Ideas for continuous genomic evaluation for newly genotyped Walloon Holstein females and males

S. NADERI[1], R. R. MOTA[1], S. VANDERICK[1], N. GENGLER[1]

[1] Gembloux Agro-Bio Tech, ULiège, B-5030 Gembloux, Belgium

Current Situation

➢ Number of genotyped animals in the Walloon genomic evaluations~ 9,000

➢ Single-step genomic bayesian procedure (ssGBayes)

  ➢ Blending genomic, local and MACE information
  ➢ Subtract Walloon information contributing to MACE

➢ Delay between genotyping animals and official GEBV
  In the worst case scenario 4 months

Why preliminary genomic evaluations ?

➢ cullling animal at calf-hood reducing rearing costs

➢ reduce time span between DNA sampling and delivering the genomic evaluation to the farmers

➢ An official evaluation and generates GEBV and GREL
    processing time would increase

Objectives

Generate preliminary genomic evaluations that are:

- Simple and calculated quickly enough that monthly or even weekly evaluations would be practical

- Similar enough to official routine evaluations

Possible approches

A. SNP effect based methods using our routine evaluations as the sources of SNP effects ➔ polygenic contributions ???

B. Genomic selection index based methods ➔ correct (co)variance structures "**H**" based ???

Decomposition of GEBV

$$GEBV_i = w_1 PA + w_2 YD + w_3 DGV + w_4 PC + w_5 PP$$

$$\sum w_i = 1$$

PA: Parent average

YD: yield deviation

PC: Progeny contribution

PP: pedigree prediction based
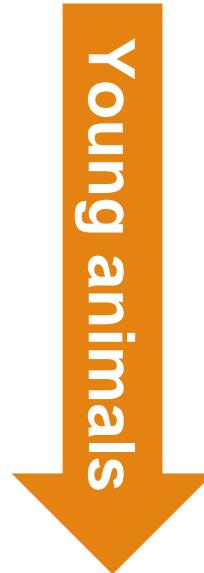
Young animals ↓

$$GEBV_i \approx w_1 PA + w_2 DGV$$

(Lourenco et al., 2015)

A- Group I: Animals without progeny

$$DGV_i = -\left(\sum_j g^{ij}\, GEBV^i\, / g^{ii}\right)$$

$$GEBV_i \approx w_1 PA_G + w_2 DGV_i$$

$$PA_i = (GEBV_s + GEBV_d)/2$$

GEBV of Young bulls without progeny was used to derive W$_i$

A-Group II: Animals with progeny

$$GEBV_i \approx w_1 PA_G + w_2 DGV_i + w_3 PA_C + w_4 EBV_i$$

$$PA_i = (EBV_s + EBV_d)/2$$

GEBV of ~3000 genotyped animals with progeny was used to derive W$_i$

Requirements of the method

- **Combined Pedigree**
- **SNP effects (previous evaluation)**
- **Parent average**
- **Proper regression coefficients**

Running postGS
(solution of previous evaluation)

↓

SNP sol

DGV

Running own code
(Parents average all animals)

