STØTTET AF
Mælkeafgiftsfonden

Analysis of Temperament trait

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Introduction

The Temperament trait for a bull is a measure of the genetic potential of his offspring to have easy handling. Phenotypes are only collected on females and is given as a subjective judgement by the farmer on a 1-10 scale.

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`. Due to an observed outsized influence of the dams breeding value on the predicted breeding value of her offspring, the phenotypic records of sire dams have been removed from the dataset.

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_ss	m_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor
2009	temp1	142	93.71	93.82	95.09	9.4	8.96	8.79	0.92
2010	temp1	108	93.85	94.34	95.31	9.46	9.24	9.1	0.93
2011	temp1	93	95.35	96.05	97.02	9.99	10.61	10.37	0.93
2012	temp1	101	96.31	96.83	97.65	9.03	9.21	9.14	0.94
2013	temp1	96	98.44	99.46	99.7	7.34	7.31	7.38	0.92
2014	temp1	74	95.57	96.39	96.45	9.46	9.42	9.3	0.95
2015	temp1	69	101.0	101.58	101.39	7.9	8.17	7.99	0.95
2016	temp1	50	100.3	100.48	100.38	10.14	10.16	10.01	0.95
2017	temp1	51	100.27	100.67	100.27	9.49	9.23	8.96	0.96
2018	temp1	54	101.43	101.59	100.87	9.53	9.53	9.52	0.97
2019	temp1	37	104.03	102.32	101.46	9.02	8.94	8.83	0.98
2020	temp1	25	100.32	99.44	98.48	8.15	8.82	8.76	0.9

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	temp1	230	93.65	92.67	9.21	9.91	1.62	0.98
2010	temp1	197	94.53	93.69	8.94	9.46	1.55	0.98
2011	temp1	157	95.29	94.38	9.23	9.87	1.64	0.98
2012	temp1	171	97.28	96.81	8.78	9.47	1.39	0.98
2013	temp1	157	97.96	97.6	7.12	7.75	1.54	0.97
2014	temp1	118	96.92	97.22	9.24	10.33	2.07	0.97
2015	temp1	88	100.47	101.2	7.49	8.6	2.1	0.96

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2016	temp1	68	98.91	98.25	9.42	8.27	4.51	0.79
2017	temp1	71	99.61	100.41	9.0	8.74	4.18	0.83
2018	temp1	77	101.48	101.84	8.87	6.96	4.91	0.7
2019	temp1	60	102.1	104.25	8.16	7.31	4.32	0.81
2020	temp1	57	101.67	102.42	7.51	6.75	4.68	0.61
2021	temp1	17	101.41	103.41	7.8	7.93	4.24	0.81

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	temp1	309	94.21	93.29	8.46	8.98	1.92	0.97
2010	temp1	397	95.09	94.35	8.83	9.69	1.87	0.97
2011	temp1	974	94.78	93.91	8.32	8.75	1.93	0.96
2012	temp1	1458	94.97	94.11	8.59	9.09	1.98	0.97
2013	temp1	2543	95.41	94.69	8.48	8.98	1.92	0.97
2014	temp1	3065	95.43	94.65	8.55	9.06	1.93	0.97
2015	temp1	3872	96.33	95.71	8.53	9.06	1.97	0.96
2016	temp1	6165	97.1	96.66	7.86	8.3	1.98	0.95
2017	temp1	8871	97.97	98.13	7.52	7.92	2.0	0.95
2018	temp1	11611	98.26	98.15	7.89	7.96	2.59	0.9
2019	temp1	11728	99.26	99.35	7.85	7.59	3.22	0.85
2020	temp1	13061	99.81	100.37	7.91	7.67	3.58	0.84
2021	temp1	14025	100.49	101.93	7.83	7.35	3.89	0.81
2022	temp1	13782	101.03	102.64	7.8	7.33	3.83	0.82
2023	temp1	2634	101.93	103.29	7.74	7.45	3.82	0.8

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

BYR	n	cor1
2009	142	0.986
2010	108	0.987
2011	93	0.994
2012	101	0.988
2013	96	0.99
2014	74	0.993
2015	69	0.989
2016	50	0.992
2017	51	0.992
2018	54	0.994
2019	37	0.995
2020	25	0.991

Table 5: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1
−5.0	1
−4.0	0
−3.0	6
−2.0	28
−1.0	85
0.0	64
1.0	27
2.0	3
3.0	1
4.0	2

Table 6: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1
2009	142	0.921
2010	108	0.925
2011	93	0.933
2012	101	0.94
2013	96	0.922

