

Analysis of Youngstock survival traits

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Introduction

The Youngstock survival index for a bull is a measure of the genetic potential of his offspring to survive the early months of its life (direct effect). We use four traits to calculate this index:

1. Heifer survival, early
2. Heifer survival, later
3. Bull survival, early
4. Bull survival, later

All traits are a binary 0/1 score, indicating whether the animal survived or not. Early period denotes the first 30 days of life, later period denote 30 days until a year. Since Youngstock survival is not an Interbull trait, no foreign information is included.

The model and genetic parameters are the same as those used in the current official NAV evaluation. For each breeds evaluation, we only use phenotypic data from animals with the correct breed in their id_nor. For the genotypes, we only include genotypes of AI bulls in the evaluations, to combat bias problems since dead calves are not genotyped. Other genotyped animals get a genomic breeding value based on calculated SNP solutions, similar to the existing weekly and monthly evaluations.

For compactness of tables, we will use abbreviations throughout. They are mentioned here:

- yss: youngstock survival
- ss: single-step breeding value
- rss: reduced information single-step breeding value
- ebv: tradition pedigree-based breeding value
- rebv: reduced information pedigree-based breeding value
- cor: correlation
- m_*: mean value of *
- s_*: standard deviation of *

Holstein

Genetic trends

Here, we exhibit the genetic trends of our evaluations for each trait. We see that the levels of breeding values are generally in agreement across evaluations.

Table 1: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2009	HP1	224	95.3	96.3	97.22	11.22	11.26	11.18	0.96
2010	HP1	193	93.24	94.04	95.06	11.88	11.86	11.81	0.96
2011	HP1	155	94.94	95.72	96.57	11.81	12.05	12.02	0.97
2012	HP1	171	98.7	99.04	99.92	11.93	11.59	11.46	0.98
2013	HP1	151	97.88	97.62	98.5	11.72	11.54	11.48	0.97
2014	HP1	113	100.81	100.86	101.44	13.25	13.21	13.0	0.98
2015	HP1	82	99.38	99.43	99.85	11.01	11.05	10.79	0.98
2016	HP1	65	102.54	102.6	102.35	10.69	10.77	10.6	0.98
2017	HP1	66	99.97	99.76	99.81	10.27	10.79	10.78	0.98
2018	HP1	78	102.91	101.78	101.77	10.45	10.97	10.79	0.97
2019	HP1	56	107.14	105.98	105.49	9.6	9.79	9.67	0.94
2020	HP1	56	105.64	105.09	104.35	9.55	10.03	9.98	0.96
2021	HP1	46	107.26	105.85	104.97	11.02	11.18	11.22	0.96
2022	HP1	44	105.82	104.2	103.33	11.26	11.12	11.01	0.95

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2023	HP1	4	111.75	110.75	109.56	4.35	2.06	1.81	0.21
2009	HP2	224	97.1	97.92	98.54	8.78	9.01	9.02	0.97
2010	HP2	193	95.27	96.04	96.69	10.7	10.76	10.87	0.98
2011	HP2	155	96.87	97.51	98.07	10.3	10.73	10.78	0.98
2012	HP2	171	99.56	100.26	100.79	9.91	10.13	10.22	0.98
2013	HP2	151	99.69	100.2	100.57	11.25	11.45	11.49	0.98
2014	HP2	113	99.03	99.8	100.06	11.03	11.09	11.07	0.98
2015	HP2	82	99.93	99.96	99.95	9.98	10.44	10.35	0.99
2016	HP2	65	103.91	103.88	103.74	8.23	8.39	8.35	0.99
2017	HP2	66	99.45	98.76	98.5	11.14	11.17	11.28	0.99
2018	HP2	78	103.41	102.63	102.44	10.2	10.95	10.94	0.98
2019	HP2	56	105.04	104.04	103.43	8.05	8.37	8.5	0.95
2020	HP2	53	105.15	104.17	103.5	6.89	7.04	7.09	0.93
2021	HP2	40	103.4	102.05	101.33	9.2	9.59	9.84	0.98
2022	HP2	4	107.5	106.25	105.34	14.73	13.6	14.01	1.0
2009	BP1	224	95.46	96.32	97.39	10.65	10.63	10.72	0.95
2010	BP1	193	92.95	93.54	94.58	11.84	11.86	12.01	0.96
2011	BP1	154	95.64	96.38	97.24	11.37	11.59	11.76	0.96
2012	BP1	171	98.39	98.57	99.41	11.58	11.23	11.23	0.97
2013	BP1	151	98.0	97.65	98.39	11.27	11.08	11.2	0.96
2014	BP1	114	101.46	101.25	101.69	13.03	13.16	13.21	0.98
2015	BP1	82	99.26	99.09	99.27	11.16	11.17	11.16	0.98
2016	BP1	66	103.08	102.88	102.52	10.28	10.08	10.22	0.98
2017	BP1	66	100.27	99.8	99.49	10.92	11.07	11.31	0.98
2018	BP1	78	102.09	100.91	100.53	10.28	10.4	10.56	0.96
2019	BP1	56	106.7	105.68	105.21	10.06	10.28	10.43	0.94
2020	BP1	55	105.78	105.16	104.25	10.22	10.78	10.95	0.96
2021	BP1	46	107.07	105.63	104.75	11.05	10.8	11.01	0.95
2022	BP1	42	105.48	104.4	103.37	11.83	11.38	11.42	0.95
2023	BP1	3	113.33	110.0	109.07	3.21	1.73	1.77	0.99
2009	BP2	224	97.15	97.72	98.8	8.86	8.93	8.88	0.97
2010	BP2	193	95.29	95.66	96.78	10.93	10.98	10.97	0.98
2011	BP2	154	97.52	98.14	99.04	9.74	10.12	10.05	0.98

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2012	BP2	171	99.2	99.74	100.48	10.13	10.34	10.25	0.98
2013	BP2	151	99.98	100.34	100.88	11.05	11.21	11.16	0.98
2014	BP2	113	99.35	100.02	100.33	10.62	10.78	10.7	0.98
2015	BP2	82	99.9	99.82	99.73	9.82	10.05	9.92	0.99
2016	BP2	66	104.35	104.23	104.04	8.42	8.24	8.21	0.98
2017	BP2	66	99.42	98.65	98.37	11.06	11.22	11.11	0.99
2018	BP2	78	102.73	101.99	101.69	9.47	10.09	10.0	0.98
2019	BP2	56	104.07	103.48	102.8	7.75	8.16	8.12	0.95
2020	BP2	54	104.98	103.83	103.14	7.19	7.61	7.54	0.94
2021	BP2	42	102.67	101.6	100.86	9.01	8.76	8.92	0.96
2022	BP2	32	104.53	103.34	102.62	8.08	8.28	8.24	0.95

Table 2: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	HP1	265	96.4	97.03	10.6	10.1	1.71	0.98
2010	HP1	223	94.56	94.98	11.29	10.88	1.66	0.98
2011	HP1	184	96.29	96.72	10.87	10.37	1.87	0.98
2012	HP1	205	99.38	99.39	11.13	10.7	2.16	0.97
2013	HP1	191	98.23	97.73	10.72	10.47	2.46	0.95
2014	HP1	156	99.97	99.03	12.18	11.76	2.54	0.97
2015	HP1	123	97.63	96.49	10.43	9.55	3.36	0.93
2016	HP1	98	100.23	98.38	10.37	9.49	6.06	0.72
2017	HP1	102	98.74	97.12	9.26	8.23	6.15	0.63
2018	HP1	113	101.39	99.41	9.84	8.7	5.79	0.68
2019	HP1	89	104.0	99.26	10.15	8.07	7.17	0.63
2020	HP1	87	103.06	99.24	10.42	8.8	6.23	0.78
2021	HP1	74	104.66	100.91	11.34	8.66	7.35	0.66
2022	HP1	62	105.52	100.98	10.2	7.89	7.76	0.59
2023	HP1	18	106.61	100.56	7.55	7.23	8.06	0.44
2009	HP2	264	98.06	98.0	8.52	8.65	1.14	0.98
2010	HP2	222	96.19	95.96	10.62	10.5	1.31	0.98
2011	HP2	182	97.54	97.52	9.83	10.01	1.48	0.98
2012	HP2	201	100.12	100.14	9.61	9.7	1.7	0.97

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2013	HP2	190	100.2	100.0	10.5	10.39	2.0	0.96
2014	HP2	154	99.29	98.38	9.9	10.35	2.28	0.96
2015	HP2	119	100.02	99.79	9.0	9.3	2.6	0.93
2016	HP2	98	102.82	101.6	8.48	8.34	5.6	0.65
2017	HP2	99	99.16	99.75	9.87	8.21	6.18	0.61
2018	HP2	109	102.81	102.27	9.64	7.43	6.76	0.48
2019	HP2	85	103.68	101.32	8.08	8.22	5.94	0.61
2020	HP2	82	104.28	102.0	7.76	7.76	5.79	0.63
2021	HP2	65	102.88	102.72	8.9	7.24	5.82	0.61
2022	HP2	11	105.73	105.45	10.06	10.72	4.82	0.83
2009	BP1	265	97.15	97.78	10.03	9.59	1.69	0.98
2010	BP1	225	94.95	95.33	11.27	10.88	1.76	0.98
2011	BP1	185	97.5	97.86	10.41	9.91	1.83	0.97
2012	BP1	199	99.61	99.7	10.77	10.35	2.12	0.97
2013	BP1	193	99.21	98.52	10.18	10.03	2.38	0.95
2014	BP1	157	101.53	100.17	11.51	11.0	2.62	0.96
2015	BP1	123	99.16	97.48	10.12	9.27	3.13	0.94
2016	BP1	105	101.21	99.29	9.64	8.34	5.89	0.69
2017	BP1	94	100.95	98.95	9.47	7.32	6.11	0.62
2018	BP1	110	102.01	100.42	9.19	7.52	5.46	0.65
2019	BP1	88	104.44	99.49	9.9	6.43	7.55	0.52
2020	BP1	94	104.12	100.12	10.09	7.48	5.98	0.76
2021	BP1	69	106.01	101.67	10.83	7.29	7.54	0.61
2022	BP1	60	106.37	100.67	10.18	7.32	7.73	0.63
2023	BP1	12	107.25	99.83	6.11	7.36	8.58	0.43
2009	BP2	262	98.61	98.56	8.56	8.55	1.09	0.99
2010	BP2	223	96.97	96.77	10.58	10.44	1.27	0.98
2011	BP2	184	98.56	98.5	9.29	9.48	1.29	0.98
2012	BP2	198	100.23	100.42	9.65	9.68	1.75	0.97
2013	BP2	191	100.85	100.55	10.14	10.1	1.93	0.97
2014	BP2	156	100.44	99.41	9.31	9.66	2.19	0.96
2015	BP2	120	100.87	100.27	8.7	8.82	2.45	0.93
2016	BP2	104	103.56	102.34	8.31	7.31	5.3	0.66

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2017	BP2	93	100.74	101.2	9.72	7.65	5.75	0.64
2018	BP2	109	103.22	102.77	8.6	6.04	6.27	0.41
2019	BP2	85	103.53	101.66	7.42	6.99	5.4	0.54
2020	BP2	92	104.51	102.14	7.66	6.81	5.43	0.62
2021	BP2	67	102.9	102.67	8.31	6.3	5.54	0.58
2022	BP2	48	105.96	102.83	7.79	8.02	6.17	0.61
2023	BP2	2	111.0	109.5	1.41	2.12	1.5	1.0

Table 3: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic cows with genotype and phenotype

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	HP1	979	93.3	95.8	32.02	28.19	13.66	0.85
2010	HP1	1396	89.78	92.17	34.34	29.11	13.5	0.87
2011	HP1	3041	90.91	94.55	32.5	28.19	13.57	0.86
2012	HP1	4780	94.1	96.16	32.99	28.37	13.3	0.87
2013	HP1	8320	96.66	97.61	31.78	27.28	13.17	0.85
2014	HP1	9755	98.26	98.58	31.54	27.42	13.05	0.85
2015	HP1	12507	97.26	97.27	32.14	27.86	13.11	0.86
2016	HP1	19813	99.64	99.66	31.26	26.96	12.99	0.85
2017	HP1	29712	100.63	99.99	32.01	27.39	13.41	0.85
2018	HP1	41675	102.32	101.46	31.15	26.64	13.32	0.84
2019	HP1	46874	104.14	103.11	31.59	26.67	13.87	0.84
2020	HP1	56168	103.08	102.06	31.55	26.57	13.98	0.83
2021	HP1	59967	104.83	102.41	31.59	26.39	14.44	0.82
2022	HP1	68021	105.16	102.56	31.55	26.4	14.49	0.82
2023	HP1	74900	105.37	102.01	31.63	26.16	14.75	0.82
2024	HP1	79234	106.04	102.66	31.66	25.91	15.1	0.81
2025	HP1	24030	106.18	102.6	31.93	25.87	15.32	0.81
2009	HP2	978	92.43	93.02	27.53	25.61	9.94	0.89
2010	HP2	1395	91.41	91.87	27.93	25.83	10.1	0.89
2011	HP2	3036	93.21	94.31	27.66	25.47	10.08	0.89
2012	HP2	4768	94.87	96.05	27.4	25.11	10.07	0.89
2013	HP2	8309	97.59	98.15	27.08	24.87	9.97	0.89
2014	HP2	9714	98.24	98.7	26.62	24.49	10.08	0.88