↓

$PA_i = (GEBV_s + GEBV_d)/2$

From BOTTOM to the TOP

Fill the gaps with GEBV or EBV

Regression coefficient derivation

↓

Regular variance and covariance of vectors of PA ,DGV
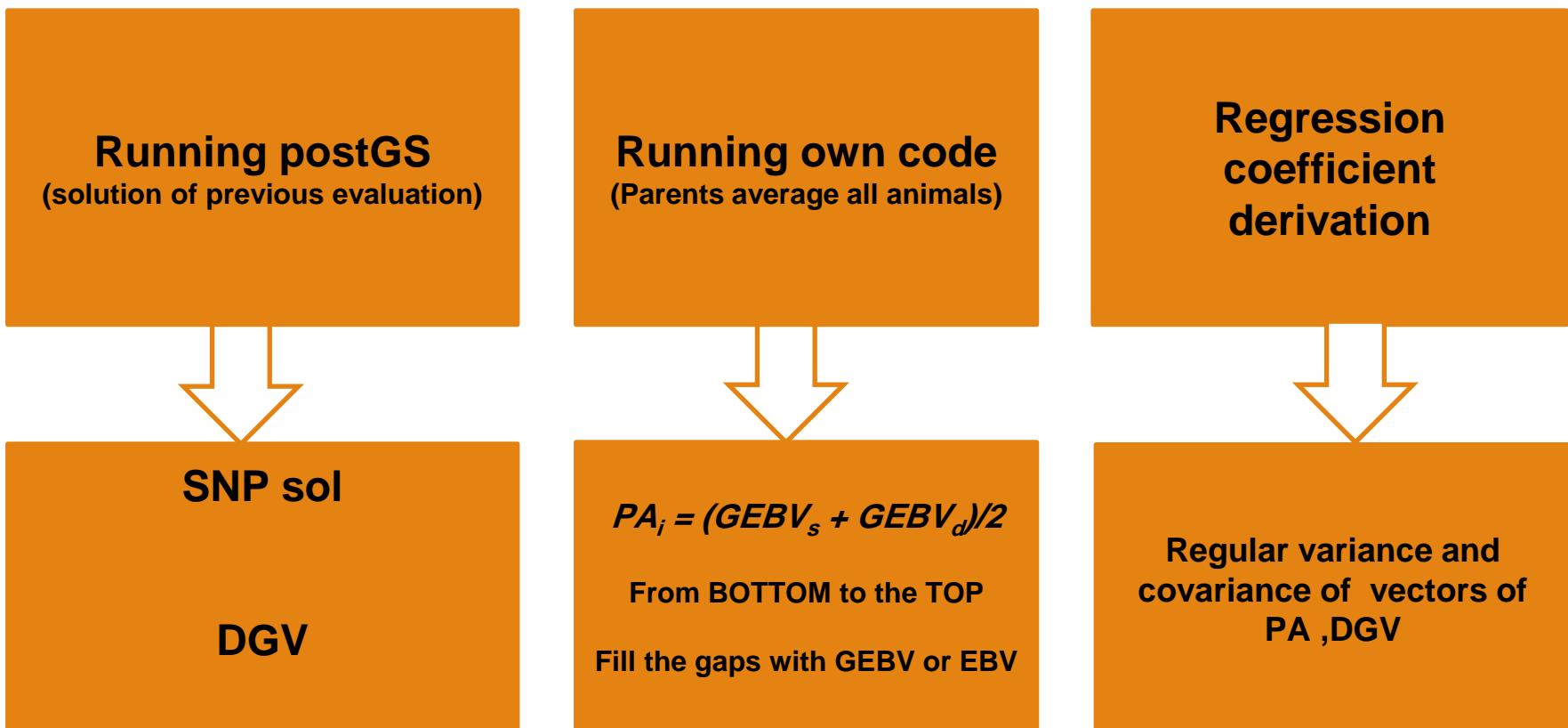
Milk

Group/Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.92	762.79	698.04
Group I/ August 2017	23	0.90	685.70	572.49
Group II/ August 2017	120	0.97	645.85	646.18