BYR	n	cor1
2014	74	0.95
2015	69	0.949
2016	50	0.951
2017	51	0.961
2018	54	0.967
2019	37	0.978
2020	25	0.896

Table 7: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1
−10.0	2
−9.0	1
−8.0	0
−7.0	5
−6.0	3
−5.0	8
−4.0	12
−3.0	18
−2.0	31
−1.0	33
0.0	45
1.0	26
2.0	9
3.0	10
4.0	7
5.0	1
6.0	3
7.0	1
8.0	0
9.0	1
10.0	0
11.0	1

Table 8: 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	142	0.968
2010	108	0.967
2011	93	0.976
2012	101	0.973
2013	96	0.96
2014	74	0.976
2015	69	0.978
2016	50	0.981
2017	51	0.982
2018	54	0.981
2019	37	0.987
2020	25	0.946

Table 9: 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	dif1
−6.0	1
−5.0	5
−4.0	7
−3.0	14
−2.0	40
−1.0	46
0.0	49
1.0	27
2.0	13
3.0	6
4.0	4
5.0	4
6.0	0
7.0	0
8.0	1

Table 10: Correlations between current two-step and new Single-step for genotyped nordic bulls with no offspring born after 2020

BYR	n	cor
2020	3194	0.911
2021	3208	0.909
2022	3270	0.901
2023	3079	0.893
2024	3001	0.876
2025	1276	0.861

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

dif	dif1
−16.0	2
−15.0	0
−14.0	1
−13.0	8
−12.0	12
−11.0	48
−10.0	88
−9.0	107
−8.0	295
−7.0	402
−6.0	670
−5.0	887
−4.0	1163
−3.0	1486
−2.0	1601
−1.0	1633
0.0	1424
1.0	1281
2.0	998
3.0	697
4.0	462
5.0	266

dif	dif1
6.0	165
7.0	90
8.0	32
9.0	9
10.0	7

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 12: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
temp1	0.86	0.588	111

EBV:

