

Project on adapting use of Snell Score to NAV evaluation of calving traits

Jørn Pedersen, December 2020

Snell score

How is Snell score calculated ?

- The first step is to define groups (Strata). We have chosen to use the same strata as in the current HV-correction. It is country and 5-year group with sex of calf added. In the current HV-correction sex of calf is not included because the sex ration has been nearly 50:50 until recently.
 - In DNK the 5-year periods start in 1985
 - In FIN the 5-year periods start in 1985 for stillbirth and in 2005 for calving ease
 - In SWE the 5-year periods start in 1985 for stillbirth and calving ease on the old 2-point scale and in 2010 for calving ease on the new 4-point scale
 - The last 5-year period can embrace up to 9 years before it is divided into 2 period
- Next step is to calculate the frequency of observations in each category of the traits within each stratum (e.g. frequency of calving ease score 1 for DNK male calves born 2015-20)
- Finally, the Snell score calculated using the method recommended by Eurogenomic group. This method is based on an assumption of an underlying normal distribution. The Snell score for each category is estimated using a truncated normal distribution (the `etruncnorm`-function I R). The procedure is adapted to SAS-programming by Freddy Fikse.

Within each stratum the average will be zero, but the standard deviation (SD) can be different. One outstanding question is: Should the SD of Snell scores be standardized (HV-correction) to the same across all strata. This question I currently discussed in the expert group of Eurogenomic Group.

SD of Snell scores

Figure 1-5 show the SD for RDC for calf survival and calving ease. Results for HOL and Jersey are quite similar. The results are somewhat similar to the SD of phenotypic data. However, the differences between the groups have become smaller, but they still exists. There are still time trends (especially in DNK) and there are differences between countries and sex of calf.

