.83	0.47	0.62	137	0.16	0.40	0.18
dCE2	138	0.75	0.47	0.59	138	0.12	0.38	0.15
dCS2	68	0.71	0.50	0.47	68	0.19	0.53	0.21

JER snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	69	1.07	0.51	0.75	69	0.35	0.56	0.28
dCE1	65	0.98	0.51	0.67	65	0.33	0.46	0.21
dCS1	65	0.62	0.50	0.54	65	0.19	0.50	0.34
dSB2	89	1.14	0.54	0.73	89	0.35	0.55	0.22
dCE2	87	1.30	0.59	0.76	87	0.56	0.46	0.13
dCS2	86	0.62	0.56	0.48	86	0.20	0.47	0.28

B: Bull index full and parent index reduced

Bulls. AI. Nordic. Bull has >50 offspring in full model and zero offspring in reduced model.

Father has >50 offspring in reduced and MGS has >50 offspring in reduced.

Model1: own_index_full = mother_index_reduc + father_index_reduc

Model2: own_index_full = mgs_index_reduc + father_index_reduc

HOL current

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	90	0.29	0.42	0.27	97	0.18	0.41	0.27
dCE1	91	0.35	0.29	0.19	98	0.26	0.32	0.23
dCS1	80	0.32	0.19	0.09	84	0.21	0.24	0.08
dSB2	100	0.04	0.32	0.12	107	0.10	0.32	0.15
dCE2	98	0.22	0.05	0.05	105	0.29	0.15	0.12
dCS2	86	0.32	0.32	0.13	92	0.29	0.40	0.19

HOL current direct

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	90	0.25	0.39	0.24	97	0.17	0.40	0.25
dCE1	91	0.33	0.26	0.17	98	0.22	0.29	0.16
dCS1	80	0.32	0.15	0.09	84	0.23	0.20	0.08
dSB2	100	0.01	0.31	0.12	107	0.05	0.31	0.14
dCE2	98	0.20	0.02	0.04	105	0.29	0.13	0.11
dCS2	86	0.28	0.29	0.11	92	0.29	0.38	0.17

HOL snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	90	0.35	0.45	0.31	97	0.20	0.44	0.30
dCE1	91	0.32	0.25	0.15	98	0.25	0.29	0.20
dCS1	78	0.28	0.15	0.06	82	0.19	0.20	0.06
dSB2	100	-0.01	0.35	0.14	107	0.10	0.36	0.16
dCE2	98	0.23	-0.05	0.05	105	0.33	0.07	0.14
dCS2	85	0.29	0.30	0.11	91	0.29	0.39	0.18

RDC snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	69	0.22	0.22	0.07	71	-0.03	0.23	0.05
dCE1	64	0.13	0.35	0.16	65	0.03	0.34	0.15
dCS1	25	-0.17	0.46	0.21	26	-0.08	0.48	0.21
dSB2	84	0.33	0.26	0.12	87	0.08	0.23	0.08
dCE2	83	0.40	0.34	0.16	86	0.06	0.27	0.08
dCS2	38	0.09	0.49	0.17	39	0.05	0.49	0.16

JER snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	41	0.44	0.55	0.23	41	0.18	0.58	0.20
dCE1	37	0.12	0.38	0.14	37	0.04	0.38	0.14
dCS1	37	0.08	0.50	0.35	37	0.15	0.54	0.38
dSB2	47	0.54	0.56	0.17	47	0.29	0.54	0.14
dCE2	47	-0.12	0.23	0.03	48	-0.15	0.17	0.03
dCS2	47	0.07	0.61	0.31	47	0.26	0.63	0.43

B2: Bull index full and parent index reduced

Bulls. AI. Nordic. Bull has >250 offspring in full model and zero offspring in reduced model.

Father has >250 offspring in reduced and MGS has >250 offspring in reduced.