trait	b1	rsquare	n
temp1	0.853	0.3	111

Interbull test

An Interbull test was performed with a passing grade.

```
735 brd pop trt evaldate m ntest    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 tem 20250904 1    45  101.7962    8.9431 GM  101.9763    7.9593   17.8528   12.1315  0.8230  0.0924   102
0.0241  0.9727 52.8  N 2015   YYNY  PASS
735 HOL DFS tem 20250904 2    45  101.7962    8.9431 GM  100.6108    6.2251   19.2849   18.3093  0.8197  0.1817   102
0.0000  1.0000 32.1  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 13: 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**
2010	878	−0.192
2011	991	−0.484
2012	1376	0.042
2013	2330	0.088
2014	3720	−0.041
2015	5110	0.005
2016	6648	−0.029
2017	9125	−0.055
2018	12758	−0.103
2019	18532	−0.092
2020	26813	−0.034
2021	33928	0.09
2022	41426	0.072
2023	31494	0.012
2024	6103	0.141

Table 14: 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**
2001	63656.0	−0.01
2002	65388.0	−0.02
2003	69048.0	−0.016
2004	69120.0	−0.006
2005	68289.0	−0.017
2006	70814.0	0.019
2007	64762.0	0.005
2008	62985.0	−0.006

BYR	n	m1
2009	59962.0	−0.028
2010	57556.0	−0.009
2011	53964.0	0.0
2012	50286.0	0.032
2013	48411.0	0.021
2014	48428.0	0.069
2015	45967.0	0.093
2016	44343.0	0.082
2017	38427.0	0.071
2018	32879.0	0.074
2019	28418.0	0.112
2020	24230.0	0.106
2021	20960.0	0.076
2022	15956.0	0.029
2023	3293.0	0.091

Reliabilities

Table 15: 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	noff	edc	rel_edc	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	temp1	142	137.42	253.07	221.58	87.48	72.32	72.54	5.27	10.8286	10.5116	0.979524
2010	temp1	108	266.79	419.26	480.42	89.41	75.07	75.14	5.82	12.214	12.0416	0.968025
2011	temp1	93	149.62	266.94	281.31	90.7	75.91	76.12	4.43	10.0051	9.7571	0.963834
2012	temp1	101	212.11	349.21	458.69	93.08	79.47	79.52	4.63	11.5299	11.4118	0.961042
2013	temp1	96	213.53	351.84	541.5	93.84	79.62	79.75	4.28	11.167	10.9565	0.952313
2014	temp1	74	284.65	441.51	948.01	96.81	84.3	84.37	3.03	11.1312	11.0588	0.909886
2015	temp1	69	375.53	538.62	1540.38	97.39	84.4	84.58	2.75	11.894	11.6958	0.897907
2016	temp1	50	398.36	650.73	1810.15	97.5	84.17	84.35	2.6	12.0758	11.84	0.794066
2017	temp1	51	387.96	614.97	2095.06	97.97	83.35	83.61	2.36	13.5568	13.213	0.905881
2018	temp1	54	344.13	443.88	2149.87	97.92	81.77	82.21	2.32	13.3944	12.828	0.894726
2019	temp1	37	347.95	430.48	2605.96	98.74	82.77	83.13	1.09	11.2091	10.794	0.897456
2020	temp1	25	171.42	239.95	3150.92	99.21	74.93	75.47	0.72	12.6572	12.204	0.484754

Table 16: 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	3194	64.654	74.291	2.527	1.696	0.774
2021	3208	64.769	74.032	4.069	1.814	0.524
2022	3270	64.525	73.565	4.67	1.927	0.457
2023	3079	61.28	71.03	3.238	2.391	0.814
2024	3001	59.375	69.103	1.739	1.243	0.758
2025	1276	58.499	68.379	2.095	1.365	0.83

Jersey

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 17: 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	temp1	16	99.94	101.31	99.69	10.69	9.48	9.17	0.92
2010	temp1	15	99.2	99.2	98.0	8.87	7.57	7.67	0.94
2011	temp1	9	102.67	101.78	100.56	12.06	12.42	11.63	0.88
2012	temp1	10	102.0	100.8	99.7	9.2	8.34	7.96	0.96
2013	temp1	11	98.0	98.27	97.55	10.3	9.2	8.66	0.97
2014	temp1	12	90.92	91.58	89.08	15.89	15.45	14.61	0.97
2015	temp1	19	98.42	97.63	96.32	12.13	12.77	12.91	0.96
2016	temp1	14	100.93	100.43	99.43	6.2	6.32	6.89	0.94
2017	temp1	23	97.39	98.09	97.48	12.32	11.37	10.99	0.97
2018	temp1	7	104.57	105.71	105.71	7.23	6.78	7.57	0.92
2019	temp1	20	100.15	99.65	99.15	9.73	10.59	10.27	0.95
2020	temp1	13	98.38	97.69	missing	12.35	12.27	missing	missing