Figure 1. SD of Snell score of survival rate of RDC calves at 1st calving

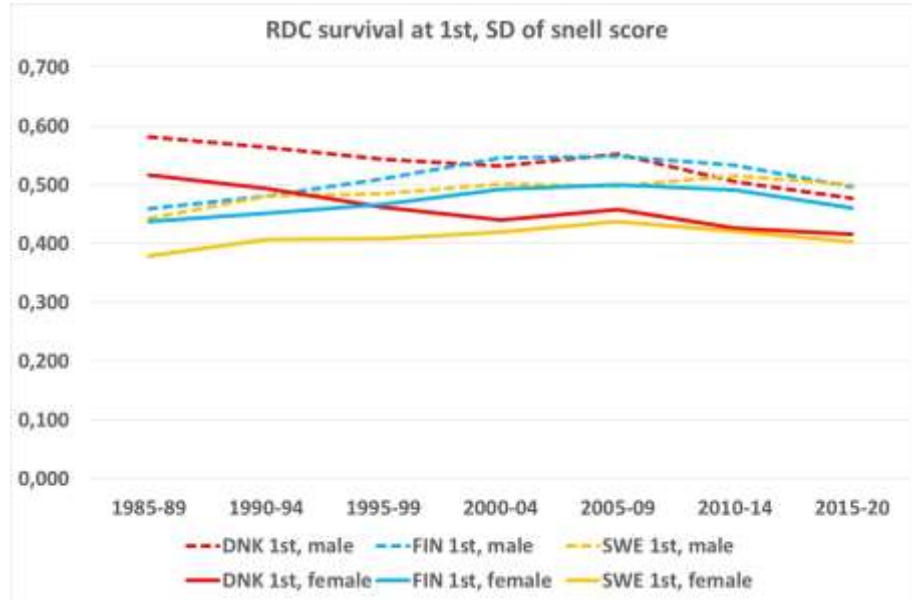


Figure 2. SD of Snell score of survival rate of RDC calves at later calving

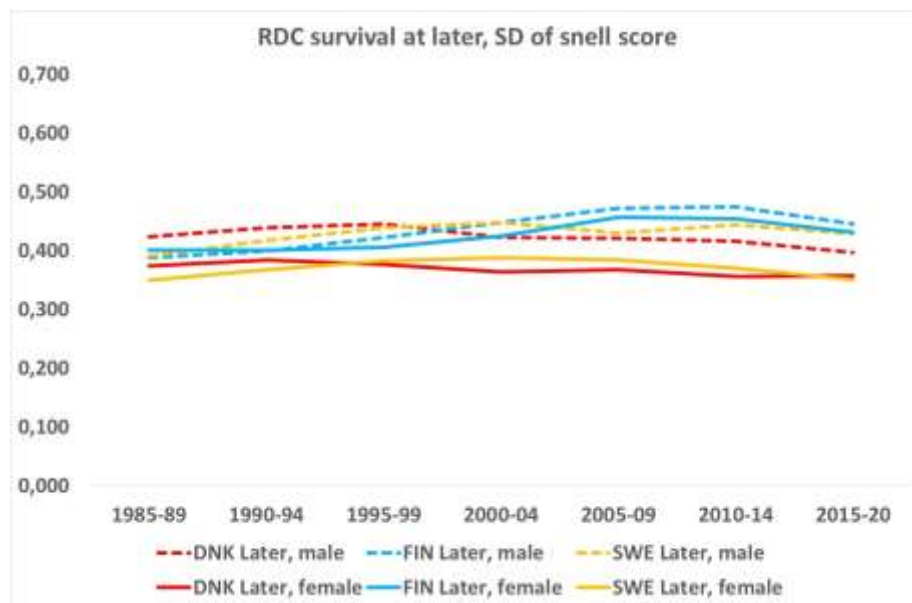


Figure 3. SD of Snell score of calving ease of RDC calves at 1st calving

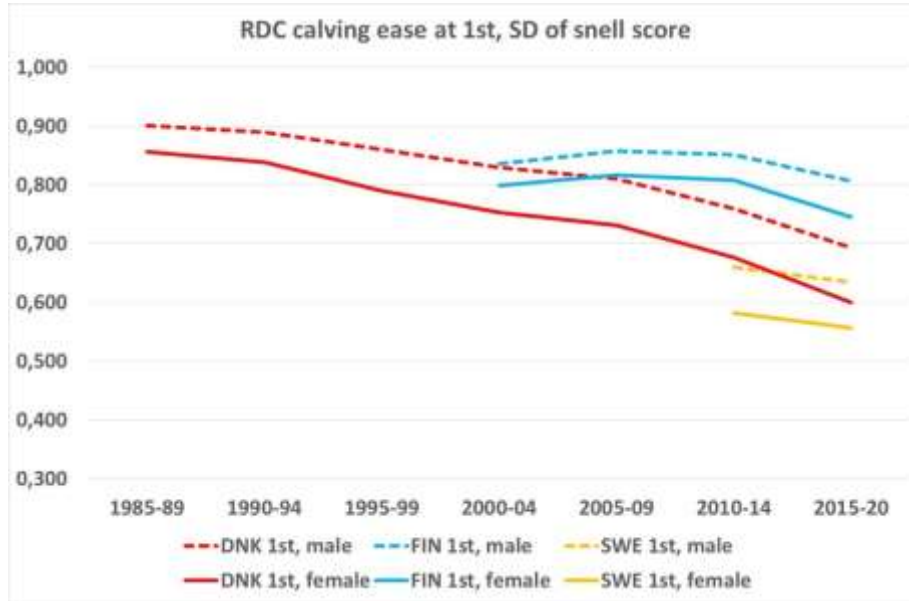


Figure 4. SD of Snell score of calving ease of RDC calves at later calvings

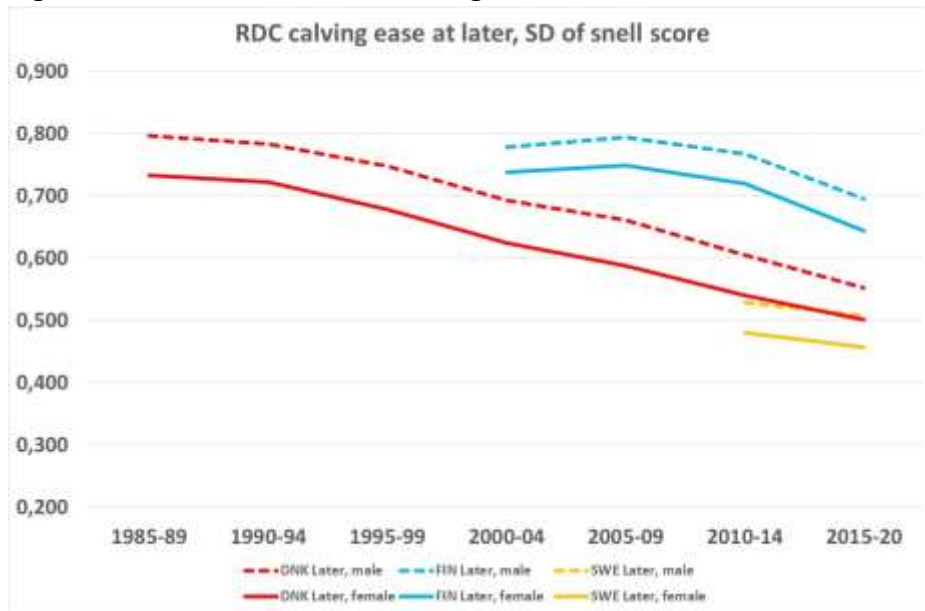
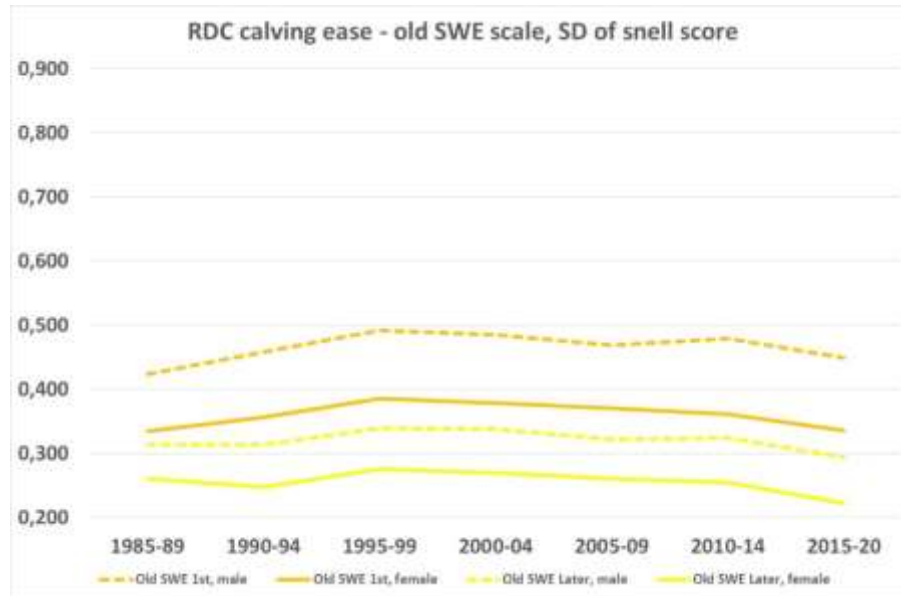


Figure 5. SD of Snell score of calving ease of SWE RDC calves by the old scale



Estimation of genetic parameters

HV correction

In the current evaluation model, the phenotypic standard deviation is standardized to same SD across countries and 5-year periods (but not sex of calves, because up to the recent years the sex ratio was 50:50).

The question is now: Should Snell scores be standardized in a similar way. That is currently discussed in the Eurogenomic Harmonisation Group. Arguments against standardization is that it will more or less correct for differences in heritability due to differences in frequencies.

We still wait for the conclusions of the discussion in Eurogenomic Harmonisation Group

Estimation of genetic parameters

The changes in model would require reestimation of genetic parameters. I anticipate that:

- Change of input to Snell score would not change genetic parameters very much (heritability and correlations would not change – but of course the size of genetic and environmental variance change due to change of scale)
- If data is not standardized, we must expect some changes in genetic parameters
- We need to estimate genetic parameters for permanent effect at later calvings