Model1: own_index_full = mother_index_reduc + father_index_reduc

Model2: own_index_full = mgs_index_reduc + father_index_reduc

HOL current

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	42	0.02	0.43	0.23	45	0.10	0.44	0.25
dCE1	42	0.32	0.17	0.13	45	0.26	0.25	0.18
dCS1	28	0.55	-0.16	0.26	31	0.34	0.14	0.16
dSB2	79	0.03	0.39	0.14	84	0.10	0.39	0.17
dCE2	78	0.20	0.02	0.04	81	0.22	0.17	0.06
dCS2	60	0.32	0.47	0.21	63	0.25	0.54	0.25

HOL snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	42	0.08	0.48	0.25	45	0.11	0.48	0.27
dCE1	42	0.26	0.11	0.09	45	0.24	0.20	0.15
dCS1	28	0.54	-0.18	0.20	31	0.35	0.11	0.15
dSB2	79	-0.01	0.38	0.16	84	0.14	0.39	0.19
dCE2	78	0.18	-0.12	0.04	81	0.23	0.05	0.06
dCS2	61	0.30	0.46	0.18	64	0.25	0.52	0.24

RDC snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	40	0.16	0.13	0.03	40	0.21	0.12	0.07
dCE1	37	0.12	0.31	0.13	37	0.21	0.36	0.21
dCS1	4	-0.92	-0.03	0.98	4	-0.26	-0.44	0.92
dSB2	67	0.45	0.26	0.11	67	0.22	0.24	0.09
dCE2	56	0.25	0.34	0.12	56	0.14	0.37	0.12
dCS2	10	-0.08	0.17	0.02	10	0.06	0.22	0.02

JER snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	20	0.32	0.66	0.18	20	0.13	0.65	0.16
dCE1	20	0.22	0.27	0.11	20	0.09	0.27	0.10
dCS1	18	0.19	0.58	0.41	18	0.28	0.60	0.50
dSB2	32	0.50	0.41	0.14	32	0.23	0.41	0.11
dCE2	30	-0.22	0.28	0.04	30	-0.14	0.26	0.04
dCS2	30	0.30	0.60	0.46	30	0.28	0.60	0.52

C: Bull index full and parent index full

Bulls born between 2010 and 2015 both years included. AI. Nordic. Bull has >50 offspring for full.

Father has >50 offspring in full and MGS has >50 offspring in full.

Model1: own_index_full = mother_index_full + father_index_full

Model2: own_index_full = mgs_index_full + father_index_full

HOL current

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	624	0.76	0.42	0.59	624	0.27	0.43	0.23
dCE1	607	0.68	0.45	0.58	607	0.20	0.43	0.24
dCS1	495	0.63	0.45	0.54	495	0.20	0.37	0.21
dSB2	670	0.76	0.37	0.51	670	0.26	0.33	0.12
dCE2	668	0.68	0.37	0.51	668	0.28	0.31	0.17
dCS2	581	0.60	0.41	0.52	581	0.20	0.34	0.20

HOL snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	629	0.76	0.44	0.64	629	0.26	0.45	0.28
dCE1	610	0.71	0.46	0.58	610	0.21	0.45	0.22
dCS1	485	0.66	0.46	0.56	485	0.20	0.38	0.21
dSB2	672	0.80	0.43	0.61	672	0.26	0.41	0.21
dCE2	668	0.75	0.39	0.55	668	0.29	0.35	0.17
dCS2	580	0.62	0.42	0.55	580	0.19	0.35	0.21

RDC snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	401	1.03	0.46	0.62	401	0.26	0.34	0.14
dCE1	389	0.89	0.50	0.66	389	0.27	0.44	0.24
dCS1	59	0.92	0.42	0.53	59	0.07	0.23	0.05
dSB2	496	0.86	0.45	0.63	496	0.24	0.39	0.24
dCE2	489	0.84	0.47	0.64	489	0.27	0.43	0.25
dCS2	171	0.88	0.49	0.61	171	0.21	0.43	0.21