Table 18: 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	temp1	52	99.31	98.33	8.08	8.78	2.02	0.96

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2010	temp1	55	98.62	97.96	7.93	8.51	2.11	0.95
2011	temp1	47	100.11	99.4	9.42	10.29	2.62	0.95
2012	temp1	47	101.62	100.09	8.33	9.51	2.6	0.95
2013	temp1	50	99.9	99.1	8.93	9.71	3.0	0.92
2014	temp1	37	98.3	98.3	11.13	12.93	3.19	0.94
2015	temp1	30	98.87	97.93	10.02	10.76	3.2	0.93
2016	temp1	26	99.92	99.85	7.46	6.72	4.23	0.7
2017	temp1	30	97.07	96.93	10.29	9.86	6.2	0.68
2018	temp1	21	101.05	100.0	8.33	6.8	5.05	0.49
2019	temp1	31	99.87	100.58	9.61	5.9	7.1	0.4
2020	temp1	22	99.27	99.45	9.41	8.54	5.91	0.67
2021	temp1	5	98.8	97.0	5.22	6.16	4.2	0.67

Table 19: 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	temp1	30	100.0	100.1	7.15	7.35	2.1	0.93
2010	temp1	462	99.86	98.94	8.14	8.8	2.35	0.95
2011	temp1	774	100.97	100.16	7.84	8.52	2.35	0.94
2012	temp1	639	99.73	98.76	7.54	8.21	2.48	0.93
2013	temp1	597	99.71	98.85	7.86	8.39	2.61	0.93
2014	temp1	579	99.26	98.33	8.14	8.98	2.71	0.93
2015	temp1	672	98.6	96.57	8.46	9.0	3.18	0.93
2016	temp1	976	97.33	96.17	8.54	9.39	3.08	0.92
2017	temp1	993	98.42	97.17	9.2	10.01	3.13	0.93
2018	temp1	980	99.74	97.79	7.96	8.13	3.85	0.86
2019	temp1	1220	99.03	98.42	8.17	7.29	4.73	0.71
2020	temp1	1316	100.78	99.27	8.31	7.66	4.85	0.73
2021	temp1	1297	99.29	98.79	7.84	6.66	4.94	0.64
2022	temp1	1604	99.75	99.19	7.76	6.77	4.62	0.69
2023	temp1	499	101.09	99.96	8.42	6.55	5.03	0.67

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

BYR	n	cor1
2009	16	0.986
2010	15	0.978
2013	11	0.99
2014	12	0.996
2015	19	0.994
2016	14	0.96
2017	23	0.988
2019	20	0.937
2020	11	0.739

Table 21: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1
−12.0	1
−11.0	0
−10.0	1
−9.0	1
−8.0	1
−7.0	1
−6.0	0
−5.0	2
−4.0	2
−3.0	5
−2.0	9
−1.0	12
0.0	15
1.0	8
2.0	6
3.0	2

dif	dif1
4.0	3
5.0	0
6.0	0
7.0	1
8.0	1
9.0	2
10.0	1
11.0	0
12.0	0
13.0	0
14.0	0
15.0	0
16.0	0
17.0	1

Table 22: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1
2009	16	0.924
2010	15	0.942
2013	11	0.966
2014	12	0.972
2015	19	0.962
2016	14	0.941
2017	23	0.971
2019	20	0.949
2020	11	0.739

Table 23: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1
−13.0	2
−12.0	0
−11.0	0
−10.0	1

dif	dif1
−9.0	1
−8.0	1
−7.0	0
−6.0	1
−5.0	2
−4.0	1
−3.0	6
−2.0	10
−1.0	11
0.0	13
1.0	6
2.0	4
3.0	5
4.0	4
5.0	2
6.0	1
7.0	1
8.0	1
9.0	1
10.0	0
11.0	0
12.0	0
13.0	0
14.0	0
15.0	0
16.0	0
17.0	0
18.0	1

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 24: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
temp1	0.794	0.51	35

EBV:

trait	b1	rsquare	n
temp1	0.605	0.22	35

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 25: 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
2010	164	0.058
2011	268	−0.039
2012	1014	−0.248
2013	1523	−0.202
2014	2151	−0.149
2015	2919	0.036
2016	3232	0.069
2017	4044	0.069
2018	5223	−0.016
2019	7172	0.016
2020	10389	0.08

BYR	n	m1
2021	11988	−0.01
2022	13241	−0.011
2023	8514	−0.086
2024	1622	−0.145

Table 26: 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
2001	4300.0	0.055
2002	4157.0	0.0
2003	4802.0	0.037
2004	5073.0	0.04
2005	5692.0	−0.061
2006	6315.0	−0.021
2007	6633.0	−0.053
2008	6850.0	−0.054
2009	7584.0	−0.009
2010	4947.0	−0.011
2011	4887.0	0.037
2012	4789.0	0.016
2013	4665.0	0.154
2014	4483.0	0.003
2015	4982.0	0.131
2016	4851.0	0.16
2017	4480.0	0.011
2018	4752.0	0.098
2019	4272.0	0.048
2020	3931.0	0.074
2021	3425.0	−0.036
2022	2885.0	0.044
2023	918.0	−0.058

Reliabilities