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2015	HP2	12404	99.36	100.03	26.55	24.44	9.9	0.88
2016	HP2	19612	100.51	100.93	26.94	24.72	10.01	0.89
2017	HP2	29364	100.41	100.71	27.1	24.9	10.04	0.89
2018	HP2	41256	102.3	103.56	26.58	24.33	10.2	0.88
2019	HP2	46259	104.08	105.07	26.51	24.32	10.39	0.87
2020	HP2	55040	103.28	103.61	26.47	23.98	10.74	0.86
2021	HP2	58945	103.77	103.79	26.58	23.9	11.08	0.85
2022	HP2	66564	104.05	103.55	26.42	23.85	10.96	0.85
2023	HP2	73502	103.69	102.94	26.32	23.7	11.05	0.85
2024	HP2	16958	103.79	103.45	26.3	23.63	11.12	0.85

Table 4: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic bulls with genotype and phenotype

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	BP1	717	93.11	94.52	26.48	22.88	9.48	0.87
2010	BP1	706	90.04	93.01	27.66	23.95	10.47	0.87
2011	BP1	1338	92.79	95.41	29.13	25.08	11.19	0.87
2012	BP1	1706	94.97	96.21	28.87	24.01	11.32	0.86
2013	BP1	1801	97.4	97.81	27.88	24.05	11.21	0.86
2014	BP1	2376	98.34	99.13	28.8	25.25	11.44	0.87
2015	BP1	2012	98.82	97.76	28.84	24.84	11.7	0.86
2016	BP1	2155	101.3	100.43	28.36	24.6	12.09	0.84
2017	BP1	2446	101.42	100.11	29.09	24.27	12.4	0.85
2018	BP1	2347	103.22	101.85	28.3	23.75	12.39	0.84
2019	BP1	2516	105.15	102.02	28.25	23.45	12.87	0.83
2020	BP1	2400	105.53	102.87	29.74	24.41	13.02	0.84
2021	BP1	2199	106.28	102.46	28.26	23.48	13.21	0.82
2022	BP1	2302	107.24	102.93	29.57	23.93	13.58	0.83
2023	BP1	2245	107.73	102.64	28.81	23.08	14.2	0.81
2024	BP1	1901	107.91	103.1	29.08	23.24	14.18	0.81
2025	BP1	754	107.12	101.01	28.52	23.07	13.84	0.83
2009	BP2	634	95.04	94.82	22.39	20.66	7.18	0.89
2010	BP2	633	92.61	93.51	25.33	22.94	7.55	0.92
2011	BP2	1157	94.63	95.0	23.8	21.52	8.68	0.88

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2012	BP2	1528	95.55	96.25	24.16	21.92	8.22	0.9
2013	BP2	1555	98.71	99.45	24.04	22.62	8.44	0.89
2014	BP2	2076	97.89	98.32	24.96	23.23	8.57	0.9
2015	BP2	1804	100.81	100.84	24.54	22.55	8.72	0.89
2016	BP2	1966	101.87	101.61	23.72	22.39	8.79	0.88
2017	BP2	2276	101.51	101.48	24.99	23.01	9.16	0.89
2018	BP2	2162	102.45	103.36	24.29	21.96	9.19	0.88
2019	BP2	2297	104.88	105.23	24.2	22.17	9.51	0.87
2020	BP2	2192	105.21	104.75	24.14	21.53	9.54	0.87
2021	BP2	1994	105.82	105.56	23.99	21.46	10.1	0.85
2022	BP2	2058	106.17	104.65	23.68	21.21	10.07	0.85
2023	BP2	2022	104.68	103.77	23.43	21.17	10.15	0.84
2024	BP2	1669	106.68	105.64	23.42	21.26	10.3	0.84

Correlations

Here, we give correlation tables and tables of differences between the relevant evaluations. We test that we didn't change the model by comparing our new model without genomic information to the breeding values of the traditional pedigree-based model and expect very high correlations for tested animals. We test the change by incorporating genomic information, compared to a non-genomic evaluation, and expect to see some changes even in tested animals, but not too large.

Table 5: Correlations between current EBV and new EBV for Nordic AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	224	0.998	0.997	0.998	0.997
2010	193	0.998	0.998	0.997	0.997
2011	155	0.998	0.998	0.998	0.998
2012	171	0.998	0.998	0.998	0.998
2013	151	0.998	0.998	0.998	0.998
2014	113	0.999	0.999	0.999	0.999
2015	82	0.999	0.999	0.998	0.998
2016	65	0.998	0.999	0.998	0.999
2017	66	0.999	0.999	0.999	0.999
2018	78	0.999	0.999	0.999	0.999
2019	56	0.999	0.999	0.999	0.999

BYR	n	cor1	cor2	cor3	cor4
2020	56	0.998	0.998	0.999	0.998
2021	46	0.999	0.998	0.999	0.998
2022	44	0.999	0.998	0.999	0.998

Table 6: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-3.0	0	0	1	0
-2.0	22	7	31	8
-1.0	165	168	198	187
0.0	193	223	169	213
1.0	34	16	15	7
2.0	0	1	1	0
3.0	1	0	0	0

Table 7: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	224	0.96	0.968	0.953	0.969
2010	193	0.963	0.979	0.959	0.98
2011	155	0.966	0.975	0.965	0.978
2012	171	0.977	0.98	0.975	0.984
2013	151	0.967	0.981	0.96	0.982
2014	113	0.981	0.985	0.978	0.984
2015	82	0.981	0.987	0.983	0.985
2016	65	0.983	0.988	0.98	0.984
2017	66	0.976	0.991	0.979	0.989
2018	78	0.97	0.982	0.965	0.983
2019	56	0.936	0.948	0.944	0.949
2020	56	0.956	0.924	0.954	0.937
2021	46	0.96	0.961	0.953	0.955
2022	44	0.951	0.899	0.943	0.897

Table 8: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-15.0	1	0	0	0
-14.0	0	0	0	0
-13.0	0	0	1	0
-12.0	0	1	0	0
-11.0	0	2	0	1
-10.0	1	1	4	2
-9.0	4	2	4	3
-8.0	5	7	10	4
-7.0	11	4	4	6
-6.0	8	13	5	6
-5.0	23	13	28	12
-4.0	21	18	26	22
-3.0	37	28	46	44
-2.0	56	85	59	71
-1.0	82	89	76	110
0.0	79	91	69	71
1.0	29	29	34	25
2.0	27	17	22	20
3.0	11	9	9	8
4.0	10	1	5	5
5.0	3	3	5	3
6.0	3	1	4	1
7.0	1	1	1	1
8.0	2	0	1	0
9.0	0	0	1	0
10.0	0	0	0	0
11.0	1	0	0	0
12.0	0	0	0	0
13.0	0	0	1	0

Table 9: Correlations between current two-step and new Single-step (combined YSS index) for genotyped AI bulls born after 2009 with > 30 offspring

BYR	n	cor
2009	223	0.954

BYR	n	cor
2010	193	0.922
2011	154	0.956
2012	171	0.969
2013	151	0.902
2014	113	0.984
2015	82	0.985
2016	65	0.977
2017	66	0.98
2018	78	0.87
2019	56	0.968
2020	56	0.946
2021	46	0.913
2022	44	0.886

Table 10: Table of differences between current two-step and new Single-step (combined YSS index) for genotyped AI bulls with > 30 offspring born after 2015

dif	dif5
-11.0	1
-10.0	1
-9.0	1
-8.0	1
-7.0	4
-6.0	4
-5.0	9
-4.0	13
-3.0	33
-2.0	79
-1.0	86
0.0	66
1.0	39
2.0	35
3.0	18
4.0	9
5.0	8

dif	dif5
6.0	1
7.0	0
8.0	2
9.0	2
10.0	1
11.0	0
12.0	1
13.0	0
14.0	0
15.0	0
16.0	0
17.0	0
18.0	0
19.0	0
20.0	0
21.0	0
22.0	0
23.0	0
24.0	0
25.0	0
26.0	0
27.0	0
28.0	0
29.0	0
30.0	0
31.0	0
32.0	0
33.0	0
34.0	0
35.0	0
36.0	0
37.0	0
38.0	0

dif	dif5
39.0	0
40.0	0
41.0	0
42.0	1

Table 11: Correlations between current two-step and new Single-step for genotyped nordic bulls with no offspring born after 2020

BYR	n	cor
2020	3090	0.66
2021	3050	0.671
2022	3119	0.646
2023	3009	0.662
2024	3001	0.629
2025	1276	0.659

Table 12: Table of differences between current two-step and new Single-step for genotyped nordic bulls born after 2020 with no offspring

dif	dif5
-93.0	1
-92.0	0
-91.0	0
-90.0	1
-89.0	0
-88.0	0
-87.0	0
-86.0	0
-85.0	0
-84.0	0
-83.0	0
-82.0	1
-81.0	0
-80.0	0
-79.0	4
-78.0	0
-77.0	2

dif	dif5
-76.0	2
-75.0	1
-74.0	2
-73.0	0
-72.0	2
-71.0	2
-70.0	1
-69.0	2
-68.0	1
-67.0	3
-66.0	0
-65.0	5
-64.0	5
-63.0	8
-62.0	10
-61.0	7
-60.0	11
-59.0	13
-58.0	11
-57.0	21
-56.0	18
-55.0	15
-54.0	17
-53.0	26
-52.0	25
-51.0	31
-50.0	27
-49.0	34
-48.0	46
-47.0	46
-46.0	29
-45.0	36
-44.0	37

dif	dif5
-43.0	50
-42.0	55
-41.0	63
-40.0	63
-39.0	72
-38.0	82
-37.0	78
-36.0	87
-35.0	85
-34.0	92
-33.0	96
-32.0	131
-31.0	113
-30.0	111
-29.0	110
-28.0	124
-27.0	126
-26.0	143
-25.0	156
-24.0	144
-23.0	164
-22.0	165
-21.0	183
-20.0	188
-19.0	220
-18.0	196
-17.0	191
-16.0	191
-15.0	194
-14.0	227
-13.0	205
-12.0	209
-11.0	196

dif	dif5
-10.0	220
-9.0	230
-8.0	254
-7.0	228
-6.0	235
-5.0	263
-4.0	267
-3.0	264
-2.0	282
-1.0	226
0.0	231
1.0	248
2.0	238
3.0	220
4.0	228
5.0	203
6.0	224
7.0	177
8.0	239
9.0	224
10.0	182
11.0	185
12.0	194
13.0	160
14.0	179
15.0	179
16.0	161
17.0	141
18.0	147
19.0	134
20.0	147
21.0	128
22.0	138

dif	dif5
23.0	127
24.0	128
25.0	112
26.0	90
27.0	86
28.0	88
29.0	83
30.0	74
31.0	71
32.0	70
33.0	62
34.0	63
35.0	46
36.0	46
37.0	43
38.0	43
39.0	37
40.0	41
41.0	36
42.0	27
43.0	34
44.0	30
45.0	23
46.0	14
47.0	27
48.0	17
49.0	17
50.0	13
51.0	10
52.0	16
53.0	12
54.0	15
55.0	6

dif	dif5
56.0	8
57.0	9
58.0	7
59.0	3
60.0	6
61.0	3
62.0	3
63.0	3
64.0	2
65.0	2
66.0	4
67.0	2
68.0	1
69.0	1
70.0	2
71.0	0
72.0	0
73.0	0
74.0	2
75.0	0
76.0	0
77.0	0
78.0	1

Table 13: Genotyped nordic bulls with no offspring and a difference between single-step and two-step of more than 50 index points.!

nav_id	country	BYR	dif	twobv	ssbv5	sire_ss	dam_ss
1023737136	DNK	2021	-77.91	89.91	12.0	101.0	108.0
1024855096	DNK	2022	77.28	118.72	196.0	121.0	88.0
1025453835	DNK	2022	93.25	114.75	208.0	115.0	144.0
1026006869	DNK	2023	75.15	120.85	196.0	114.0	148.0
1027213597	DNK	2024	75.63	105.37	181.0	missing	90.0
1027806470	DNK	2024	82.45	115.55	198.0	112.0	161.0
1027909818	DNK	2024	76.24	105.76	182.0	104.0	142.0

nav_id	country	BYR	diff	twobv	ssbv5	sire_ss	dam_ss
1028125186	DNK	2025	78.6	114.4	193.0	109.0	184.0
1214083955	FIN	2021	79.04	110.96	190.0	107.0	156.0
1214261715	FIN	2022	90.31	104.69	195.0	108.0	164.0
1214600832	FIN	2022	79.17	106.83	186.0	86.0	171.0
1320503163	SWE	2022	79.49	120.51	200.0	120.0	121.0
1320951532	SWE	2023	76.72	116.28	193.0	110.0	135.0

Legarra-Reverter test

The Legarra-Reverter test is a test for bias in evaluations. We perform two calculations of breeding values, one with all information available and one where offspring of sires born after 2018 has their records removed. Then we perform a linear regression on genotyped, nordic bulls, who has no data in the reduced dataset and with more than 30 offspring in the full dataset. We also require that their sires are not in the focal group, so we remove bulls whose father meets the same criteria.