JER snell score

trait	model1 N	model1 b1mother	model1 b1father	model1 Rsqr	Model2 N	model2 b1mgs	model2 b1father	model2 Rsqr
dSB1	190	1.02	0.51	0.71	190	0.13	0.40	0.20
dCE1	175	0.93	0.55	0.71	175	0.23	0.49	0.32
dCS1	138	0.74	0.61	0.69	138	0.15	0.61	0.36
dSB2	262	1.08	0.51	0.67	262	0.20	0.38	0.12
dCE2	262	1.08	0.53	0.67	262	0.30	0.49	0.20
dCS2	261	0.72	0.50	0.60	261	0.20	0.45	0.26

Phenotypic means for direct CE2

I have looked further into the data used for HOL current for dCE2.

It is for the same bulls as used in A and in B.

- bull_dCE2_mean is the mean of the offspring of the bull in the full data
- father_dCE2_mean is the mean of the offspring of the sire in the full data
- mgs_dCE2_mean is the mean of the offspring of the maternal grand sire in the full data
- father_dCE2_mean_reduc is the mean of the offspring of the sire in the reduced data
- mgs_dCE2_mean_reduc is the mean of the offspring of the maternal grand sire in the reduced data

for the 215 bulls in A:

Mean and STD:				Correlations		
Bull_dCE2_mean	215	3.932	0.029			Bull_dCE2_mean
father_dCE2_mean	215	3.909	0.043	father_dCE2_mean	215	0.223
mgs_dCE2_mean	215	3.876	0.050	mgs_dCE2_mean	215	0.220

For the 105 bulls in B:

Mean and STD:				Correlations		
Bull_dCE2_mean	105	3.924	0.029			Bull_dCE2_mean
father_dCE2_mean_reduc	105	3.913	0.034	father_dCE2_mean_reduc	105	0.118
mgs_dCE2_mean_reduc	105	3.860	0.044	mgs_dCE2_mean_reduc	105	0.089

The correlation between bull and father for B is lower than expected based on the heritability and the number of offspring, but it is in line with results shown on BV in section B. We expect a heritability of 7-8% for dCE2.

Number of offspring pr bull, pr father and pr mgs	r^2_{AI} for sire index		
	bull_full	father_reduc	mgs_reduc
50-70	0	5	0
71-100	1	4	3
101-200	1	11	3
201-500	21	16	13
501-1000	25	13	9
1001-2000	10	9	14
2001-	47	47	63
Min	100	56	73
Max	11992	8743	39099

Number of offspring	h^2		
	0.02	0.08	0.32
1	0.01	0.02	0.08
10	0.05	0.17	0.47
50	0.20	0.51	0.81
100	0.33	0.67	0.90
200	0.50	0.80	0.95
1000	0.83	0.95	0.99
10000	0.98	1.00	1.00

Test of heritabilities for calving traits

Offspring of the bull is split randomly in two groups. Each group has a minimum off calves of 50, 250 or 500. The calves are split by country.

Based on the expected heritability (these are from Jørrn) and the minimum number of offspring the reliability of the bulls' progeny mean is calculated (called r50, r250 or r500). The mean of the first group is correlated with the mean of the second group for the bulls (called c50, c250 or c500). The number of bulls in the correlation is called N50, N250 and N500. The expectation is that r and c is at similar level if the heritability is correct.

We will not focus on r50 and c50 since this is not many offspring and therefore randomness can affect the progeny mean and create noise. In stead we will focus on r250 and c250 since we have many offspring and still not too few bulls.

For the current HOL evaluation there is overall high similarity between r250 and c250. However, we have highlighted with yellow where the c250 is much lower than r250. The biggest problem is seen for SB2 for FIN where the c250 is negative, which is highly unexpected.

For snell score HOL evaluation the results are overall similar with current HOL. The c250 is for many of the traits and countries either at same level or higher for snell score than for current, as an example see SB1

SWE. An exception is SB2 DNK where the c250 is 0.11 for snell score and 0.35 for current. Furthermore, it is still problematic for SB2 FIN with negative value for c250.

