# Mælkeafgiftsfonden

Reliability type trait calculation

### 09.15.2022 Ulrik Nielsen

Procedures described in "Approximation of reliabilities in large-scale single-step genomic evaluation" have been used for most of linear type traits for HOL. There are 7 steps and total clock time for running all 7 steps is 5-6 hours per trait.

Reliabilities from two step and SS were compared for different groups of animals. For bulls born between 1996 and 2008 and with 20 to 100 classified progenies reliabilities have declined. I twostep method genomic information is included, but not for Single step. The statistic shown below is for stature.

correlation for tested bulls born after 1996- 2008, 20 < obs < 100 6 13:04 Thursday, September 15, 2022

### The CORR Procedure

### 3 Variables: rai newrel1 obs

### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	3839	0.96565	0.00836	3707	0.90000	0.99000	rel two step
newrel1	3839	0.91493	0.02608	3512	0.79721	0.98467	new rel
obs	3839	62.44178	18.12389	239714	21.00000	99.00000	obs clasified

### Pearson Correlation Coefficients, N = 3839 Prob > |r| under H0: Rho=0

	rai	newrel1	obs
rai	1.00000	0.74008	0.64113
rel two step		<.0001	<.0001
newrel1	0.74008	1.00000	0.90180
new rel	<.0001		<.0001
obs	0.64113	0.90180	1.00000
obs clasified	<.0001	<.0001	

## For bulls born after 2008 with genomic information in both evaluations and 20 to 100 classified progenies mean reliability was the same.

correlation for tested bulls born after 2008, 20 < obs < 100

13:04 Thursday, September 15, 2022

### The CORR Procedure

### 3 Variables: rai newrel1 obs

### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	1011	0.96907	0.00866	979.73000	0.83000	0.99000	rel two step
newrel1	1011	0.96839	0.01012	979.04211	0.91911	0.99800	new rel
obs	1011	61.74184	22.13343	62421	21.00000	99.00000	obs clasified

### Pearson Correlation Coefficients, N = 1011 Prob > |r| under H0: Rho=0

	rai	newrel1	obs
rai	1.00000	0.56802	0.43188
rel two step		<.0001	<.0001
newrel1	0.56802	1.00000	0.70874
new rel	<.0001		<.0001
obs	0.43188	0.70874	1.00000
obs clasified	<.0001	<.0001	

For tested bulls born in DFS countries and born after 2018 with no classified daughters. Mean was slightly lower for Single trait than for two step. But for some bulls, reliabilities were extremely high.

tested bull born after 2018 1	13:04 Thursday, September 15, 2022
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### The CORR Procedure

3 Variables: rai newrel1 obs

### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	9669	0.81262	0.01997	7857	0.64000	0.85000	rel two step
newrel1	9669	0.78240	0.02696	7565	0.56973	0.99838	new rel
obs	9669	0	0	0	0	0	obs clasified

### Pearson Correlation Coefficients, N = 9669 Prob > |r| under H0: Rho=0

	rai	newrel1	obs
rai	1.00000	0.83907	
rel two step		<.0001	
newrel1	0.83907	1.00000	·
new rel	<.0001		

### 51 bulls with no progeny tested have a reliability above 0.91.

### tested bull born after 2018 , newrel1 > 0.91 13:04 Thursday, September 15,

### The CORR Procedure

### 3 Variables: rai newrel1 obs

### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	51	0.83922	0.00744	42.80000	0.81000	0.85000	rel two step
newrel1	51	0.96709	0.02462	49.32160	0.91146	0.99838	new rel
obs	51	0	0	0	0	0	obs clasified

### Pearson Correlation Coefficients, N = 51 Prob > |r| under H0: Rho=0

	rai	newrel1	obs
rai rel two step	1.00000	0.40545 0.0032	
newrel1 new rel	0.40545 0.0032	1.00000	•

These animals have no progeny classified but a lot of tested offspring with no pheno-type.

no progeny tested for tested bulls born after 2018 , newrel1 > 0.91 \$13:04\$ Thursday,