The slope of the regression indicates the bias, with a slope of one meaning no bias, a slope less than one indicating that the estimated values of unproven animals are too extreme, and a slope higher than one indicating that the estimated breeding values of unproven animals are too conservative.

As can be seen, we have some issues with the Legarra-Reverter test. We're looking into it.

Table 14: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
HP1	0.781	0.385	153
HP2	0.754	0.34	151
BP1	0.822	0.412	154
BP2	0.818	0.394	154

EBV:

trait	b1	rsquare	n
HP1	0.74	0.282	153
HP2	0.64	0.183	151
BP1	0.803	0.314	154
BP2	0.711	0.225	154

Interbull test

Youngstock survival is not an Interbull trait, but for quality control we performed n Interbull GEBV test and got a with a failing grade.

735	brd	pop	trt	evaldate	m	n	test	mean_y	std_y	dv	mean_x	std_x	b0	se_b0	b1	se_b1	ncand
i_est	Exp_b1	R2	fb	year		tests	pass										
735	HOL	DFS	HP1	20250710	1	108	101.5926	10.5518	GM	100.4030	6.9174	38.0047	13.0049	0.6332	0.1136	108	
0.0000	1.0000	18.5	N	2015		NNNY	FAIL										
735	HOL	DFS	HP1	20250710	2	108	101.5926	10.5518	GM	99.8157	7.4034	53.8017	12.6674	0.4796	0.1265	108	
0.0000	1.0000	11.9	N	2015		----	----										
735	HOL	DFS	HP2	20250710	1	109	100.3237	10.3698	GM	101.9881	5.7398	0.9810	14.4941	0.9747	0.1635	109	
0.0000	1.0000	30.7	N	2015		YYYY	PASS										
735	HOL	DFS	HP2	20250710	2	109	100.3237	10.3698	GM	100.6661	5.9745	24.9744	14.7559	0.7502	0.1461	109	
0.0000	1.0000	19.8	N	2015		----	----										
735	HOL	DFS	BP1	20250710	1	106	102.4019	10.2447	GM	99.9411	6.8071	33.1106	12.6334	0.6941	0.1145	106	
0.0000	1.0000	22.6	N	2015		NNNY	FAIL										
735	HOL	DFS	BP1	20250710	2	106	102.4019	10.2447	GM	99.2408	7.0187	49.3901	12.8715	0.5361	0.1293	106	
0.0000	1.0000	14.2	N	2015		----	----										
735	HOL	DFS	BP2	20250710	1	122	101.2708	10.0788	GM	101.6393	5.7495	14.3831	13.6390	0.8567	0.1502	122	
0.0000	1.0000	25.5	N	2015		YYNY	PASS										
735	HOL	DFS	BP2	20250710	2	122	101.2708	10.0788	GM	100.3036	5.8418	42.4173	14.2927	0.5898	0.1421	122	
0.0000	1.0000	12.5	N	2015		----	----										

The set of bulls chosen by the Interbull test program is different from the focal group selected for the Legarra-Reverter test. Hence, we get different slope coefficients.

Mendelian sampling

The mendelian sampling of an animals is its deviation of its breeding values from the expected breeding value, which is the average of its parents breeding values. Some mendelian samling is expected on the individual level (this is what enables breeding), but across all animals we expect it to be close to zero. Otherwise, this indicates a bias in the set of animals in the evaluation, which violates the unbiasedness of the BLUP model. We conclude that the mendelian sampling is generally close to 0.

Table 15: Average mendelian sampling by birth year. Animals are only included if they are genotyped, their sire has > 30 offspring and their dam is genotyped.

BYR	n	m1	m2	m3	m4
2010	915	-6.911	-7.461	-6.325	-6.717
2011	995	-5.133	-5.159	-5.469	-5.048
2012	1456	-1.44	-1.875	-1.506	-1.811
2013	2511	0.848	0.617	0.733	0.594
2014	4034	0.795	0.607	0.833	0.6
2015	5792	0.835	0.45	0.937	0.504
2016	7436	0.313	0.258	0.302	0.308
2017	9986	0.393	0.758	0.546	0.839
2018	13820	0.542	0.094	0.524	0.095
2019	19959	1.709	1.324	1.66	1.232
2020	29234	1.246	0.815	1.125	0.678
2021	37462	-0.113	0.066	-0.14	0.064
2022	46903	-0.067	0.019	-0.136	0.029
2023	51705	-0.179	-0.13	-0.199	-0.075
2024	56322	-0.215	-0.236	-0.258	-0.175

Table 16: Average mendelian sampling by birth year. Animals are only included if they are not genotyped, their sire has > 30 offspring and their dam isn't genotyped.

BYR	n	m1	m2	m3	m4
2001	404420.0	0.036	0.037	0.001	-0.007
2002	398066.0	0.023	0.011	0.01	0.006
2003	413840.0	-0.019	0.02	0.027	0.042
2004	460421.0	-0.007	0.001	0.002	0.004
2005	452597.0	0.014	-0.031	-0.042	0.005
2006	459008.0	-0.01	-0.032	-0.041	-0.012
2007	445404.0	-0.003	-0.021	-0.016	-0.0
2008	502261.0	-0.001	0.005	0.006	0.002

BYR	n	m1	m2	m3	m4
2009	517513.0	0.028	0.007	0.004	0.018
2010	525251.0	0.03	-0.022	-0.008	-0.002
2011	518430.0	0.017	-0.036	0.009	-0.034
2012	513149.0	0.025	-0.014	0.018	-0.045
2013	507190.0	0.003	0.009	-0.001	-0.002
2014	506877.0	-0.002	0.007	0.009	0.019
2015	500677.0	0.001	-0.008	-0.012	-0.003
2016	485189.0	0.004	-0.007	-0.017	0.019
2017	451130.0	-0.002	-0.023	0.01	0.005
2018	433674.0	-0.002	-0.023	0.0	-0.005
2019	402778.0	-0.005	-0.001	0.001	-0.006
2020	392908.0	0.008	-0.01	0.014	-0.021
2021	375996.0	-0.023	-0.037	-0.029	-0.026
2022	347727.0	0.006	-0.026	-0.013	-0.005
2023	315019.0	-0.022	-0.042	-0.036	-0.013
2024	292717.0	-0.033	-0.035	-0.052	-0.002

Reliabilities

Table 17: Comparison of reliabilities between single-step (ss), new EBV (ebv) and current official evaluation (cur) for nordic AI bulls with > 30 offspring and correlation between single-step and current evaluation.

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	HP1	224	72.48	61.63	61.65	7.58	11.08	11.03	0.98
2010	HP1	193	73.0	62.57	62.6	8.73	13.28	13.29	0.99
2011	HP1	155	74.35	65.22	65.3	8.18	11.14	11.11	0.97
2012	HP1	171	76.57	67.79	67.79	9.19	14.08	14.09	0.99
2013	HP1	151	76.75	67.88	67.87	9.43	14.43	14.43	0.99
2014	HP1	113	80.96	74.22	74.2	10.59	16.23	16.26	0.99
2015	HP1	82	83.97	79.61	79.61	9.07	14.03	14.07	0.99
2016	HP1	65	83.24	78.39	78.38	9.26	13.62	13.65	0.99
2017	HP1	66	83.77	79.17	79.24	9.66	14.44	14.41	0.99
2018	HP1	78	81.27	75.36	75.37	10.05	15.63	15.62	0.99
2019	HP1	56	81.53	75.66	75.59	9.88	15.51	15.54	0.99
2020	HP1	56	78.83	70.95	70.98	12.48	20.06	20.08	0.99

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2021	HP1	46	77.8	68.49	68.48	13.96	23.25	23.28	0.99
2022	HP1	44	76.24	66.8	66.77	13.78	22.81	22.86	0.99
2009	HP2	224	72.49	61.63	72.85	7.65	11.08	9.07	0.95
2010	HP2	193	73.03	62.57	73.26	8.82	13.28	10.47	0.97
2011	HP2	155	74.38	65.22	75.82	8.24	11.14	8.94	0.96
2012	HP2	171	76.61	67.79	77.68	9.24	14.08	10.94	0.96
2013	HP2	151	76.77	67.88	77.65	9.43	14.43	11.1	0.97
2014	HP2	113	80.99	74.22	82.36	10.62	16.23	12.51	0.97
2015	HP2	82	84.29	79.61	86.73	9.43	14.03	9.95	0.98
2016	HP2	65	83.35	78.39	85.98	9.42	13.62	9.48	0.98
2017	HP2	66	83.85	79.17	85.89	9.75	14.44	10.75	0.97
2018	HP2	78	81.41	75.36	82.83	10.21	15.63	12.04	0.97
2019	HP2	56	81.65	75.66	82.46	10.01	15.51	12.48	0.96
2020	HP2	53	79.94	72.96	79.38	11.94	18.67	15.98	0.98
2021	HP2	40	80.46	73.2	76.05	13.06	21.17	19.67	0.96
2009	BP1	224	72.44	61.63	60.4	7.5	11.08	11.05	0.98
2010	BP1	193	72.89	62.57	61.45	8.52	13.28	13.23	0.99
2011	BP1	154	74.51	65.47	64.03	6.98	10.74	10.73	0.99
2012	BP1	171	76.46	67.79	66.44	9.08	14.08	13.92	0.99
2013	BP1	151	76.59	67.88	66.27	9.27	14.43	14.26	0.99
2014	BP1	114	80.56	73.87	72.24	10.6	16.58	16.3	0.99
2015	BP1	82	83.68	79.61	77.91	8.77	14.03	14.01	0.99
2016	BP1	66	82.39	77.72	75.82	9.25	14.57	14.52	0.99
2017	BP1	66	83.27	79.17	76.92	9.12	14.44	14.43	0.99
2018	BP1	78	80.98	75.36	73.01	9.8	15.63	15.51	0.99
2019	BP1	56	81.18	75.66	73.0	9.54	15.51	15.2	0.98
2020	BP1	55	78.87	71.65	68.56	12.0	19.54	18.44	0.99
2021	BP1	46	77.44	68.49	65.91	13.81	23.25	21.94	0.99
2022	BP1	42	77.14	68.52	64.98	13.41	21.89	20.33	0.99
2009	BP2	224	72.37	61.63	73.5	7.83	11.08	9.56	0.91
2010	BP2	193	72.97	62.57	74.02	9.12	13.28	10.77	0.94
2011	BP2	154	74.55	65.47	76.71	7.42	10.74	8.74	0.94
2012	BP2	171	76.52	67.79	78.43	9.35	14.08	11.11	0.95

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2013	BP2	151	76.7	67.88	78.23	9.5	14.43	11.38	0.95
2014	BP2	113	80.87	74.22	83.15	10.68	16.23	12.6	0.97
2015	BP2	82	84.3	79.61	87.56	9.6	14.03	9.89	0.98
2016	BP2	66	82.92	77.72	85.98	10.04	14.57	10.8	0.96
2017	BP2	66	83.83	79.17	86.55	9.93	14.44	10.77	0.97
2018	BP2	78	81.41	75.36	83.38	10.44	15.63	12.14	0.97
2019	BP2	56	81.71	75.66	82.68	10.29	15.51	12.67	0.95
2020	BP2	54	79.48	72.3	78.65	12.33	19.12	16.61	0.97
2021	BP2	42	79.46	71.39	75.0	13.63	22.22	21.02	0.96
2022	BP2	32	82.0	76.8	66.22	11.11	17.23	19.59	0.82

Table 18: Comparison of reliabilities between single-step and current official evaluation (two-step) for nordic genotyped bulls with no offspring

BYR	n	ss_rel	two_rel	s_ss_rel	s_two_rel	cor
2020	3079	53.727	62.005	0.0	2.271	0.0
2021	3047	53.727	61.458	0.0	2.63	0.0
2022	3109	53.727	61.347	0.0	2.704	-0.0
2023	2982	53.727	60.266	0.0	3.528	-0.0
2024	2941	53.727	58.285	0.0	3.399	-0.0
2025	1275	53.727	54.865	0.0	3.153	-0.0

Jersey

```

r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
1. Filling remaining columns with `missing`
  @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
2. Filling remaining columns with `missing`
  @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
3. Filling remaining columns with `missing`
  @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
4. Filling remaining columns with `missing`
  @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
5. Filling remaining columns with `missing`
  @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
6. Filling remaining columns with `missing`
  @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592

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L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
94. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
95. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
96. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
97. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
98. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
99. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
100. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
101. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1: too many warnings, silencing any further warnings
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:597
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
1. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
2. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
3. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
4. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
5. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
6. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
7. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:
8. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
└ Warning: thread = 1 warning: only found 15 / 20 columns around data row:

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r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
96. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
97. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
98. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
99. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
100. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1 warning: only found 15 / 20 columns around data row:
101. Filling remaining columns with `missing`
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:592
r Warning: thread = 1: too many warnings, silencing any further warnings
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:597

```

Genetic trends

Here, we exhibit the genetic trends of our evaluations for each trait. We see that the levels of breeding values are generally in agreement across evaluations.