Milk
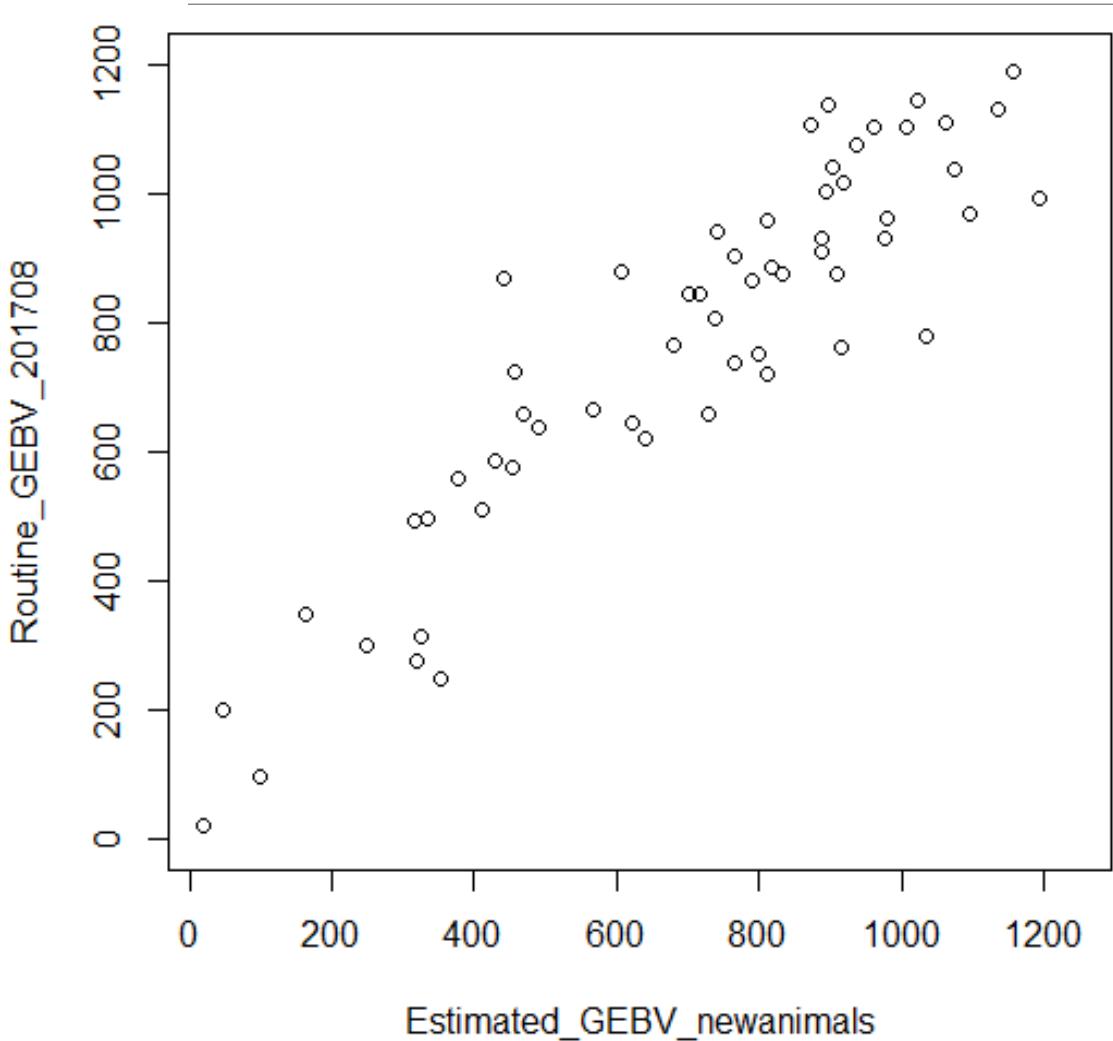
Mean_R_GEBV	Mean_E_GEBV
762.79	698.04
685.70	572.49
645.85	646.18

Fat

Group/ Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.95	32.57	32.77
Group I/ August 2017	23	0.84	27.42	26.42
Group II/ August 2017	120	0.88	26.46	26.04