The FREQ Procedure

nav_sid	Frequency	Percent	Cumulative Frequency	Cumulative Percent
1020200212	572	2.62	572	2.62
1020229996	1770	8.10	2342	10.71
1020259142	1665	7.62	4007	18.33
1020270800	57	0.26	4064	18.59
1020282953	301	1.38	4365	19.97
1020332836	205	0.94	4570	20.91
1020336363	183	0.84	4753	21.74
1020339659	204	0.93	4957	22.68
1020363913	2899	13.26	7856	35.94
1020369473	2487	11.38	10343	47.32
1020515953	57	0.26	10400	47.58
1020524257	483	2.21	10883	49.79
1020530830	259	1.18	11142	50.97
1020548509	1626	7.44	12768	58.41
1020552413	826	3.78	13594	62.19
1020565524	74	0.34	13668	62.53
1020609281	2276	10.41	15944	72.94
1020664509	182	0.83	16126	73.77
1020697833	638	2.92	16764	76.69
1020727457	357	1.63	17121	78.32
1020759267	52	0.24	17173	78.56
1020790235	351	1.61	17524	80.17
1020794003	60	0.27	17584	80.44
1020805158	652	2.98	18236	83.43
1020837648	126	0.58	18362	84.00
1020845408	186	0.85	18548	84.85
1020845810	101	0.46	18649	85.31
1020847489	324	1.48	18973	86.80
1020886655	857	3.92	19830	90.72
1020904809	144	0.66	19974	91.38
1020939655	100	0.46	20074	91.83
1020945719	67	0.31	20141	92.14
1020969920	46	0.21	20187	92.35
1020975264	184	0.84	20371	93.19
1020983239	202	0.92	20573	94.12
1021066348	106	0.48	20679	94.60
1021161957	30	0.14	20709	94.74
1021166958	35	0.16	20744	94.90
1021202788	59	0.27	20803	95.17
1021283984	89	0.41	20892	95.58
1212700637	95	0.43	20987	96.01
1212761590	58	0.27	21045	96.28
1212761610	150	0.69	21195	96.96
1212995240	154	0.70	21349	97.67
1213298725	49	0.22	21398	97.89
1213458478	47	0.22	21445	98.11
1213470447	37	0.17	21482	98.28
1319322499	146	0.67	21628	98.94
1319389835	40	0.18	21668	99.13
1319476453	56	0.26	21724	99.38
1319643937	135	0.62	21859	100.00

DATAFILE pheno.txt 2 3 INTEGER animal ones # ones indicates a column of 1 4 5 REAL ERCss1 ERCss2 ERCss3 milk1 milk2 milk3 6 7 MISSING -999.0 8 9 DATASORT PEDIGREECODE=animal 10 11 PEDFILE example.ped 12 15 13 PEDIGREE G am # animal model 14 15 PARFILE VC.var 16 17 model 18 milk1 = ones G(animal) !weight=ERCss1 19 milk2 = ones G(animal) !weight=ERCss2 20 milk3 = ones G(animal) !weight=ERCss3 • The content in apax99.dir 1 # Type of analysis: 4 = Tier and Meyer approach 24

Step7 in the procedure is according to the "cookbook" as shown. Every animal in the

3 # Maximum number of non-zeros in the sparse matrix

pedigree animal has a data record.

4 600000

5 # Original directive file given to mix99i (or -):

### 6 Mix99\_DIR.DIR

```
7 # Number of breeding values
8 3
9 #weight to make breeding values
10 1 0 0
11 0 1 0
12 0 0 1
13 # Absorption level effect
```

14 2

### Suggested alternative method.

According to the description all animals in the pedigree should be included in the data file, also genomic tested animals with no progeny. The alternative method includes only animals with own type record or sires with progeny with type records. Genomic tested animals with no type record or progeny with no type record are deleted from the data record but kept in the pedigree. For these genomic tested animals the output of the model will be a reliability based on the pedigree index. The reliability is transformed to ERC (ERCped). The total ERC (ERCtotal) is the sum of ERCss and ERCped. For 1<sup>st</sup> lactation it will be:

ERCtotal1 = ERCss1 + ERCped1

ERCtotal can then be transformed to a reliability.

This procedure has been tried and tested for stature, and the statistics for the groups of animals are:

Tested bulls born after 1996- 2008, 20 < obs < 100

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### The CORR Procedure

3 Variables: rai newrel1 obs

### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	3839	0.96565	0.00836	3707	0.90000	0.99000	rel two step
newrel1	3839	0.91461	0.02609	3511	0.79709	0.98347	new rel
obs	3839	62.44178	18.12389	239714	21.00000	99.00000	obs clasified

Tested bulls born after 2008, 20 < obs < 100

### The CORR Procedure

3 Variables: rai newrel1 obs

#### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	1011	0.96907	0.00866	979.73000	0.83000	0.99000	rel two step
newrel1	1011	0.96567	0.01055	976.28989	0.91874	0.98700	new rel
obs	1011	61.74184	22.13343	62421	21.00000	99.00000	obs clasified

Tested bull born after 2018

#### The CORR Procedure

3 Variables: rai newrel1 obs

### Simple Statistics

Variable	Ν	Mean	Std Dev	Sum	Minimum	Maximum	Label
rai	9669	0.81262	0.01997	7857	0.64000	0.85000	rel two step
newrel1	9669	0.73151	0.03531	7073	0.52470	0.79941	new rel
obs	9669	0	0	0	0	0	obs classified

For the first groups there are no changes compared to the original method. For the candidate bulls there is a decrease. No bulls have now a reliability above 0.90. The contribution from the pedigree will also be less because many of these bulls also have candidates as sires, and these sires have a reliability, which is biased upwards of their candidate offspring.