Table 19: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2009	HP1	50	96.16	96.4	96.59	6.22	6.4	6.14	0.98
2010	HP1	55	95.64	96.13	96.41	11.12	11.36	10.86	0.99
2011	HP1	47	90.4	90.77	91.23	8.35	8.77	8.38	0.98
2012	HP1	47	96.15	96.45	96.75	7.92	8.17	7.77	0.98
2013	HP1	50	93.6	94.12	94.57	9.28	9.33	8.94	0.99
2014	HP1	36	96.78	97.11	97.42	7.21	7.25	6.88	0.98
2015	HP1	30	95.6	95.73	96.21	8.12	8.42	8.05	0.99
2016	HP1	26	100.69	100.5	100.65	7.54	7.59	7.25	0.99
2017	HP1	29	100.59	100.48	100.45	7.82	7.61	7.21	0.99
2018	HP1	20	100.25	99.9	99.74	8.07	8.22	7.81	0.98
2019	HP1	29	102.72	102.55	102.01	9.31	9.56	9.14	1.0
2020	HP1	25	101.6	101.56	100.97	8.31	8.29	7.99	1.0
2021	HP1	14	105.93	105.71	105.02	5.65	5.47	5.25	0.99
2022	HP1	16	102.44	101.56	101.09	8.04	8.29	7.9	1.0

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor
2023	HP1	1	104.0	105.0	104.07	NaN	NaN	NaN
2009	HP2	50	92.28	92.14	92.79	10.88	11.34	11.09
2010	HP2	55	93.15	93.04	93.66	9.57	9.31	9.03
2011	HP2	47	95.91	96.32	96.87	9.9	10.11	9.92
2012	HP2	47	97.13	97.21	97.65	12.46	12.42	12.11
2013	HP2	50	95.86	95.88	96.38	11.35	11.14	10.88
2014	HP2	36	99.33	99.11	99.43	10.2	9.69	9.5
2015	HP2	30	95.57	95.6	95.77	12.06	11.87	11.48
2016	HP2	26	101.31	101.5	101.52	10.34	10.36	10.19
2017	HP2	29	99.38	99.21	99.07	19.83	19.91	19.51
2018	HP2	20	102.1	101.15	101.13	11.48	11.83	11.69
2019	HP2	29	99.62	99.66	99.27	14.75	14.81	14.45
2020	HP2	24	103.29	103.17	102.62	13.05	13.22	12.92
2021	HP2	13	105.15	104.15	103.61	10.5	10.4	10.18
2022	HP2	2	108.5	107.5	107.07	7.78	4.95	4.76
2009	BP1	41	96.37	96.29	96.67	5.78	6.05	5.82
2010	BP1	35	94.54	94.8	95.28	10.81	11.25	10.67
2011	BP1	22	93.73	93.68	94.19	6.41	6.61	6.29
2012	BP1	16	98.5	98.31	98.59	6.98	7.37	6.99
2013	BP1	17	95.06	95.65	96.03	7.68	7.74	7.52
2014	BP1	16	98.25	98.25	98.72	7.22	7.28	6.9
2015	BP1	29	95.79	95.79	96.27	7.7	8.08	7.71
2016	BP1	19	101.32	101.21	101.31	6.73	6.69	6.33
2017	BP1	26	100.65	100.62	100.61	7.41	7.17	6.87
2018	BP1	14	101.5	101.43	101.31	7.86	7.71	7.3
2019	BP1	26	102.04	101.65	101.32	9.54	9.81	9.31
2020	BP1	21	101.67	101.38	100.91	8.34	8.26	7.98
2021	BP1	13	105.46	104.92	104.34	5.44	5.69	5.3
2022	BP1	13	101.08	100.23	99.84	8.17	8.26	7.98
2009	BP2	34	92.97	92.74	93.35	9.53	9.71	9.51
2010	BP2	30	92.8	92.67	93.25	8.51	8.18	7.94
2011	BP2	18	97.17	97.44	98.07	6.96	7.16	6.97
2012	BP2	15	96.73	97.2	97.44	14.96	15.26	14.86

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2013	BP2	15	100.47	100.8	101.02	5.21	5.28	5.3	0.94
2014	BP2	16	101.06	100.88	101.17	10.93	10.91	10.59	1.0
2015	BP2	28	97.25	97.25	97.32	10.42	10.63	10.35	0.99
2016	BP2	19	101.42	101.0	101.13	10.43	10.46	10.29	1.0
2017	BP2	25	99.84	99.52	99.48	19.39	19.25	18.84	1.0
2018	BP2	12	102.25	101.75	101.49	11.5	11.72	11.47	1.0
2019	BP2	26	99.0	98.81	98.46	14.69	14.66	14.37	1.0
2020	BP2	20	103.8	103.65	103.07	12.32	12.61	12.45	0.99
2021	BP2	11	103.55	102.45	102.0	10.1	10.1	9.94	0.99
2022	BP2	6	97.5	99.0	98.84	12.45	13.46	13.53	0.94

Table 20: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	HP1	55	97.22	97.51	6.03	6.14	1.05	0.98
2010	HP1	60	96.6	96.58	10.83	11.03	1.05	0.99
2011	HP1	51	92.14	92.22	8.4	8.37	1.37	0.98
2012	HP1	50	96.84	97.2	7.61	7.8	1.32	0.98
2013	HP1	52	94.5	94.98	9.2	9.07	1.44	0.98
2014	HP1	39	97.67	97.31	7.19	6.85	2.05	0.93
2015	HP1	34	96.82	96.03	7.7	8.19	1.85	0.95
2016	HP1	28	101.61	98.14	7.29	4.99	4.82	0.68
2017	HP1	31	101.39	98.94	7.63	6.58	5.29	0.63
2018	HP1	23	101.61	97.35	7.8	4.21	6.26	0.55
2019	HP1	33	103.61	100.21	8.7	5.25	6.79	0.41
2020	HP1	32	103.47	98.91	7.54	3.18	7.12	0.15
2021	HP1	21	105.1	98.38	5.42	4.65	6.9	0.58
2022	HP1	18	102.78	99.11	7.55	3.23	7.33	0.23
2023	HP1	3	108.67	99.67	4.16	2.52	9.0	0.99
2009	HP2	55	94.02	94.2	11.03	11.12	1.75	0.98
2010	HP2	60	94.63	94.2	9.81	9.43	1.67	0.98
2011	HP2	50	97.2	97.12	10.02	10.05	1.4	0.98
2012	HP2	50	98.04	98.14	12.52	12.36	1.58	0.99
2013	HP2	52	96.65	96.88	11.36	11.1	2.04	0.97

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2014	HP2	39	100.03	99.46	9.99	10.29	2.92	0.93
2015	HP2	34	96.24	96.59	12.51	10.73	3.47	0.93
2016	HP2	28	102.46	99.32	10.42	6.32	7.07	0.62
2017	HP2	31	100.29	99.81	19.46	8.81	12.42	0.53
2018	HP2	23	104.48	101.52	11.73	5.99	7.91	0.62
2019	HP2	33	101.21	101.18	14.22	6.16	10.64	0.38
2020	HP2	30	106.13	100.3	12.45	5.72	11.7	0.26
2021	HP2	17	105.47	102.06	10.01	3.83	7.88	0.35
2022	HP2	5	99.8	102.0	12.48	4.85	6.2	0.74
2009	BP1	51	97.12	97.43	5.81	5.95	0.98	0.98
2010	BP1	55	96.49	96.64	10.32	10.51	1.02	0.99
2011	BP1	51	92.33	92.51	8.35	8.35	1.35	0.98
2012	BP1	48	97.17	97.69	7.29	7.55	1.35	0.98
2013	BP1	51	94.98	95.35	8.82	8.78	1.31	0.98
2014	BP1	38	97.21	97.03	6.9	6.66	2.24	0.92
2015	BP1	32	97.34	96.75	8.16	8.42	1.72	0.97
2016	BP1	27	101.3	98.26	7.15	5.04	4.52	0.71
2017	BP1	30	101.5	99.43	7.15	6.29	5.2	0.6
2018	BP1	22	101.23	97.73	7.52	4.3	5.68	0.59
2019	BP1	33	103.45	100.27	8.8	5.0	7.18	0.39
2020	BP1	29	103.21	99.1	7.44	3.34	6.59	0.22
2021	BP1	22	105.05	99.0	5.03	4.21	6.23	0.61
2022	BP1	18	102.17	98.78	7.73	3.04	6.39	0.49
2023	BP1	2	108.0	99.5	4.24	2.12	8.5	1.0
2009	BP2	51	93.35	93.51	10.14	10.34	1.61	0.98
2010	BP2	55	94.18	93.95	8.43	8.08	1.47	0.98
2011	BP2	51	98.0	97.86	9.15	9.15	1.47	0.98
2012	BP2	48	97.96	98.19	11.38	11.35	1.48	0.98
2013	BP2	51	97.29	97.53	10.11	9.98	2.04	0.97
2014	BP2	38	99.47	99.16	9.44	9.84	2.68	0.94
2015	BP2	32	98.06	98.0	11.76	10.41	3.06	0.95
2016	BP2	26	101.73	99.19	9.6	6.13	6.54	0.56
2017	BP2	30	100.43	100.13	18.49	7.99	11.77	0.55

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2018	BP2	21	103.0	101.57	10.56	5.82	6.76	0.67
2019	BP2	32	100.34	101.09	13.42	5.75	9.81	0.37
2020	BP2	28	104.89	100.29	11.73	5.42	10.61	0.25
2021	BP2	21	103.95	101.0	8.57	5.52	6.67	0.48
2022	BP2	13	98.23	100.69	10.83	2.84	8.46	0.4

Table 21: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic cows with genotype and phenotype

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	HP1	194	96.57	97.27	10.65	9.16	4.64	0.82
2010	HP1	2263	94.03	94.95	11.85	10.89	4.92	0.86
2011	HP1	4200	93.54	94.46	11.58	10.95	4.87	0.86
2012	HP1	4797	93.92	95.0	11.95	11.0	4.78	0.87
2013	HP1	3801	93.22	93.79	11.71	10.75	4.81	0.86
2014	HP1	4752	93.71	94.26	11.16	10.12	4.69	0.85
2015	HP1	5686	95.76	96.14	11.15	10.07	4.64	0.85
2016	HP1	6763	95.46	95.53	10.91	9.67	4.62	0.85
2017	HP1	8438	96.49	96.56	11.36	10.07	4.71	0.85
2018	HP1	10364	97.74	96.7	11.0	9.37	4.92	0.83
2019	HP1	12600	98.8	97.65	10.91	9.23	5.19	0.81
2020	HP1	15309	99.59	97.44	10.88	8.95	5.59	0.79
2021	HP1	14904	101.54	98.7	11.05	8.8	6.14	0.76
2022	HP1	15706	101.83	98.33	10.9	8.5	6.5	0.74
2023	HP1	15351	101.89	98.39	11.03	8.23	6.9	0.71
2024	HP1	16021	103.1	98.82	10.56	8.08	6.75	0.74
2025	HP1	5200	103.26	98.96	10.75	8.03	6.75	0.75
2009	HP2	194	96.17	93.79	16.16	13.55	7.88	0.8
2010	HP2	2262	94.85	94.48	15.91	12.74	7.23	0.82
2011	HP2	4200	95.93	95.07	16.41	12.95	7.55	0.82
2012	HP2	4797	95.62	94.9	16.53	13.27	7.45	0.82
2013	HP2	3782	96.6	95.87	17.07	13.68	7.51	0.83
2014	HP2	4712	96.47	96.01	16.68	13.32	7.56	0.82
2015	HP2	5617	97.37	97.11	16.82	13.73	7.61	0.82
2016	HP2	6329	97.72	97.08	16.22	12.8	7.68	0.81