Table 27: 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	noff	edc	rel_edc	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	temp1	16	149.19	241.33	741.25	92.42	70.75	63.07	5.36	13.7443	16.09077	0.823702
2010	temp1	15	75.53	131.33	257.34	94.74	73.35	65.02	2.38	7.75037	9.181027	0.849301
2013	temp1	11	99.45	168.09	620.4	96.93	73.99	63.82	1.8	11.7315	15.36664	0.831591
2014	temp1	12	132.92	208.69	837.4	98.2	80.48	70.08	0.98	8.65775	13.64015	0.850356
2015	temp1	19	201.05	289.76	1432.34	98.82	84.79	77.76	0.75	7.73884	11.99011	0.830956
2016	temp1	14	125.86	181.61	1045.09	98.42	79.9	67.96	1.12	7.8911	14.87956	0.526305
2017	temp1	23	181.52	243.94	1541.93	98.85	82.94	75.78	0.84	8.01492	11.41086	0.788997
2019	temp1	20	176.73	213.39	1811.99	99.17	80.97	73.34	0.49	10.0487	14.15028	0.883242
2020	temp1	13	124.62	160.07	1920.19	99.21	76.46	67.38	0.48	9.82416	14.46047	0.403005

Table 28: 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	492	54.829	56.721	4.871	4.279	0.695
2021	422	55.848	56.161	8.094	3.774	0.38
2022	487	55.512	55.949	8.385	3.626	0.393
2023	633	50.778	52.048	4.476	3.744	0.772
2024	674	49.174	49.733	2.495	2.691	0.795
2025	261	47.628	48.597	2.445	1.996	0.738

RDC

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 29: 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_ss	m_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor
2009	temp1	134	98.49	98.67	missing	8.84	9.01	missing	missing
2010	temp1	128	100.34	100.61	missing	9.91	10.11	missing	missing

BYR	trait	n	m_ss	m_newebv	m_offebv	s_ss	s_newebv	s_offebv	cor
2011	temp1	134	99.99	100.04	missing	8.32	8.79	missing	missing
2012	temp1	137	99.93	99.9	missing	8.8	8.77	missing	missing
2013	temp1	98	98.66	98.85	missing	8.26	8.39	missing	missing
2014	temp1	73	99.32	99.23	missing	8.62	8.76	missing	missing
2015	temp1	64	97.56	97.44	missing	7.32	7.22	missing	missing
2016	temp1	63	100.21	100.14	missing	7.49	7.73	missing	missing
2017	temp1	53	97.96	97.57	missing	8.29	8.6	missing	missing
2018	temp1	39	103.85	103.9	missing	7.41	7.27	missing	missing
2019	temp1	43	99.6	99.74	missing	9.31	9.75	missing	missing
2020	temp1	33	103.09	102.73	missing	7.4	8.02	missing	missing

Table 30: 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	temp1	170	99.39	98.69	9.14	9.91	1.43	0.99
2010	temp1	184	100.6	99.96	9.89	10.54	1.44	0.99
2011	temp1	178	100.52	99.97	8.12	8.85	1.53	0.98
2012	temp1	183	100.25	99.86	8.69	9.3	1.56	0.98
2013	temp1	136	98.94	98.48	8.8	9.28	1.6	0.98
2014	temp1	96	99.05	98.9	9.23	9.84	1.47	0.98
2015	temp1	83	97.93	97.83	8.35	9.23	1.95	0.97
2016	temp1	81	100.17	100.28	7.61	7.1	5.02	0.64
2017	temp1	76	98.93	98.53	8.79	6.86	5.78	0.62
2018	temp1	63	102.11	101.46	8.32	7.08	4.59	0.75
2019	temp1	60	99.2	98.03	8.8	7.25	6.0	0.57
2020	temp1	55	102.51	101.96	8.06	7.44	5.27	0.62

BYR	trait	n	m_f	m_r	s_f	s_r	mean_diff	cor
2021	temp1	14	104.29	104.29	7.61	7.05	3.86	0.76

Table 31: 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	temp1	237	98.56	98.07	8.34	8.96	1.86	0.97
2010	temp1	2209	99.52	98.79	8.11	8.61	1.78	0.97
2011	temp1	3618	100.07	99.42	8.01	8.5	1.82	0.97
2012	temp1	3444	100.24	99.54	8.18	8.66	1.81	0.97
2013	temp1	3523	99.27	98.56	8.04	8.54	1.91	0.96
2014	temp1	3699	99.8	99.21	7.47	7.92	1.88	0.96
2015	temp1	4824	99.96	99.49	7.67	8.14	1.95	0.95
2016	temp1	7009	99.87	99.56	7.26	7.75	1.98	0.95
2017	temp1	7630	99.33	99.13	7.27	7.65	2.08	0.94
2018	temp1	8348	99.46	99.42	7.16	7.31	2.77	0.88
2019	temp1	8379	100.21	99.84	7.48	6.97	3.85	0.78
2020	temp1	9368	100.39	99.98	7.03	6.66	3.43	0.8
2021	temp1	9217	101.32	100.32	7.22	6.47	4.1	0.73
2022	temp1	8778	100.56	99.55	7.19	6.58	4.1	0.72
2023	temp1	1354	101.2	99.96	7.32	6.54	4.08	0.74