The genetic parameters were estimated by the MCEM-method described by Lidauer et al. (2015) in “TECHNICAL REFERENCE GUIDE FOR MIX99 SOLVER”. In order to reduce computing time, the input data was reduced by deleting data on calves born before 2005 and data from small herds. Additionally, data was deleted herdwise until manageable input datasets was obtained.

The following models have been analysed (up to now). All models include fixed effects, random herd x year effect, direct and maternal genetic effects and random cow effect for traits with more calvings (SB2 and CE2)

- Single trait analyses of
 - SB1: Calf survival at 1st calving
 - SB2: Calf survival at later calvings (2nd – 5th)
 - CE1: Calving Ease at 1st calving
 - CE2: Calving Ease at later calvings (2nd – 5th)
- Two trait analyses of:
 - SB1-SB2
 - CE1-CE2
 - SB1-CE1
 - SB2-CE2
 - SB1-CE2
 - SB2-CE1

Results from single trait estimation of parameters using Snell scores as input (not HV corrected)

The variances and covariances will change due to the rescaling of input data to Snell score. Therefore it is most relevant to compare heritabilities and correlations (table 1)

In general:

- The herd x year variance (within 5-year periods) was much smaller compared to total variance than assumed in the current evaluation. Actually, it was quite close to zero.
- The permanent cow variance was of the same size as the maternal variance. Therefore, it is important to include this effect in the model. It is not included in the current evaluation model.
- In most cases, the genetic correlation between direct and maternal effect is slightly negative. That is often observed for models that include direct and maternal effects and for various reasons the negative correlations sometime get quite large. These results show larger negative correlations specially for calving ease in later lactation. That might have some effect on estimates of heritability. In the current evaluation model all genetic correlations between direct and maternal effects are assumed to be zero.