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2017	HP2	8176	97.33	97.4	16.64	12.99	7.97	0.8
2018	HP2	10188	100.79	99.57	15.85	12.12	8.01	0.78
2019	HP2	12202	99.47	99.69	17.24	12.0	9.33	0.72
2020	HP2	14986	100.24	100.63	18.39	11.99	9.84	0.72
2021	HP2	14406	100.86	100.15	17.2	11.75	9.75	0.7
2022	HP2	15151	101.88	100.77	16.9	11.09	9.8	0.69
2023	HP2	14944	102.54	100.71	16.58	11.01	9.89	0.68
2024	HP2	3195	102.88	101.35	16.39	10.89	9.61	0.68

Table 22: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic bulls with genotype and phenotype

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	BP1	132	97.02	98.04	7.37	6.36	2.89	0.86
2010	BP1	214	95.02	95.9	10.39	9.37	3.25	0.91
2011	BP1	359	94.68	95.65	9.21	8.74	3.57	0.87
2012	BP1	393	95.4	96.08	9.5	9.19	3.31	0.9
2013	BP1	408	94.88	95.24	9.48	8.66	3.32	0.89
2014	BP1	432	95.81	96.2	9.38	8.53	3.62	0.87
2015	BP1	491	97.36	97.38	9.28	8.06	3.73	0.86
2016	BP1	423	98.12	97.68	8.73	7.57	3.83	0.84
2017	BP1	467	97.47	97.15	8.93	8.23	3.81	0.85
2018	BP1	308	99.28	97.0	9.34	7.63	4.55	0.83
2019	BP1	370	99.96	98.92	8.9	6.94	4.46	0.78
2020	BP1	348	101.16	98.1	8.55	7.08	4.9	0.78
2021	BP1	213	101.6	99.01	9.61	6.97	5.59	0.74
2022	BP1	281	102.45	98.58	9.47	6.64	6.19	0.7
2023	BP1	317	100.6	98.09	8.89	6.69	5.44	0.7
2024	BP1	354	101.83	98.49	9.36	6.88	5.95	0.7
2025	BP1	132	102.8	99.19	8.49	6.58	5.7	0.72
2009	BP2	132	95.54	94.72	11.74	10.14	3.98	0.88
2010	BP2	214	93.09	93.32	11.78	9.91	4.59	0.85
2011	BP2	357	97.25	96.85	11.77	10.25	5.08	0.83
2012	BP2	385	98.38	97.67	13.79	11.37	5.76	0.83
2013	BP2	401	97.63	97.17	13.27	10.87	5.63	0.83

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2014	BP2	421	98.05	97.9	13.0	10.07	5.77	0.81
2015	BP2	470	97.6	97.81	13.85	11.45	5.56	0.86
2016	BP2	393	98.82	98.49	12.83	9.85	6.33	0.79
2017	BP2	458	97.11	97.41	14.48	10.92	6.77	0.81
2018	BP2	304	101.53	99.91	12.8	9.96	6.25	0.8
2019	BP2	362	99.4	100.63	15.1	9.73	7.79	0.75
2020	BP2	339	103.27	101.1	13.51	9.34	7.98	0.69
2021	BP2	209	99.99	101.23	14.07	9.84	8.24	0.68
2022	BP2	264	102.69	100.94	13.28	8.76	8.29	0.67
2023	BP2	282	100.97	100.72	14.37	8.72	9.04	0.63
2024	BP2	311	100.36	101.41	13.96	8.42	9.02	0.59

Correlations

Here, we give correlation tables and tables of differences between the relevant evaluations. We test that we didn't change the model by comparing our new model without genomic information to the breeding values of the traditional pedigree-based model and expect very high correlations for tested animals. We test the change by incorporating genomic information, compared to a non-genomic evaluation, and expect to see some changes even in tested animals, but not too large.

Table 23: Correlations between current EBV and new EBV for Nordic AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	50	0.999	1.0	0.998	0.999
2010	55	1.0	0.999	1.0	0.999
2011	47	0.999	0.999	0.999	0.999
2012	47	0.999	1.0	0.999	0.999
2013	50	0.999	1.0	1.0	0.999
2014	36	0.999	0.999	0.999	0.999
2015	30	1.0	1.0	0.999	1.0
2016	26	0.999	1.0	0.999	0.999
2017	29	0.999	1.0	0.999	1.0
2018	20	0.999	1.0	1.0	0.999
2019	29	1.0	1.0	0.999	1.0
2020	25	0.999	1.0	0.999	0.999
2021	14	0.998	0.999	0.999	0.999

BYR	n	cor1	cor2	cor3	cor4
2022	16	0.999	1.0	0.999	0.999

Table 24: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-2.0	1	1	0	0
-1.0	54	46	38	52
0.0	90	105	108	98
1.0	15	8	14	9
2.0	0	0	0	1

Table 25: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	50	0.976	0.979	0.975	0.979
2010	55	0.991	0.979	0.992	0.976
2011	47	0.984	0.983	0.984	0.979
2012	47	0.982	0.983	0.985	0.981
2013	50	0.987	0.975	0.986	0.97
2014	36	0.985	0.98	0.984	0.979
2015	30	0.989	0.989	0.986	0.99
2016	26	0.992	0.988	0.99	0.99
2017	29	0.994	0.998	0.993	0.998
2018	20	0.984	0.992	0.987	0.993
2019	29	0.997	0.994	0.997	0.993
2020	25	0.995	0.993	0.992	0.991
2021	14	0.994	0.989	0.989	0.99
2022	16	0.996	0.955	0.994	0.959

Table 26: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-6.0	0	1	0	1
-5.0	0	2	0	0
-4.0	1	5	0	4

dif	dif1	dif2	dif3	dif4
-3.0	3	6	2	7
-2.0	18	25	18	21
-1.0	61	43	63	53
0.0	55	40	52	37
1.0	15	20	19	18
2.0	6	8	3	10
3.0	1	6	3	6
4.0	0	1	0	2
5.0	0	2	0	0
6.0	0	0	0	0
7.0	0	0	0	1
8.0	0	1	0	0

Legarra-Reverter test

The Legarra-Reverter test is a test for bias in evaluations. We perform two calculations of breeding values, one with all information available and one where offspring of sires born after 2018 has their records removed. Then we perform a linear regression on genotyped, nordic bulls, who has no data in the reduced dataset and with more than 30 offspring in the full dataset. We also require that their sires are not in the focal group, so we remove bulls whose father meets the same criteria.

The slope of the regression indicates the bias, with a slope of one meaning no bias, a slope less than one indicating that the estimated values of unproven animals are too extreme, and a slope higher than one indicating that the estimated breeding values of unproven animals are too conservative.

As can be seen, we have some issues with the Legarra-Reverter test. We're looking into it.

Table 27: Legarra-Reverter scores

Singlestep:

trait	b1	rsquare	n
HP1	0.925	0.464	58
HP2	1.165	0.333	58
BP1	0.786	0.422	45
BP2	1.208	0.285	44

EBV:

trait	b1	rsquare	n
HP1	0.874	0.371	58

trait	b1	rsquare	n
HP2	1.076	0.238	58
BP1	0.746	0.329	45
BP2	0.94	0.153	44

Interbull test

Youngstock survival is not an Interbull trait, but for quality control we performed an Interbull GEBV test and got a passing grade.

735	brd	pop	trt	evaldate	m	n	test	mean_y	std_y	dv	mean_x	std_x	b0	se_b0	b1	se_b1	ncand
i_est	Exp_b1	R2	fb	year		tests	pass										
735	JER	DFS	HP1	20250711	1	50	100.3974	8.2795	GM	97.1136	4.8737	12.3803	17.3066	0.9069	0.1809	50	
0.0000	1.0000	35.3	N	2015		YYY-	PASS										
735	JER	DFS	HP1	20250711	2	50	100.3974	8.2795	GM	97.3515	5.1968	23.8670	17.0594	0.7867	0.1743	50	
0.0000	1.0000	29.8	N	2015		----	----										
735	JER	DFS	HP2	20250711	1	50	101.1954	13.0235	GM	99.4791	6.4620	-13.1887	25.1105	1.1455	0.3335	50	
0.0000	1.0000	30.2	N	2015		YYYY	PASS										
735	JER	DFS	HP2	20250711	2	50	101.1954	13.0235	GM	99.2989	6.8309	20.0914	25.7571	0.8140	0.2585	50	
0.0000	1.0000	17.1	N	2015		----	----										
735	JER	DFS	BP1	20250711	1	50	100.8428	8.4411	GM	97.3476	4.8072	8.3950	17.7733	0.9493	0.1910	50	
0.0000	1.0000	36.2	N	2015		YYY-	PASS										
735	JER	DFS	BP1	20250711	2	50	100.8428	8.4411	GM	97.3871	4.8615	15.7119	18.4460	0.8742	0.1886	50	
0.0000	1.0000	30.9	N	2015		----	----										
735	JER	DFS	BP2	20250711	1	50	101.3888	12.9585	GM	99.6916	6.1700	-15.6553	26.3332	1.1704	0.3407	50	
0.0000	1.0000	29.2	N	2015		YYYY	PASS										
735	JER	DFS	BP2	20250711	2	50	101.3888	12.9585	GM	99.4308	6.4981	18.3688	27.0844	0.8325	0.2717	50	
0.0000	1.0000	16.4	N	2015		----	----										

The set of bulls chosen by the Interbull test program is different from the focal group selected for the Legarra-Reverter test. Hence, we get different slope coefficients.

Mendelian sampling

The mendelian sampling of an animal is its deviation of its breeding values from the expected breeding value, which is the average of its parents breeding values. Some mendelian sampling is expected on the individual level (this is what enables breeding), but across all animals we expect it to be close to zero. Otherwise, this indicates a bias in the set of animals in the evaluation, which violates the unbiasedness of the BLUP model. We conclude that the mendelian sampling is generally close to 0.

Table 28: Average mendelian sampling by birth year. Animals are only included if they are genotyped, their sire has > 30 offspring and their dam is genotyped.

BYR	n	m1	m2	m3	m4
2010	171	1.327	2.731	1.523	2.488
2011	285	1.084	1.44	0.893	1.177
2012	1096	-0.389	0.413	-0.232	0.498
2013	1745	-0.297	0.66	-0.117	0.714
2014	2581	0.073	0.656	0.112	0.653
2015	3220	0.202	0.811	0.225	0.719
2016	3539	0.308	-0.132	0.249	-0.025
2017	4551	0.175	0.059	0.12	0.098
2018	5619	0.187	0.009	0.094	-0.071
2019	7710	-0.079	0.259	-0.011	0.18
2020	10977	0.021	0.228	0.039	0.229
2021	12765	-0.044	0.109	0.022	0.127
2022	14298	-0.011	0.038	0.03	-0.018
2023	14527	0.057	-0.071	-0.05	-0.111
2024	15056	0.016	-0.173	-0.039	-0.198

Table 29: Average mendelian sampling by birth year. Animals are only included if they are not genotyped, their sire has > 30 offspring and their dam isn't genotyped.

BYR	n	m1	m2	m3	m4
2001	47194.0	-0.011	-0.054	-0.02	0.049
2002	42994.0	0.019	-0.082	-0.005	-0.024
2003	43665.0	0.005	-0.062	-0.039	0.003
2004	40987.0	-0.013	-0.028	-0.012	0.018
2005	38413.0	0.025	0.019	0.063	0.029
2006	40435.0	0.005	0.042	0.051	0.034
2007	38218.0	-0.017	0.0	-0.008	-0.011
2008	37740.0	-0.064	-0.028	-0.016	0.032

BYR	n	m1	m2	m3	m4
2009	39728.0	-0.046	-0.015	-0.021	0.032
2010	37728.0	-0.027	-0.001	-0.037	0.014
2011	36891.0	-0.053	-0.003	-0.037	-0.003
2012	37338.0	-0.005	-0.025	-0.056	0.025
2013	35451.0	0.003	-0.062	-0.033	0.012
2014	33499.0	0.021	-0.038	-0.011	0.048
2015	32058.0	-0.003	-0.04	0.01	0.02
2016	30677.0	-0.049	-0.095	-0.051	0.018
2017	28265.0	-0.032	-0.093	-0.03	-0.037
2018	30253.0	0.004	-0.059	0.003	-0.083
2019	28917.0	-0.075	-0.038	0.002	-0.065
2020	30874.0	-0.036	-0.086	-0.013	-0.033
2021	30339.0	-0.085	-0.116	0.001	-0.047
2022	30621.0	-0.085	-0.003	-0.014	-0.049
2023	27016.0	-0.03	-0.041	-0.083	-0.09
2024	26221.0	0.001	0.027	-0.035	-0.032

Reliabilities

Table 30: Comparison of reliabilities between single-step (ss), new EBV (ebv) and current official evaluation (cur) for nordic AI bulls with > 30 offspring and correlation between single-step and current evaluation.

