

STØTTET AF

Mælkeafgiftsfonden

RDC parameters

Maternal current

	Residual	New genetic	h2	Heritability and correlations			SB2	CE2	CS2	Variances and covariances					
				SB1	CE1	CS1				SB1	CE1	CS1	SB2	CE2	CS2
SB1	0.15900	0.00400	0.025	0.025						0.00400	0.00735	0.00158	0.00156	0.00226	0.00060
CE1	0.51750	0.02760	0.051		0.700	0.051					0.00735	0.02760	-0.01545	0.00438	0.01289
CS1	0.46400	0.03200	0.065		0.140	-0.520	0.065				0.00158	-0.01545	0.03200	-0.00317	-0.00807
SB2	0.14110	0.00170	0.012		0.598	0.639	-0.430	0.012			0.00156	0.00438	-0.00317	0.00170	0.00303
CE2	0.44550	0.01100	0.024		0.341	0.740	-0.430	0.701	0.024		0.00226	0.01289	-0.00807	0.00303	0.01100
CS2	0.47005	0.03555	0.070		0.050	-0.860	0.700	-0.580	-0.540	0.070	0.00060	-0.02694	0.02361	-0.00451	0.03555

Maternal new (after putting estimates < 0.05 equal to 0 and checking eigenvalues)

	Residual	Genetic	h2	Heritability and correlations			SB2	CE2	CS2	Calculated genetic variances and covariances					
				SB1	CE1	CS1				SB1	CE1	CS1	SB2	CE2	CS2
SB1	0.14825	0.00580	0.038	0.038						0.00580	0.00501	0.00000	0.00221	0.00267	0.00000
CE1	0.38965	0.02704	0.065	0.400	0.065						0.00501	0.02704	0.00000	0.00257	0.01026
CS1	0.48285	0.03062	0.060	0.000	0.000	0.060					0.00000	0.00000	0.03062	0.00000	0.01507
SB2	0.10450	0.00199	0.019	0.651	0.350	0.000	0.019				0.00221	0.00257	0.00000	0.00199	0.00186
CE2	0.30208	0.01082	0.035	0.336	0.600	0.000	0.400	0.035			0.00267	0.01026	0.00000	0.00186	0.01082
CS2	0.48285	0.02965	0.058	0.000	0.000	0.500	0.000	0.000	0.058		0.00000	0.00000	0.01507	0.00000	0.02965

Maternal - GAPs new proposal (my 1st correction)

	Residual	Genetic	h2	Heritability and correlations			SB2	CE2	CS2	Calculated genetic variances and covariances					
				SB1	CE1	CS1				SB1	CE1	CS1	SB2	CE2	CS2
SB1	0.14825	0.00380	0.025	0.025						0.00380	0.00406	0.00000	0.00143	0.00216	0.00000
CE1	0.38965	0.02704	0.065	0.400	0.065					0.00406	0.02704	0.00000	0.00205	0.01026	0.00000
CS1	0.48285	0.03062	0.060	0.000	0.000	0.060				0.00000	0.00000	0.03062	0.00000	0.00000	0.01507
SB2	0.10450	0.00127	0.012	0.651	0.350	0.000	0.012			0.00143	0.00205	0.00000	0.00127	0.00148	0.00000
CE2	0.30208	0.01082	0.035	0.336	0.600	0.000	0.400	0.035		0.00216	0.01026	0.00000	0.00148	0.01082	0.00000
CS2	0.48285	0.02965	0.058	0.000	0.000	0.500	0.000	0.000	0.058	0.00000	0.00000	0.01507	0.00000	0.00000	0.02965

Maternal - GAPs new proposal (my 2nd correction)

	Residual	Genetic	h2	Heritability and correlations			SB2	CE2	CS2	Calculated genetic variances and covariances					
				SB1	CE1	CS1				SB1	CE1	CS1	SB2	CE2	CS2
SB1	0.14825	0.00580	0.038	0.038						0.00580	0.00501	0.00000	0.00177	0.00267	0.00000
CE1	0.38965	0.02704	0.065	0.400	0.065					0.00501	0.02704	0.00000	0.00205	0.01026	0.00000
CS1	0.48285	0.03062	0.060	0.000	0.000	0.060				0.00000	0.00000	0.03062	0.00000	0.00000	0.01507
SB2	0.10450	0.00127	0.012	0.651	0.350	0.000	0.012			0.00177	0.00205	0.00000	0.00127	0.00148	0.00000
CE2	0.30208	0.01082	0.035	0.336	0.600	0.000	0.400	0.035		0.00267	0.01026	0.00000	0.00148	0.01082	0.00000
CS2	0.48285	0.02965	0.058	0.000	0.000	0.500	0.000	0.000	0.058	0.00000	0.00000	0.01507	0.00000	0.00000	0.02965

Correlations calculated with Trines program

Between current and new model (snell + model + parameters)

	Low h2		
	Basic model, no het.	for mSB1 and	Low h2 for mSB2
dSB1	0.98	0.98	0.98
dCE1	0.99	0.99	0.99
dSB2	0.97	0.97	0.97
dCE2	0.97	0.97	0.97
mSB1	0.950	0.953	0.955
mCE1	0.99	0.99	0.99
mSB2	0.810	0.815	0.810
mCE2	0.96	0.95	0.95