Fat

Mean_R_GEBV	Mean_E_GEBV
32.57	32.77
27.42	26.42
26.46	26.04
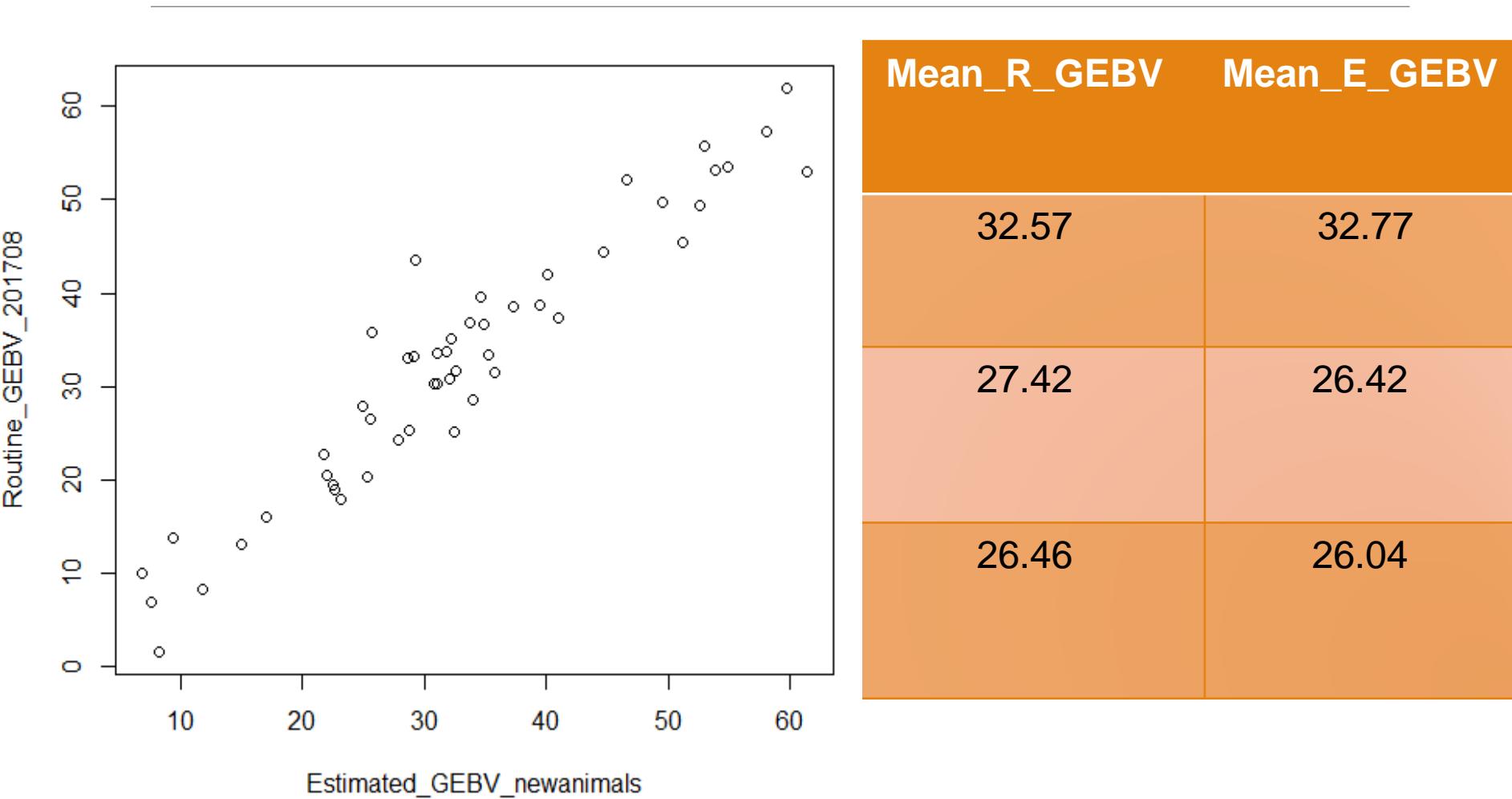
Protein

Group/ Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.93	25.15	24.86
Group I/ August 2017	23	0.89	26.17	22.56
Group II/ August 2017	120	0.95	22.22	21.34