Current HOL

trait	country	h ²	r50	c50	N50	r250	c250	N250	r500	c500	N500
SB1	DNK	0.049	0.38	0.31	73	0.76	0.74	46	0.86	0.80	35
SB1	FIN	0.049	0.38	0.68	43	0.76	0.49	19	0.86	0.32	8
SB1	SWE	0.049	0.38	0.44	46	0.76	0.43	14	0.86	0.28	7
CE1	DNK	0.101	0.56	0.29	70	0.87	0.84	46	0.93	0.85	35
CE1	FIN	0.101	0.56	0.43	41	0.87	0.71	11	0.93	1.00	2
CE1	SWE	0.101	0.56	0.58	45	0.87	0.41	13	0.93	0.62	7
CS1	DNK	0.247	0.77	0.75	63	0.94	0.87	40	0.97	0.87	30
SB2	DNK	0.012	0.13	0.17	102	0.43	0.35	68	0.60	0.47	52
SB2	FIN	0.012	0.13	0.25	60	0.43	-0.16	27	0.60	-0.18	17
SB2	SWE	0.012	0.13	-0.08	68	0.43	0.37	32	0.60	0.28	17
CE2	DNK	0.061	0.44	0.38	100	0.79	0.61	62	0.89	0.76	51
CE2	FIN	0.061	0.44	0.45	52	0.79	0.71	23	0.89	0.86	9
CE2	SWE	0.061	0.44	0.35	67	0.79	0.38	32	0.89	0.35	18
CS2	DNK	0.222	0.75	0.78	88	0.94	0.90	56	0.97	0.95	46

Snell score HOL

trait	country	h ²	r50	c50	N50	r250	c250	N250	r500	c500	N500
SB1	DNK	0.040	0.34	0.53	73	0.72	0.83	46	0.83	0.91	35
SB1	FIN	0.040	0.34	0.59	43	0.72	0.41	19	0.83	0.21	7
SB1	SWE	0.040	0.34	0.50	46	0.72	0.64	14	0.83	0.56	8
CE1	DNK	0.117	0.60	0.40	70	0.88	0.78	46	0.94	0.78	35
CE1	FIN	0.117	0.60	0.68	40	0.88	0.89	10	0.94	1.00	2
CE1	SWE	0.117	0.60	0.53	47	0.88	0.52	13	0.94	0.73	7
CS1	DNK	0.223	0.75	0.86	62	0.94	0.94	40	0.97	0.93	30
SB2	DNK	0.011	0.12	0.06	103	0.41	0.11	67	0.58	0.36	52
SB2	FIN	0.011	0.12	0.24	61	0.41	-0.10	27	0.58	-0.18	17
SB2	SWE	0.011	0.12	0.10	69	0.41	0.32	32	0.58	0.23	18
CE2	DNK	0.077	0.50	0.42	102	0.83	0.68	63	0.91	0.68	51
CE2	FIN	0.077	0.50	0.42	53	0.83	0.64	23	0.91	0.68	9
CE2	SWE	0.077	0.50	0.09	66	0.83	0.57	31	0.91	0.41	18
CS2	DNK	0.206	0.73	0.75	88	0.93	0.91	56	0.96	0.95	46