Table 1. Estimates of genetic parameters from single trait models.

	New estimates			Current parameters		
	HOL	RDC	JER	HOL	RDC	JER
SB1 -direct, h^2	0.041	0.055	0.035	0.049	0.042	0.036
SB1-maternal, h^2	0.037	0.029	0.024	0.042	0.025	0.024
SB1 dir-mat corr	0.007	-0.009	-0.002	0.000	0.000	0.000
SB2 -direct, h^2	0.011	0.020	0.017	0.012	0.012	0.012
SB2-maternal, h^2	0.078	0.018	0.017	0.106	0.072	0.012
SB2 dir-mat corr	-0.049	-0.032	-0.011	0.000	0.000	0.000
CE1 -direct, h^2	0.123	0.094	0.023	0.101	0.074	0.012
CE1-maternal, h^2	0.095	0.065	0.044	0.078	0.051	0.024
CE1 dir-mat corr	-0.058	0.020	-0.006	0.000	0.000	0.000
CE2 -direct, h^2	0.076	0.116	0.026	0.061	0.024	0.012
CE2-maternal, h^2	0.047	0.077	0.025	0.038	0.024	0.012
CE2 dir-mat corr	-0.080	-0.111	-0.042	0.000	0.000	0.000

Besides the single trait models, series of 2-trait models are analysed in order to obtain all the needed correlations between traits. The combinations analysed are:

- SB1_CE1
- SB2_CE2
- SB1_SB2
- CE1_CE2
- SB1_CE2
- CE1_SB2

Estimates of the random variables

The estimates of the random variables are shown in table 2-4

The heritabilities of the diagonal and the correlation between direct and maternal effects for one traits is average of results obtained in single trait analyses and in the 2-trait analyses.

Real size of variances and covariances (evaluated on size of residual) compared to current evaluation model

- SB: In RDC and JER they are slightly lower – in HOL they are slightly higher
- CE: Ce variances are in general somewhat lower than assumed in the current evaluation model (reduced to 50-70% of the current)

HxY: (within 5-year periods) variances are substantially reduced compared to the values currently used. Currently, it is assumed that HxY variance is 18-20% of the residual variance. The new estimates are 1-2% of the residual variance for SB and 2-6% for CE.

Permanent cow effect (for 2nd to 5th calving) are not included in the current model, but the new estimates show that they are nearly of the same size as the maternal effect.

Table 2. Estimates of HOL heritabilities and genetic correlations. Heritabilities on diagonal, genetic correlations above diagonal. Upper number is the new estimates. Lower number is the values used in the current evaluation

	dSB1	dCE1	dCS1	dSB2	dCE2	dCS2	mSB1	mCE1	mCS1	mSB2	mCE2	mCS2
dSB1	0.041 0.049	0.709 0.720	-	0.617 0.621	0.532 0.550	-	-0.002 0.0	-0.022 0.0	-	-0.002 0.0	-0.031 0.0	-
dCE1		0.018 0.012	-	0.584 0.600	0.608 0.241	-	-0.017 0.0	-0.051 0.0	-	-0.032 0.0	-0.059 0.0	-
dCS1	-	-	-	-	-	-	-	-	-	-	-	-
dSB2			-	0.110 0.101	0.631 0.649	-	-0.002 0.0	-0.028 0.0	-	-0.021 0.0	-0.043 0.0	-
dCE2			-		0.076 0.061	-	-0.019 0.0	-0.087 0.0	-	-0.038 0.0	-0.062 0.0	-
dCS2	-	-	-	-	-	-	-	-	-	-	-	-
mSB1			-			-	0.037 0.043	0.590 0.600	-	0.598 0.191	0.329 0.340	-
mCE1			-			-		0.091 0.078	-	0.623 0.203	0.716 0.740	-
mCS1	-	-	-	-	-	-	-	-	-	-	-	-
mSB2			-			-			-	0.028 0.106	0.583 0.191	-
mCE2			-			-			-		0.047 0.038	-
mCS2	-	-	-	-	-	-	-	-	-	-	-	-

HOL: In table 2 the Holstein results are shown.