Protein

Mean_R_GEBV	Mean_E_GEBV
25.15	24.86
26.17	22.56
22.22	21.34

SCS
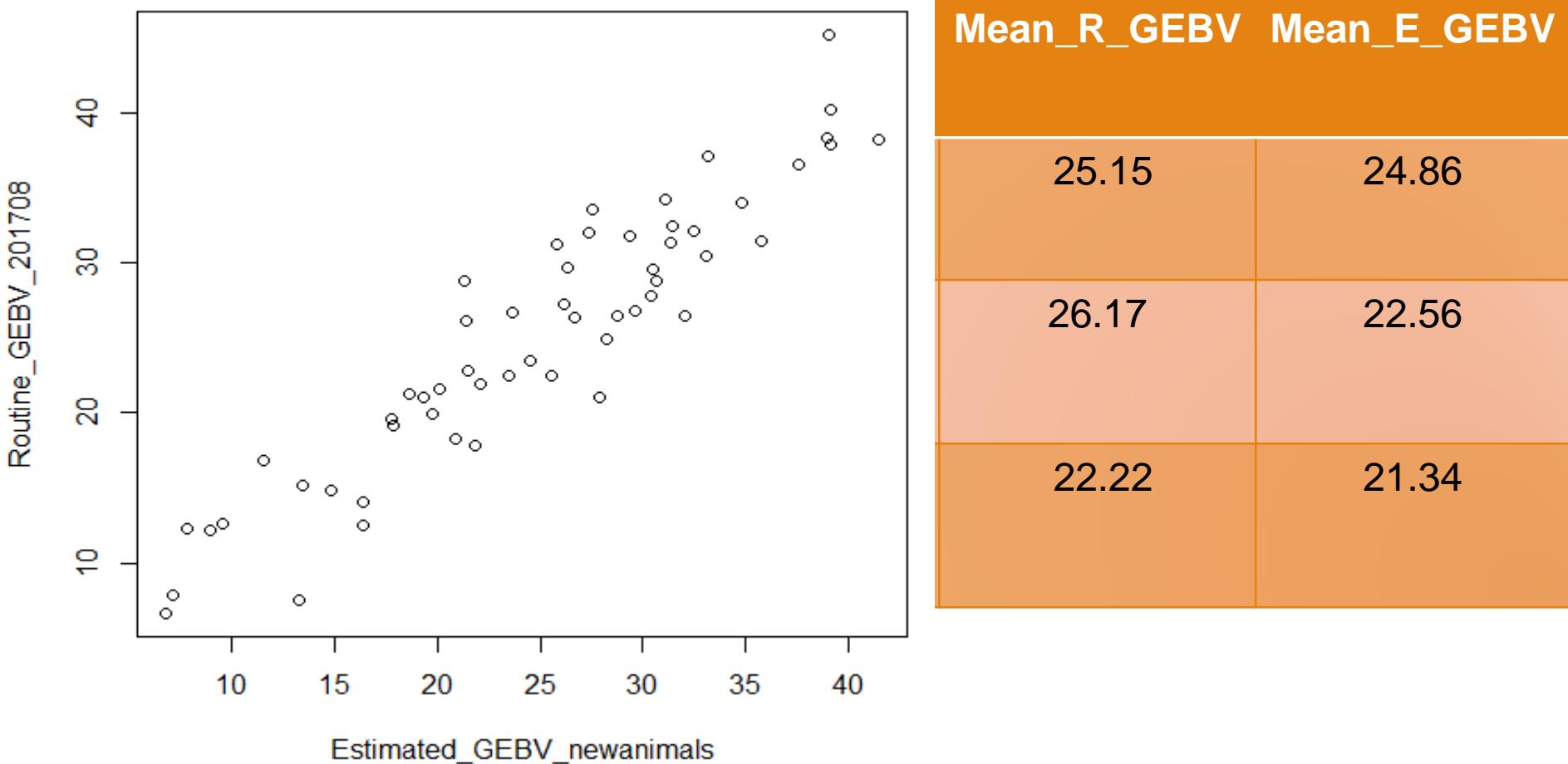
Group/ Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.90	-0.35	-0.41
Group I/ August 2017	23	0.88	-0.34	-0.38
Group II/ August 2017	120	0.93	-0.32	-0.33