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	HP1	50	71.71	66.21	NaN	8.84	10.99	NaN	NaN
2010	HP1	55	70.6	64.62	NaN	8.79	11.23	NaN	NaN
2011	HP1	47	69.43	63.2	NaN	8.02	10.29	NaN	NaN
2012	HP1	47	70.68	64.12	NaN	10.88	13.84	NaN	NaN
2013	HP1	50	68.97	61.69	NaN	10.86	14.36	NaN	NaN
2014	HP1	36	74.08	68.36	NaN	13.55	17.81	NaN	NaN
2015	HP1	30	85.62	83.31	NaN	10.51	13.26	NaN	NaN
2016	HP1	26	80.93	77.1	NaN	12.63	16.66	NaN	NaN
2017	HP1	29	87.31	85.39	NaN	10.2	12.54	NaN	NaN
2018	HP1	20	76.44	70.95	NaN	14.8	19.58	NaN	NaN
2019	HP1	29	86.95	84.61	NaN	10.4	13.82	NaN	NaN
2020	HP1	25	84.08	80.64	NaN	14.29	19.82	NaN	NaN

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2021	HP1	14	86.22	83.71	NaN	11.43	16.72	NaN	NaN
2022	HP1	16	84.13	82.3	NaN	8.41	10.18	NaN	NaN
2009	HP2	50	71.67	66.21	NaN	8.52	10.99	NaN	NaN
2010	HP2	55	70.67	64.62	NaN	8.78	11.23	NaN	NaN
2011	HP2	47	69.5	63.2	NaN	8.01	10.29	NaN	NaN
2012	HP2	47	70.72	64.12	NaN	10.87	13.84	NaN	NaN
2013	HP2	50	69.03	61.69	NaN	10.84	14.36	NaN	NaN
2014	HP2	36	74.12	68.36	NaN	13.53	17.81	NaN	NaN
2015	HP2	30	85.55	83.31	NaN	10.4	13.26	NaN	NaN
2016	HP2	26	80.98	77.1	NaN	12.6	16.66	NaN	NaN
2017	HP2	29	87.34	85.39	NaN	10.17	12.54	NaN	NaN
2018	HP2	20	76.49	70.95	NaN	14.77	19.58	NaN	NaN
2019	HP2	29	86.99	84.61	NaN	10.37	13.82	NaN	NaN
2020	HP2	24	85.32	82.34	NaN	13.22	18.3	NaN	NaN
2021	HP2	13	86.66	84.08	NaN	11.75	17.34	NaN	NaN
2009	BP1	41	72.91	67.81	NaN	8.96	11.52	NaN	NaN
2010	BP1	35	73.88	68.88	NaN	9.51	11.97	NaN	NaN
2011	BP1	22	75.43	71.23	NaN	7.65	9.53	NaN	NaN
2012	BP1	16	82.53	79.37	NaN	11.14	13.88	NaN	NaN
2013	BP1	17	80.29	76.74	NaN	11.86	15.27	NaN	NaN
2014	BP1	16	87.61	86.28	NaN	7.81	9.56	NaN	NaN
2015	BP1	29	86.25	84.18	NaN	10.13	12.61	NaN	NaN
2016	BP1	19	87.07	85.2	NaN	8.27	10.41	NaN	NaN
2017	BP1	26	89.57	88.22	NaN	7.97	9.57	NaN	NaN
2018	BP1	14	82.8	79.67	NaN	13.22	16.74	NaN	NaN
2019	BP1	26	89.25	87.71	NaN	8.29	10.8	NaN	NaN
2020	BP1	21	89.06	87.68	NaN	9.07	11.88	NaN	NaN
2021	BP1	13	88.45	87.17	NaN	8.24	11.02	NaN	NaN
2022	BP1	13	86.25	84.73	NaN	7.61	9.38	NaN	NaN
2009	BP2	34	74.18	69.61	NaN	8.87	11.79	NaN	NaN
2010	BP2	30	75.42	70.87	NaN	9.43	11.81	NaN	NaN
2011	BP2	18	77.04	73.1	NaN	7.23	9.01	NaN	NaN
2012	BP2	15	83.61	80.72	NaN	10.67	13.24	NaN	NaN

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2013	BP2	15	82.24	79.42	NaN	11.21	14.09	NaN	NaN
2014	BP2	16	87.63	86.28	NaN	7.8	9.56	NaN	NaN
2015	BP2	28	86.54	84.81	NaN	9.64	12.35	NaN	NaN
2016	BP2	19	87.09	85.2	NaN	8.26	10.41	NaN	NaN
2017	BP2	25	90.33	89.28	NaN	6.58	8.05	NaN	NaN
2018	BP2	12	85.1	83.39	NaN	11.55	15.02	NaN	NaN
2019	BP2	26	89.27	87.71	NaN	8.28	10.8	NaN	NaN
2020	BP2	20	90.67	89.83	NaN	5.45	6.78	NaN	NaN
2021	BP2	11	91.29	90.94	NaN	3.31	3.61	NaN	NaN

Table 31: Comparison of reliabilities between single-step and current official evaluation (two-step) for nordic genotyped bulls with no offspring

BYR	n	ss_rel	two_rel	s_ss_rel	s_two_rel	cor
2020	444	43.212	NaN	0.0	NaN	NaN
2021	363	43.211	NaN	0.0	NaN	NaN
2022	435	43.211	NaN	0.0	NaN	NaN
2023	593	43.212	NaN	0.0	NaN	NaN
2024	645	43.212	NaN	0.0	NaN	NaN
2025	261	43.211	NaN	0.0	NaN	NaN

It should be noted that there is no two-step evaluation for Youngstock survival for Jersey. Hence, there are no correlation or other tables regarding two-step in this section.

RDC

```

r Warning: thread = 1 warning: parsed expected 15 columns, but didn't reach
end of line around data row: 1. Parsing extra columns and widening final
columnset
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:593
r Warning: thread = 1 warning: parsed expected 15 columns, but didn't reach
end of line around data row: 1. Parsing extra columns and widening final
columnset
L @ CSV ~/.julia/packages/CSV/XLcQT/src/file.jl:593

```

Genetic trends

Here, we exhibit the genetic trends of our evaluations for each trait. We see that the levels of breeding values are generally in agreement across evaluations.

Table 32: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2009	HP1	158	96.37	96.78	96.72	8.31	8.41	8.65	0.97
2010	HP1	165	94.48	94.89	94.65	8.94	9.22	9.26	0.98
2011	HP1	168	96.18	96.67	96.51	9.13	9.56	9.62	0.98
2012	HP1	169	97.7	98.08	97.88	8.47	8.31	8.49	0.96
2013	HP1	122	96.48	96.78	96.21	9.67	9.91	9.87	0.98
2014	HP1	85	97.28	97.86	97.57	9.57	9.65	9.61	0.98
2015	HP1	71	97.24	97.48	96.79	10.83	11.34	11.49	0.99
2016	HP1	70	99.64	99.94	100.04	8.75	8.83	9.02	0.98
2017	HP1	66	102.12	101.59	101.06	11.49	11.59	11.83	0.99
2018	HP1	52	100.65	100.21	99.64	8.57	8.9	8.81	0.98
2019	HP1	50	105.04	104.56	104.49	7.51	7.63	7.92	0.98
2020	HP1	53	103.11	102.51	102.0	7.65	7.55	7.71	0.98
2021	HP1	46	104.67	103.91	104.33	6.81	6.63	6.86	0.96
2022	HP1	38	104.42	103.0	103.23	7.38	7.54	7.67	0.95
2023	HP1	3	103.67	101.0	100.47	5.51	2.65	3.19	0.85
2009	HP2	158	93.87	94.23	94.41	9.5	9.79	9.82	0.98
2010	HP2	165	94.24	94.43	94.2	10.08	10.55	10.32	0.98
2011	HP2	168	95.71	96.14	96.09	10.34	10.73	10.38	0.98
2012	HP2	169	94.98	95.08	95.1	9.49	9.63	9.56	0.98
2013	HP2	122	94.64	95.09	94.78	10.6	10.92	10.57	0.98
2014	HP2	85	95.82	96.08	96.26	9.95	10.42	9.94	0.99
2015	HP2	71	95.41	95.54	95.75	10.92	11.16	10.7	0.99
2016	HP2	70	99.29	99.11	99.47	8.86	8.89	8.59	0.99
2017	HP2	66	100.5	100.09	100.13	11.02	11.19	11.12	0.99
2018	HP2	52	102.38	102.1	102.14	7.8	8.28	8.18	0.99
2019	HP2	50	103.74	103.14	103.31	7.57	7.7	7.44	0.99
2020	HP2	51	103.27	102.84	102.95	7.75	7.95	7.87	0.98
2021	HP2	38	104.26	103.84	104.23	7.34	7.27	6.88	0.98
2022	HP2	2	106.0	105.0	106.29	1.41	1.41	2.39	1.0
2009	BP1	158	96.43	96.89	97.26	8.17	8.4	8.52	0.98
2010	BP1	165	95.15	95.75	95.84	8.72	9.03	8.98	0.98
2011	BP1	168	96.24	96.87	96.88	8.86	9.2	9.23	0.98
2012	BP1	169	97.38	97.68	97.66	8.46	8.32	8.49	0.96

BYR	trait	n	m_ssm_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor	
2013	BP1	123	96.9	97.47	97.03	9.5	9.72	9.64	0.98
2014	BP1	84	97.15	97.81	97.48	9.35	9.44	9.41	0.98
2015	BP1	71	97.01	97.44	96.74	10.43	10.8	10.9	0.99
2016	BP1	70	99.47	99.7	99.85	8.53	8.6	8.69	0.98
2017	BP1	66	101.61	101.17	100.7	11.3	11.27	11.48	0.99
2018	BP1	52	100.52	100.21	99.51	8.51	8.78	8.68	0.98
2019	BP1	50	104.84	104.52	104.31	7.45	7.54	7.81	0.98
2020	BP1	51	103.24	102.63	101.92	7.42	7.17	7.35	0.98
2021	BP1	45	104.33	103.73	104.02	6.78	6.59	6.67	0.97
2022	BP1	39	104.49	103.26	103.29	7.44	7.57	7.58	0.95
2023	BP1	2	103.5	99.5	98.17	4.95	2.12	2.7	1.0
2009	BP2	158	94.3	94.75	94.36	9.3	9.57	9.73	0.98
2010	BP2	165	95.02	95.32	94.55	10.85	11.1	11.06	0.98
2011	BP2	168	96.2	96.69	96.32	10.18	10.52	10.3	0.98
2012	BP2	169	95.12	95.36	95.13	9.35	9.55	9.69	0.98
2013	BP2	123	94.8	95.24	94.86	10.59	10.87	10.75	0.98
2014	BP2	84	95.89	96.24	96.31	9.72	9.82	9.54	0.98
2015	BP2	71	96.08	96.17	96.51	10.21	10.55	10.41	0.99
2016	BP2	70	99.64	99.14	99.24	9.17	9.02	8.97	0.99
2017	BP2	66	100.58	100.27	100.11	10.66	10.76	10.86	0.99
2018	BP2	52	102.0	101.67	102.08	7.84	8.19	8.4	0.98
2019	BP2	50	103.42	102.96	103.04	7.74	7.74	7.58	0.99
2020	BP2	49	101.55	101.18	101.32	8.42	8.71	8.69	0.98
2021	BP2	40	104.78	104.18	104.39	7.3	7.14	7.24	0.96
2022	BP2	20	103.8	102.85	103.55	6.49	7.1	7.39	0.93

Table 33: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	HP1	195	96.97	97.28	8.23	8.51	1.11	0.97
2010	HP1	183	94.85	95.08	8.84	8.77	1.19	0.98
2011	HP1	182	96.3	96.29	8.76	8.86	1.2	0.98
2012	HP1	192	97.9	98.1	7.98	7.79	1.42	0.96
2013	HP1	151	96.88	96.44	8.9	8.5	1.69	0.97