- Most heritabilities are quite similar to those currently used. One exception is the heritability of maternal calf survival at later calvings (mSB2). The new estimate is only 0.028. In the current model we assume a heritability of 0.106. The new estimate is closer to our expectations based on general knowledge of behavior of this trait.
- Many of genetic correlations are quite close to those used in the current model.
 - The correlations between direct and maternal effects are very close to zero for SB1 and SB2. For CE1 and CE2 they are slightly more negative (-0.05 to -0.09). In the current model all these correlations are assumed to be 0.
 - The genetic correlation between mSB2 and both mSB1 and mCE1 is higher than in the current model. For the correlation between mSB1 and mSB2, the new estimate is closer to our expectations.

Table 3. Estimates of RDC heritabilities and genetic correlations. Heritabilities on diagonal, genetic correlations above diagonal. Upper number is the new estimates. Lower number is the values used in the current evaluation

	dSB1	dCE1	dCS1	dSB2	dCE2	dCS2	mSB1	mCE1	mCS1	mSB2	mCE2	mCS2
dSB1	0.057 0.042	0.042 0.725	-	0.118 0.649	0.485 0.480	-	-0.002 0.0	0.009 0.0	-	0.008 0.0	-0.008 0.0	-
dCE1		0.099 0.074	-	0.435 ?	0.027 0.780	-	0.004 0.0	-0.051 0.0	-	-0.012 0.0	0.022 0.0	-
dCS1	-	-	-	-	-	-	-	-	-	-	-	-
dSB2			-	0.160 0.120	0.030 0.650	-	0.009 0.0	-0.012 0.0	-	-0.021 0.0	-0.018 0.0	-
dCE2			-		0.037 0.024	-	-0.007 0.0	0.002 0.0	-	0.018 0.0	-0.062 0.0	-
dCS2	-	-	-	-	-	-	-	-	-	-	-	-
mSB1			-			-	0.031 0.025	0.018 0.700	-	0.078 0.235	0.336 0.341	-
mCE1			-			-		0.066 0.051	-	0.631 ?	0.039 0.740	-
mCS1	-	-	-	-	-	-	-	-	-	-	-	-
mSB2			-			-			-	0.108 0.072	0.041 0.275	-
mCE2			-			-			-		0.046 0.024	-
mCS2	-	-	-	-	-	-	-	-	-	-	-	-

The RDC results are shown I table 3.

The results obtained in the first sample analysed was in many ways very strange. Therefor another sample was analysed. It turned out that the results obtained in this second sample seemed to correspond to our expectations. Some of the analysed was also verified on a third

Table 4. Estimates of JER heritabilities and genetic correlations. Heritabilities on diagonal, genetic correlations above diagonal. Upper number is the new estimates. Lower number is the values used in the current evaluation

	dSB1	dCE1	dCS1	dSB2	dCE2	dCS2	mSB1	mCE1	mCS1	mSB2	mCE2	mCS2
dSB1	0.035 0.036	0.008 0.440	-	0.787 0.789	0.334 0.340	-	-0.004 0.0	0.005 0.0	-	-0.008 0.0	-0.014 0.0	-
dCE1		0.022 0.012	-	0.388 0.389	0.803 0.811	-	0.003 0.0	-0.009 0.0	-	-0.003 0.0	-0.033 0.0	-
dCS1	-	-	-	-	-	-	-	-	-	-	-	-
dSB2			-	0.017 0.012	0.444 0.449	-	-0.005 0.0	-0.003 0.0	-	-0.012 0.0	-0.021 0.0	-
dCE2			-		0.026 0.012	-	-0.004 0.0	-0.024 0.0	-		-0.039 0.0	-
dCS2	-	-	-	-	-	-	-	-	-	-	-	-
mSB1			-			-	0.024 0.024	0.011 0.589	-	0.479 0.480	0.164 0.169	-
mCE1			-			-		0.043 0.024	-	0.238 0.239	0.511 0.529	-
mCS1	-	-	-	-	-	-	-	-	-	-	-	-
mSB2			-			-			-	0.017 0.012	0.480 0.490	-
mCE2			-			-			-		0.026 0.012	-
mCS2	-	-	-	-	-	-	-	-	-	-	-	-

The Jersey results are shown in table 4.

- The heritabilities are generally higher than assumed in the current model. The increase is largest calving ease traits. Here the heritabilities are doubled.
- The genetic correlation between direct and maternal traits are all very close to zero
- The other genetic correlations are very close to those used in the current model – except for the correlation between dSB1 and dCE1 – and between mSB1 and mCE1. They are both very low compared to those used in the current model. These results have been analysed in other samples, but the same results are obtained in these analyses. The conclusion is that the genetic correlations between SB and CE at 1st calving is very low.