SCS
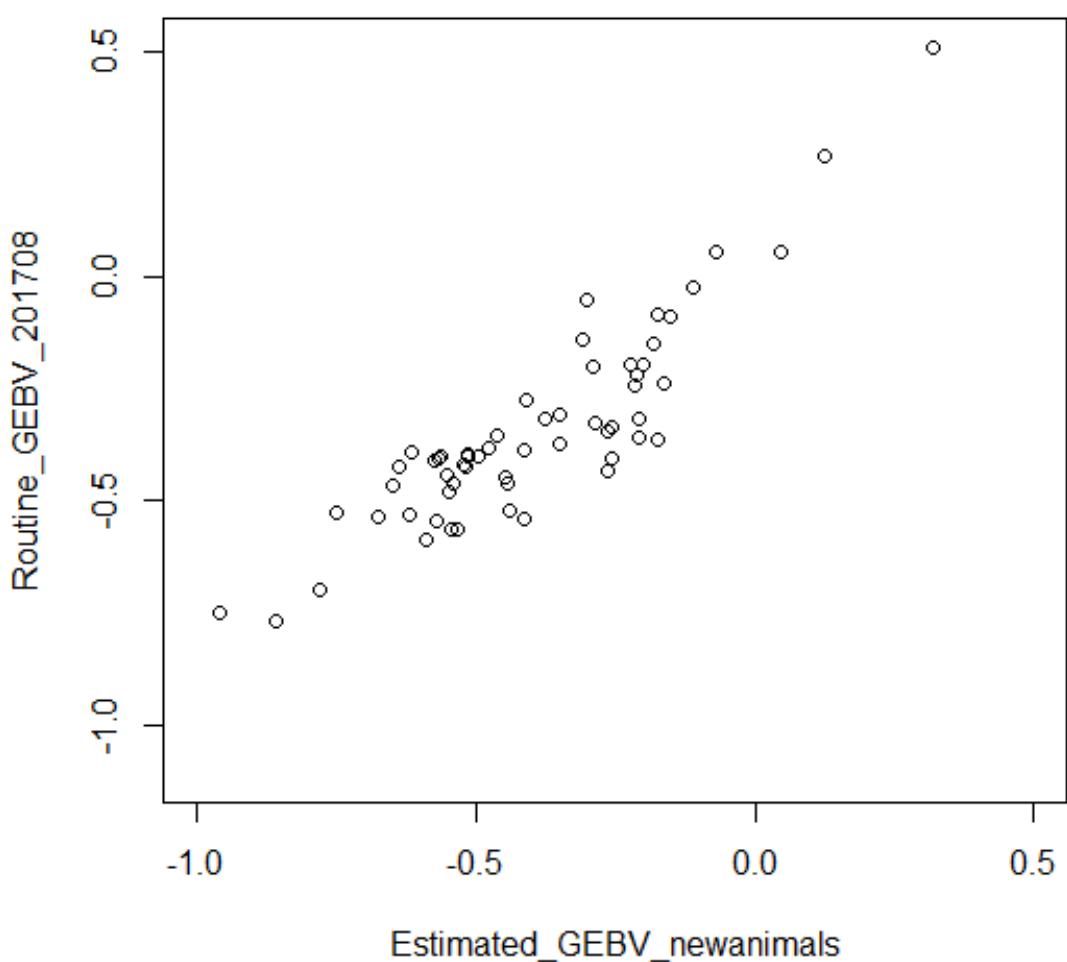
Mean_R_GEBV	Mean_E_GEBV
-0.35	-0.41
-0.34	-0.38
-0.32	-0.33

Genomic selection index based methods

- **Direct selection index difficult as inversion of "H" difficult**

- **However as shown be many researchers (e.g. Gengler et al., 1997)**
  ➜ equivalent Mixed Model Equations

- **GEBV of routine evaluation as "data" and heritability close to unity**

- **Extending GEBV for new genotyped animals**

Extending GEBV for new genotyped animals (Ext_GEBV)

- **Extract the pedigree of new genotyped animals**

- **Combined the pedigree with the routine pedigree**

- **GEBV of routine evaluation in December as priors ➔ GEBV of new genotyped animals**

Overlapping and relationship of new genotyped animals with animal in routine evaluation

New Genotype animals	Sire	P.grand sire	Ancestors	M. grand sire	P. great grand sire	M.great grand sire
71	46 (13)	31 (26)	20588 (8070)	47 (45)	133 (132)	193 (183)

	Animals in routine (December)	New genotyped animals
Animals in routine (December)	0.026	0.041
New genotyped animals	0.041	0.070

Extending GEBV for new genotyped animals

Trait	cor(EXT, EST)	Cor(R, EXT)	Mean EXT	Mean EST	Mean R
Milk	0.93	0.78	277.0	492.4	796.3
Fat	0.96	0.79	14.6	23.2	34.1
Protein	0.95	0.73	10.4	19.0	27.9

Accuracy of the preliminary evaluation could be improved

- adding new genotyped animals

    - parent average or missing (the correlation ~0.99, not shown results)
      ➔ processing time would increase

- adding a specific group of animals

    - closely linked to routine population

    - only a group of genotyped animals representing the dimensionality of the genomic information (proven and young)

➢An official evaluation and generates GEBV and GREL

Conclusion

The correlation between preliminary and official evaluations was not as high as expected (specially for approach B):

- small size of new genotyped animals

- instability of   the SNP estimates

- the proportion of residual polygenic variance in total additive genetic variance (approache B)

Acknowledgements

Thank you for your attention