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2014	HP1	109	97.4	97.85	8.91	9.03	1.81	0.97
2015	HP1	86	97.56	97.16	10.04	9.98	2.23	0.96
2016	HP1	88	99.49	99.48	8.47	6.2	5.19	0.56
2017	HP1	80	102.41	101.76	10.73	6.54	7.02	0.52
2018	HP1	76	101.54	100.16	8.38	7.12	6.09	0.55
2019	HP1	69	105.29	102.06	8.04	7.52	7.41	0.39
2020	HP1	70	103.56	98.69	7.38	5.11	7.24	0.38
2021	HP1	59	104.46	98.85	6.77	4.29	7.0	0.46
2022	HP1	57	104.63	98.72	6.75	3.45	7.32	0.29
2023	HP1	9	102.89	99.89	5.35	4.43	3.89	0.77
2009	HP2	194	95.14	95.12	9.09	8.91	0.86	0.99
2010	HP2	183	94.9	94.83	9.81	9.62	1.0	0.99
2011	HP2	181	96.17	96.03	9.82	9.75	1.15	0.99
2012	HP2	192	95.68	95.83	8.97	8.79	1.4	0.98
2013	HP2	148	95.8	95.7	10.14	10.12	1.61	0.98
2014	HP2	107	96.51	97.05	9.3	9.82	1.6	0.98
2015	HP2	86	96.72	96.69	10.29	10.4	1.8	0.98
2016	HP2	86	99.65	99.66	8.29	6.2	5.55	0.52
2017	HP2	76	101.18	101.13	10.63	6.22	6.97	0.53
2018	HP2	74	102.72	100.72	7.18	5.08	6.14	0.19
2019	HP2	62	104.21	101.61	7.76	4.51	6.18	0.46
2020	HP2	67	104.51	99.54	7.75	3.76	6.85	0.36
2021	HP2	54	104.94	100.46	6.91	4.37	6.67	0.45
2022	HP2	12	105.75	98.42	6.08	3.0	8.5	0.08
2009	BP1	188	97.15	97.41	8.03	8.14	0.9	0.99
2010	BP1	198	95.94	96.26	8.54	8.63	1.25	0.98
2011	BP1	191	96.99	97.1	8.52	8.7	1.27	0.97
2012	BP1	194	97.98	98.27	7.99	7.87	1.44	0.96
2013	BP1	155	97.9	97.66	8.64	8.52	1.81	0.96
2014	BP1	111	98.33	98.95	8.47	8.85	1.95	0.96
2015	BP1	92	98.13	97.79	9.54	9.67	2.25	0.96
2016	BP1	85	99.51	99.69	8.28	6.64	5.48	0.55
2017	BP1	84	102.37	101.33	10.24	6.08	6.61	0.52

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2018	BP1	78	102.03	100.92	8.42	7.85	6.15	0.57
2019	BP1	71	104.82	101.44	7.57	5.93	7.32	0.3
2020	BP1	70	103.87	99.71	7.07	4.95	6.81	0.35
2021	BP1	58	104.45	99.5	6.41	4.14	6.67	0.4
2022	BP1	54	104.81	99.0	6.84	3.47	7.15	0.3
2023	BP1	9	103.56	100.22	4.3	3.31	4.22	0.43
2009	BP2	187	94.67	94.57	9.05	8.86	0.73	0.99
2010	BP2	194	95.05	94.9	10.36	10.26	0.89	0.99
2011	BP2	191	96.45	96.37	9.89	9.67	1.09	0.99
2012	BP2	193	95.36	95.44	9.19	8.96	1.22	0.98
2013	BP2	149	95.52	95.53	10.17	10.28	1.58	0.98
2014	BP2	105	96.7	97.1	9.26	9.61	1.58	0.98
2015	BP2	90	97.51	97.52	10.01	10.29	1.68	0.98
2016	BP2	85	99.13	99.39	9.18	7.11	5.32	0.66
2017	BP2	83	101.48	101.27	10.47	6.46	5.88	0.66
2018	BP2	74	102.47	100.62	7.9	6.28	5.2	0.47
2019	BP2	71	103.58	101.04	8.22	4.57	5.49	0.64
2020	BP2	68	101.4	98.47	7.94	3.53	5.66	0.46
2021	BP2	57	104.95	100.86	6.67	4.41	5.95	0.51
2022	BP2	42	103.33	99.33	5.85	3.25	5.14	0.41
2023	BP2	1	101.0	101.0	NaN	NaN	0.0	NaN

Table 34: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic cows with genotype and phenotype

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	HP1	441	95.59	97.34	18.72	16.58	6.63	0.9
2010	HP1	3428	95.49	97.01	18.84	16.59	7.04	0.89
2011	HP1	6066	95.97	97.32	18.73	16.49	6.66	0.9
2012	HP1	6830	95.89	97.18	18.88	16.58	6.87	0.89
2013	HP1	7243	96.33	97.15	18.65	16.18	6.9	0.89
2014	HP1	8039	96.59	97.36	19.14	16.6	6.92	0.89
2015	HP1	10571	97.04	97.38	18.49	16.15	6.95	0.88
2016	HP1	14775	97.38	97.81	18.5	16.01	7.0	0.88
2017	HP1	17598	98.49	98.05	18.35	15.72	7.16	0.87

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2018	HP1	19923	98.45	98.12	18.22	15.63	7.27	0.87
2019	HP1	20205	100.38	99.54	18.31	14.89	8.28	0.82
2020	HP1	22509	102.15	99.18	18.17	14.92	8.51	0.83
2021	HP1	22690	102.02	99.77	17.53	14.62	8.0	0.83
2022	HP1	23554	102.33	99.68	17.32	14.26	8.19	0.82
2023	HP1	21843	102.07	99.6	17.21	13.83	8.26	0.81
2024	HP1	21870	104.68	99.98	16.91	13.76	8.91	0.8
2025	HP1	6390	105.41	100.19	16.59	13.71	9.17	0.8
2009	HP2	441	93.22	93.7	17.22	16.06	5.29	0.92
2010	HP2	3425	93.05	93.48	17.61	16.16	5.8	0.91
2011	HP2	6058	93.85	94.09	17.29	15.82	5.54	0.91
2012	HP2	6818	93.04	93.35	17.46	15.94	5.69	0.91
2013	HP2	7211	94.31	94.53	17.21	15.55	5.73	0.91
2014	HP2	7980	94.3	94.61	17.88	16.24	5.77	0.91
2015	HP2	10412	95.08	95.11	17.36	15.84	5.8	0.91
2016	HP2	14539	95.79	96.12	17.16	15.64	5.86	0.9
2017	HP2	17205	96.93	96.77	17.09	15.31	5.92	0.9
2018	HP2	19500	97.65	97.02	16.66	14.88	6.1	0.89
2019	HP2	19802	98.9	98.19	16.81	14.5	6.77	0.86
2020	HP2	22095	100.96	98.11	16.48	14.38	7.05	0.86
2021	HP2	22238	100.65	98.69	16.27	14.19	6.74	0.86
2022	HP2	23042	101.4	98.82	15.91	13.82	6.88	0.86
2023	HP2	21346	101.77	98.99	15.74	13.57	6.93	0.85
2024	HP2	4795	103.34	100.09	16.03	13.59	7.25	0.85

Table 35: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic bulls with genotype and phenotype

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2009	BP1	403	94.41	96.39	15.25	13.38	4.51	0.91
2010	BP1	690	93.82	95.36	16.9	14.17	5.61	0.9
2011	BP1	1425	96.37	96.72	16.49	14.75	5.71	0.89
2012	BP1	1815	96.01	97.18	17.53	15.17	6.3	0.89
2013	BP1	1838	96.96	97.03	17.35	15.32	6.22	0.89
2014	BP1	1839	95.53	96.21	17.57	15.64	6.32	0.89

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2015	BP1	1780	97.32	97.29	17.58	15.05	6.45	0.89
2016	BP1	1707	97.87	97.84	17.29	14.89	6.48	0.88
2017	BP1	1984	97.96	97.48	17.12	14.71	6.72	0.87
2018	BP1	1915	100.41	99.68	16.8	14.07	7.13	0.85
2019	BP1	1891	101.19	100.26	16.8	13.86	7.92	0.81
2020	BP1	2162	101.95	99.59	16.29	13.72	7.78	0.82
2021	BP1	1948	103.34	100.48	15.82	13.06	7.83	0.81
2022	BP1	1828	104.35	99.95	15.78	13.09	8.14	0.82
2023	BP1	1705	104.31	100.71	15.95	13.18	7.96	0.81
2024	BP1	1432	106.17	100.81	15.13	12.25	8.67	0.79
2025	BP1	453	106.53	100.94	15.96	13.38	8.72	0.81
2009	BP2	338	92.43	92.57	10.91	10.32	2.4	0.95
2010	BP2	575	94.26	94.3	13.14	12.08	3.1	0.95
2011	BP2	1123	95.44	95.29	11.92	11.28	3.31	0.93
2012	BP2	1385	94.04	94.09	12.5	11.51	3.76	0.92
2013	BP2	1355	94.9	94.83	12.03	11.29	3.75	0.92
2014	BP2	1452	93.75	93.8	13.0	12.08	3.78	0.93
2015	BP2	1419	94.91	94.94	12.97	11.92	3.84	0.93
2016	BP2	1382	96.01	96.19	12.78	11.53	4.18	0.91
2017	BP2	1655	97.23	97.25	12.18	10.86	4.07	0.91
2018	BP2	1627	99.3	98.65	11.98	10.28	4.87	0.86
2019	BP2	1622	98.88	98.67	12.25	10.33	5.32	0.84
2020	BP2	1837	100.64	98.46	11.33	9.66	5.11	0.85
2021	BP2	1617	101.01	99.35	11.83	9.98	5.26	0.84
2022	BP2	1495	101.44	98.81	11.31	9.59	5.49	0.83
2023	BP2	1404	102.25	99.44	11.69	9.78	5.53	0.84
2024	BP2	1158	103.72	100.03	10.97	9.04	5.86	0.82

Correlations

Here, we give correlation tables and tables of differences between the relevant evaluations. We test that we didn't change the model by comparing our new model without genomic information to the breeding values of the traditional pedigree-based model and expect very high correlations for tested animals. We test the change by incorporating genomic information, compared to a non-genomic evaluation, and expect to see some changes even in tested animals, but not too large.

Table 36: Correlations between current EBV and new EBV for Nordic AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	158	0.99	0.991	0.991	0.99
2010	165	0.994	0.992	0.994	0.992
2011	168	0.995	0.994	0.994	0.993
2012	169	0.993	0.991	0.994	0.99
2013	122	0.994	0.993	0.994	0.991
2014	85	0.995	0.995	0.994	0.992
2015	71	0.996	0.997	0.995	0.994
2016	70	0.993	0.993	0.994	0.992
2017	66	0.996	0.996	0.996	0.994
2018	52	0.994	0.993	0.993	0.991
2019	50	0.993	0.995	0.993	0.994
2020	53	0.995	0.995	0.993	0.993
2021	46	0.994	0.994	0.995	0.991
2022	38	0.99	0.981	0.989	0.984

Table 37: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-4.0	1	1	1	1
-3.0	2	1	5	3
-2.0	38	10	37	18
-1.0	96	66	110	62
0.0	147	158	140	155
1.0	77	114	70	104
2.0	11	24	12	27
3.0	6	2	3	8
4.0	0	1	0	0
5.0	0	1	0	0

Table 38: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	158	0.973	0.982	0.976	0.977

BYR	n	cor1	cor2	cor3	cor4
2010	165	0.978	0.98	0.978	0.977
2011	168	0.978	0.984	0.977	0.98
2012	169	0.962	0.978	0.962	0.978
2013	122	0.978	0.982	0.977	0.98
2014	85	0.977	0.989	0.978	0.984
2015	71	0.989	0.99	0.987	0.987
2016	70	0.984	0.989	0.985	0.986
2017	66	0.991	0.992	0.991	0.991
2018	52	0.981	0.988	0.982	0.984
2019	50	0.984	0.986	0.98	0.985
2020	53	0.979	0.98	0.976	0.98
2021	46	0.959	0.962	0.967	0.947
2022	38	0.951	0.91	0.95	0.895

Table 39: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-7.0	1	2	1	3
-6.0	1	3	2	5
-5.0	7	5	4	1
-4.0	12	5	14	8
-3.0	39	19	32	22
-2.0	66	37	71	41
-1.0	68	86	87	80
0.0	90	112	66	103
1.0	52	73	59	69
2.0	26	24	30	26
3.0	11	8	7	12
4.0	4	2	4	4
5.0	1	1	1	4
6.0	0	1	0	0

Legarra-Reverter test

The Legarra-Reverter test is a test for bias in evaluations. We perform two calculations of breeding values, one with all information available and one where offspring of sires born after

2018 has their records removed. Then we perform a linear regression on genotyped, nordic bulls, who has no data in the reduced dataset and with more than 30 offspring in the full dataset. We also require that their sires are not in the focal group, so we remove bulls whose father meets the same criteria.