Snell score RDC

trait	country	h ²	r50	c50	N50	r250	c250	N250	r500	c500	N500
SB1	DNK	0.058	0.42	0.08	26	0.79	0.81	7	0.88	.	.
SB1	FIN	0.058	0.42	0.04	44	0.79	0.29	21	0.88	0.43	9
SB1	SWE	0.058	0.42	-0.06	27	0.79	-0.13	9	0.88	.	1
CE1	DNK	0.077	0.50	0.61	25	0.83	0.81	7	0.91	.	.
CE1	FIN	0.077	0.50	0.54	36	0.83	0.83	12	0.91	1.00	2
CE1	SWE	0.077	0.50	0.44	25	0.83	0.79	9	0.91	.	1
CS1	DNK	0.247	0.77	0.80	21	0.94	0.84	5	0.97	.	.
SB2	DNK	0.021	0.21	-0.03	48	0.57	0.11	17	0.73	1.00	2
SB2	FIN	0.021	0.21	0.30	59	0.57	0.21	33	0.73	0.38	21
SB2	SWE	0.021	0.21	0.47	40	0.57	0.59	20	0.73	0.67	11
CE2	DNK	0.035	0.31	0.26	46	0.69	0.44	16	0.82	1.00	2
CE2	FIN	0.035	0.31	0.45	53	0.69	0.73	27	0.82	0.74	13
CE2	SWE	0.035	0.31	0.44	39	0.69	0.58	20	0.82	0.64	11
CS2	DNK	0.234	0.76	0.91	34	0.94	0.95	11	0.97	.	1

Snell score JER

trait	country	h ²	r50	c50	N50	r250	c250	N250	r500	c500	N500
SB1	DNK	0.034	0.30	0.37	33	0.68	0.55	22	0.81	0.82	10
CE1	DNK	0.022	0.22	0.64	31	0.58	0.31	21	0.73	0.70	8
CS1	DNK	0.150	0.66	0.59	31	0.91	0.64	21	0.95	0.85	7
SB2	DNK	0.016	0.17	0.29	45	0.50	0.11	33	0.67	0.25	26
CE2	DNK	0.026	0.25	0.21	46	0.62	0.51	33	0.77	0.39	24
CS2	DNK	0.150	0.66	0.66	45	0.91	0.81	33	0.95	0.84	22

Correlation between progeny mean for bull_full and progeny mean for father_reduc

The phenotypic correlation between progeny means for bulls having more than 250 offspring and fathers having more than 250 offspring.

Current HOL

trait	country	c250	N250	Nfathers
SB1	DNK	0.47	30	22
SB1	FIN	0.62	11	9
SB1	SWE	0.55	14	9
CE1	DNK	0.26	30	22
CE1	FIN	0.62	4	4
CE1	SWE	0.17	14	9
CS1	DNK	0.05	31	23
SB2	DNK	0.03	60	45
SB2	FIN	0.07	17	12
SB2	SWE	0.25	20	14
CE2	DNK	0.10	59	44
CE2	FIN	-0.32	13	11
CE2	SWE	0.26	20	14
CS2	DNK	0.46	58	42

Snell score HOL

trait	country	c250	N250	Nfathers
SB1	DNK	0.61	30	22
SB1	FIN	0.56	11	9
SB1	SWE	0.48	14	9
CE1	DNK	0.37	30	22
CE1	FIN	0.48	4	4
CE1	SWE	0.21	14	9
CS1	DNK	-0.02	31	23
SB2	DNK	0.04	60	45
SB2	FIN	0.06	17	12
SB2	SWE	0.21	20	14
CE2	DNK	0.12	59	44
CE2	FIN	-0.30	13	11
CE2	SWE	0.26	20	14
CS2	DNK	0.41	59	43

Snell score RDC - OBS Few bulls!

trait	country	c250	N250	Nfathers
SB1	DNK	.	1	1
SB1	FIN	0.12	14	12
SB1	SWE	0.40	7	7

CE1	DNK	.	1	1
CE1	FIN	0.37	13	11
CE1	SWE	0.39	7	7
CS1	DNK	-1.00	2	2
SB2	DNK	-0.28	8	7
SB2	FIN	0.58	19	17
SB2	SWE	0.34	12	10
CE2	DNK	0.43	8	8
CE2	FIN	0.06	16	14
CE2	SWE	0.52	12	10
CS2	DNK	0.23	8	8

Snell score JER

trait	country	c250	N250	Nfathers
SB1	DNK	0.13	18	12
CE1	DNK	0.32	18	12
CS1	DNK	0.42	18	12
SB2	DNK	-0.12	32	23
CE2	DNK	0.22	30	21
CS2	DNK	0.71	30	21