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

BYR	n	cor1
2009	132	0.989
2010	72	0.994
2011	119	0.991
2012	118	0.988
2013	88	0.984

BYR	n	cor1
2014	67	0.987
2015	60	0.987
2016	59	0.978
2017	48	0.975
2018	37	0.934
2019	38	0.843

Table 33: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1
−18.0	1
−17.0	0
−16.0	0
−15.0	0
−14.0	0
−13.0	0
−12.0	0
−11.0	0
−10.0	0
−9.0	1
−8.0	2
−7.0	0
−6.0	1
−5.0	7
−4.0	3
−3.0	8
−2.0	17
−1.0	44
0.0	36
1.0	27
2.0	15
3.0	13
4.0	6
5.0	4

dif	dif1
6.0	2
7.0	2
8.0	1
9.0	1
10.0	1

Table 34: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1
2009	132	0.965
2010	72	0.969
2011	119	0.939
2012	118	0.939
2013	88	0.954
2014	67	0.955
2015	60	0.966
2016	59	0.96
2017	48	0.964
2018	37	0.913
2019	38	0.85

Table 35: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1
−16.0	1
−15.0	0
−14.0	0
−13.0	0
−12.0	0
−11.0	0
−10.0	1
−9.0	0
−8.0	2
−7.0	0
−6.0	2

dif	dif1
−5.0	7
−4.0	6
−3.0	9
−2.0	22
−1.0	27
0.0	38
1.0	28
2.0	14
3.0	11
4.0	8
5.0	9
6.0	1
7.0	1
8.0	2
9.0	2
10.0	1

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 36: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
temp1	0.726	0.351	119

EBV:

trait	b1	rsquare	n
temp1	0.519	0.093	119

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 37: 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
2010	357	−0.056
2011	627	−0.317
2012	1483	0.179
2013	2861	−0.095
2014	4003	0.012
2015	5602	0.16
2016	6362	−0.024
2017	7454	−0.051
2018	9359	−0.033
2019	11047	0.097
2020	13713	0.106
2021	15699	0.117
2022	17471	−0.015
2023	11288	0.038
2024	2617	−0.031

Table 38: 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
2001	61945.0	−0.007
2002	60483.0	−0.013
2003	59703.0	−0.001
2004	57190.0	−0.02
2005	54527.0	−0.01

BYR	n	m1
2006	53285.0	0.01
2007	50305.0	0.007
2008	49305.0	−0.005
2009	47407.0	−0.022
2010	40717.0	−0.025
2011	36942.0	0.009
2012	31773.0	0.007
2013	30623.0	0.076
2014	28296.0	0.076
2015	24441.0	0.102
2016	20567.0	0.064
2017	16549.0	0.042
2018	13881.0	0.061
2019	10829.0	0.068
2020	9136.0	0.073
2021	6760.0	0.055
2022	4565.0	0.019
2023	657.0	0.025

Reliabilities

Table 39: 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	noff	edc	rel_edc	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	temp1	134	92.49	151.17	139.47	89.56	77.16	77.32	3.38	6.50144	6.33442	0.941192
2010	temp1	128	111.95	178.12	212.78	88.25	73.68	74.05	4.46	8.0776	7.94063	0.890532
2011	temp1	134	135.66	202.12	272.36	90.04	76.4	76.78	4.11	8.37156	8.22667	0.960524
2012	temp1	137	126.27	192.05	281.08	90.92	75.83	76.49	4.63	9.74358	9.51307	0.826459
2013	temp1	98	178.68	252.99	443.87	92.65	78.46	79.11	4.74	10.845	10.559	0.958928
2014	temp1	73	260.11	339.97	731.53	95.19	81.92	82.42	3.91	11.3967	11.097	0.952449
2015	temp1	64	273.06	347.54	915.32	96.57	83.91	84.48	2.99	10.9532	10.5537	0.944539
2016	temp1	63	263.59	329.48	947.93	96.59	81.72	82.49	2.79	11.7641	11.2007	0.829655
2017	temp1	53	327.66	387.22	1290.61	97.08	83.47	84.31	2.92	12.6852	12.0427	0.944599
2018	temp1	39	376.04	407.51	1548.59	97.71	83.64	84.38	1.94	11.6405	11.0232	0.955352

BYR	trait	n	noff	edc	rel_edc	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2019	temp1	43	269.09	295.36	1301.25	97.88	82.95	83.68	1.82	11.3927	10.6813	0.948978
2020	temp1	33	155.15	188.92	1507.62	98.54	78.76	79.75	1.09	10.1749	9.64416	0.446558

Table 40: 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	2790	63.222	70.131	2.482	2.554	0.687
2021	2789	63.282	69.622	4.326	3.123	0.464
2022	2603	62.78	68.839	4.774	2.791	0.351
2023	2316	59.181	65.389	2.953	3.765	0.724
2024	2205	57.219	63.294	1.999	3.031	0.709
2025	763	56.292	62.517	2.285	2.981	0.752