The slope of the regression indicates the bias, with a slope of one meaning no bias, a slope less than one indicating that the estimated values of unproven animals are too extreme, and a slope higher than one indicating that the estimated breeding values of unproven animals are too conservative.

As can be seen, we have some issues with the Legarra-Reverter test. We're looking into it.

Table 40: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
HP1	0.917	0.274	143
HP2	0.825	0.216	143
BP1	0.856	0.256	143
BP2	0.998	0.329	143

EBV:

trait	b1	rsquare	n
HP1	0.695	0.149	143
HP2	0.59	0.095	143
BP1	0.701	0.147	143
BP2	0.804	0.191	143

Interbull test

Youngstock survival is not an Interbull trait, but for quality control we performed n Interbull GEBV test and got a with a passing grade.

735	brd	pop	trt	evaldate	m	n	test	mean_y	std_y	dv	mean_x	std_x	b0	se_b0	b1	se_b1	ncand
i_est	Exp_b1	R2	fb	year	tests	pass											
735	RDC	DFS	HP1	20250711	1	125	99.4600	9.6656	GM	99.0771	4.6458	22.5630	17.0567	0.7767	0.1943	125	
0.0000	1.0000	14.2	N	2015	YNNY	hiSE											
735	RDC	DFS	HP1	20250711	2	125	99.4600	9.6656	GM	99.2211	5.6153	51.5824	14.7588	0.4835	0.1485	125	
0.0000	1.0000	7.9	N	2015	----	----											
735	RDC	DFS	HP2	20250711	1	127	98.9540	10.5151	GM	99.2417	4.1564	30.9926	21.3009	0.6867	0.2151	127	
0.0000	1.0000	7.6	N	2015	YNNY	hiSE											
735	RDC	DFS	HP2	20250711	2	127	98.9540	10.5151	GM	99.1470	4.7308	69.5042	19.4921	0.2990	0.1963	127	
0.0000	1.0000	1.8	N	2015	----	----											
735	RDC	DFS	BP1	20250711	1	125	99.8463	9.5846	GM	99.2998	4.5790	28.4725	17.5180	0.7195	0.1918	125	
0.0000	1.0000	11.9	N	2015	YNNY	hiSE											
735	RDC	DFS	BP1	20250711	2	125	99.8463	9.5846	GM	99.3955	5.3563	54.0501	15.5800	0.4618	0.1565	125	
0.0000	1.0000	6.6	N	2015	----	----											
735	RDC	DFS	BP2	20250711	1	127	99.1950	11.6118	GM	99.7845	4.8953	-1.4208	18.9985	1.0097	0.1949	127	
0.0000	1.0000	18.4	N	2015	YYYY	PASS											
735	RDC	DFS	BP2	20250711	2	127	99.1950	11.6118	GM	99.2161	4.8672	34.6024	20.4752	0.6523	0.2061	127	
0.0000	1.0000	7.4	N	2015	----	----											

NOTE: pass=hiSE indicates an inconclusive statistical PASS due to high SE(b1) while FAILING the practical test: b1<0.8 or b1>1.2

The set of bulls chosen by the Interbull test program is different from the focal group selected for the Legarra-Reverter test. Hence, we get different slope coefficients.

Mendelian sampling

The mendelian sampling of an animal is its deviation of its breeding values from the expected breeding value, which is the average of its parents breeding values. Some mendelian sampling is expected on the individual level (this is what enables breeding), but across all animals we expect it to be close to zero. Otherwise, this indicates a bias in the set of animals in the evaluation, which violates the unbiasedness of the BLUP model. We conclude that the mendelian sampling is generally close to 0.

Table 41: Average mendelian sampling by birth year. Animals are only included if they are genotyped, their sire has > 30 offspring and their dam is genotyped.

BYR	n	m1	m2	m3	m4
2010	355.0	-0.213	-0.811	-0.289	-0.666
2011	625.0	-0.595	-1.4	-0.551	-1.226
2012	1492.0	-1.058	-1.175	-1.043	-0.831
2013	2900.0	1.429	0.876	1.284	0.26
2014	4053.0	0.125	0.172	0.137	0.079
2015	5657.0	-0.237	-0.162	-0.219	-0.09
2016	6473.0	-0.286	-0.16	-0.3	-0.111
2017	7572.0	0.083	-0.001	0.098	-0.134
2018	9487.0	-0.148	-0.06	-0.141	0.006
2019	11333.0	0.215	0.264	0.22	0.216
2020	14052.0	0.564	0.567	0.563	0.39
2021	16051.0	-0.04	0.063	-0.017	0.081
2022	18353.0	0.294	0.247	0.235	0.149
2023	17800.0	-0.007	0.064	0.013	-0.003
2024	18521.0	0.049	0.115	0.061	0.064

Table 42: Average mendelian sampling by birth year. Animals are only included if they are not genotyped, their sire has > 30 offspring and their dam isn't genotyped.

BYR	n	m1	m2	m3	m4
2001	138582.0	0.016	0.017	0.052	-0.003
2002	146642.0	0.003	0.018	0.047	0.017
2003	158799.0	-0.008	0.019	-0.008	-0.001
2004	268936.0	0.007	0.008	-0.018	0.011
2005	256229.0	-0.009	-0.008	-0.019	0.016
2006	248058.0	-0.003	-0.008	0.017	0.019
2007	235402.0	0.009	0.017	0.011	0.001
2008	279666.0	0.0	-0.005	0.008	0.027

BYR	n	m1	m2	m3	m4
2009	277089.0	-0.011	-0.018	0.007	0.02
2010	262526.0	-0.001	-0.031	-0.012	0.01
2011	251420.0	0.031	-0.028	-0.026	0.008
2012	234857.0	0.033	-0.001	-0.013	-0.004
2013	225881.0	0.029	0.023	0.019	0.003
2014	211669.0	-0.03	0.023	-0.004	0.01
2015	190606.0	-0.026	0.012	-0.006	0.014
2016	165756.0	-0.03	0.009	-0.024	-0.002
2017	142584.0	-0.017	-0.01	-0.028	-0.038
2018	128378.0	-0.047	-0.05	-0.032	-0.043
2019	110175.0	-0.056	-0.037	-0.023	-0.024
2020	100746.0	-0.063	-0.033	-0.05	-0.01
2021	87387.0	-0.073	-0.005	-0.025	0.028
2022	73860.0	-0.012	-0.02	-0.025	-0.005
2023	62911.0	-0.017	0.008	0.002	-0.039
2024	51872.0	-0.009	-0.007	0.005	-0.017

Reliabilities

There seems to be a problem with the reported reliabilities in the official evaluation for Jersey. Please excuse us for now while we figure this out.

Table 43: Comparison of reliabilities between single-step (ss), new EBV (ebv) and current official evaluation (cur) for nordic AI bulls with > 30 offspring and correlation between single-step and current evaluation.

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	HP1	158	69.82	62.97	63.48	6.48	8.2	8.03	0.97
2010	HP1	165	68.49	60.58	61.13	7.08	9.26	9.09	0.99
2011	HP1	168	69.98	62.66	63.18	8.19	10.86	10.65	0.99
2012	HP1	169	70.18	62.79	63.25	8.78	11.64	11.41	0.99
2013	HP1	122	72.18	65.35	65.83	10.2	13.46	13.18	0.99
2014	HP1	85	76.46	70.99	71.34	10.07	13.07	12.82	0.99
2015	HP1	71	79.16	74.29	74.58	8.71	11.5	11.31	0.99
2016	HP1	70	77.31	72.26	72.6	9.23	11.87	11.67	0.99
2017	HP1	66	78.19	72.71	73.0	9.71	13.04	12.86	0.99
2018	HP1	52	78.32	73.02	73.27	9.34	12.21	12.07	0.99

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2019	HP1	50	78.16	72.67	72.9	9.92	13.35	13.14	0.99
2020	HP1	53	76.53	70.29	70.55	10.42	15.22	15.05	0.99
2021	HP1	46	72.52	64.58	64.91	12.48	18.53	18.33	1.0
2022	HP1	38	64.06	53.03	53.39	13.85	19.95	19.9	1.0
2023	HP1	3	51.86	32.83	32.67	3.15	4.01	3.79	0.97
2009	HP2	158	69.68	62.97	75.68	6.48	8.2	7.79	0.94
2010	HP2	165	68.34	60.58	72.86	7.11	9.26	8.1	0.94
2011	HP2	168	69.82	62.66	75.07	8.24	10.86	9.66	0.94
2012	HP2	169	69.99	62.79	74.97	8.83	11.64	10.31	0.96
2013	HP2	122	71.99	65.35	77.08	10.26	13.46	11.62	0.97
2014	HP2	85	76.28	70.99	82.59	10.14	13.07	10.66	0.97
2015	HP2	71	79.0	74.29	85.58	8.77	11.5	8.65	0.98
2016	HP2	70	77.14	72.26	84.13	9.29	11.87	9.02	0.97
2017	HP2	66	78.02	72.71	83.97	9.79	13.04	10.19	0.97
2018	HP2	52	78.15	73.02	84.33	9.41	12.21	9.01	0.98
2019	HP2	50	77.99	72.67	83.74	9.99	13.35	11.02	0.98
2020	HP2	51	77.15	71.6	82.29	9.86	13.93	12.79	0.96
2021	HP2	38	75.5	69.48	77.63	10.63	15.27	14.26	0.96
2022	HP2	2	88.35	86.97	83.0	1.93	2.16	1.41	1.0
2009	BP1	158	69.83	62.97	64.2	6.48	8.2	8.24	0.97
2010	BP1	165	68.5	60.58	61.78	7.08	9.26	9.22	0.98
2011	BP1	168	69.99	62.66	63.9	8.19	10.86	10.88	0.98
2012	BP1	169	70.19	62.79	64.04	8.78	11.64	11.68	0.99
2013	BP1	123	71.82	65.04	66.32	10.93	13.83	13.82	0.99
2014	BP1	84	76.72	71.39	72.71	9.84	12.62	12.42	0.99
2015	BP1	71	79.16	74.29	75.62	8.7	11.5	11.43	0.99
2016	BP1	70	77.32	72.26	73.49	9.22	11.87	11.76	0.99
2017	BP1	66	78.2	72.71	73.94	9.71	13.04	12.94	0.99
2018	BP1	52	78.32	73.02	74.15	9.33	12.21	11.93	0.99
2019	BP1	50	78.17	72.67	73.62	9.91	13.35	13.05	0.99
2020	BP1	51	77.41	71.59	72.57	9.62	13.96	13.78	0.99
2021	BP1	45	73.01	65.34	65.93	12.18	17.99	17.75	0.99
2022	BP1	39	63.72	52.47	52.41	13.84	19.99	19.41	1.0

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2023	BP1	2	52.62	34.2	34.5	4.06	4.57	4.95	1.0
2009	BP2	158	69.65	62.97	74.2	6.49	8.2	8.04	0.89
2010	BP2	165	68.32	60.58	71.52	7.12	9.26	8.28	0.91
2011	BP2	168	69.78	62.66	73.37	8.25	10.86	9.91	0.93
2012	BP2	169	69.96	62.79	73.53	8.84	11.64	10.77	0.94
2013	BP2	123	71.59	65.04	75.47	11.0	13.83	12.43	0.95
2014	BP2	84	76.52	71.39	81.62	9.92	12.62	10.57	0.97
2015	BP2	71	78.97	74.29	84.76	8.78	11.5	9.01	0.97
2016	BP2	70	77.11	72.26	82.91	9.3	11.87	9.42	0.97
2017	BP2	66	78.0	72.71	82.92	9.8	13.04	10.55	0.97
2018	BP2	52	78.12	73.02	83.1	9.42	12.21	9.55	0.98
2019	BP2	50	77.96	72.67	82.26	10.0	13.35	11.46	0.97
2020	BP2	49	77.94	72.87	81.55	9.14	12.66	11.49	0.97
2021	BP2	40	75.3	69.14	75.88	10.45	15.17	14.64	0.96
2022	BP2	20	71.84	64.73	63.0	12.73	17.66	16.95	0.97

Table 44: Comparison of reliabilities between single-step and current official evaluation (two-step) for nordic genotyped bulls with no offspring

BYR	n	ss_rel	two_rel	s_ss_rel	s_two_rel	cor
2020	2743	41.766	51.954	0.0	2.848	-0.0
2021	2703	41.766	51.216	0.0	3.495	-0.0
2022	2493	41.766	50.623	0.0	3.183	-0.0
2023	2249	41.766	49.654	0.0	4.393	-0.0
2024	2143	41.766	46.221	0.0	4.988	-0.0
2025	762	41.766	42.032	0.0	4.125	0.0