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

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Current Situation

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

- Single-step genomic Bayesian procedure (ssGBayes)
  - Blending genomic, Walloon and MACE information
  - Subtract Walloon information contributing to MACE

- Delay between genotyping animals and official GEBV

  Worst case scenario: 4 months

Why preliminary genomic evaluations ?

- Culling animals at calf-hood reducing rearing costs

- Time span reduction between DNA sampling and GEBV

- An official evaluation generating GEBV and GREL
  - Processing time may increase

Objectives

Generate preliminary genomic evaluations that are:

- Simpler and faster: practical monthly/weekly evaluations
- Quite similar to current official routine evaluations

Possible approches

A. SNP effect methods using official routine evaluations as source
➔ polygenic contributions ???

B. Genomic selection index methods
➔ correct covariance 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 used to derive W_i

A-Group II: Animals with progeny

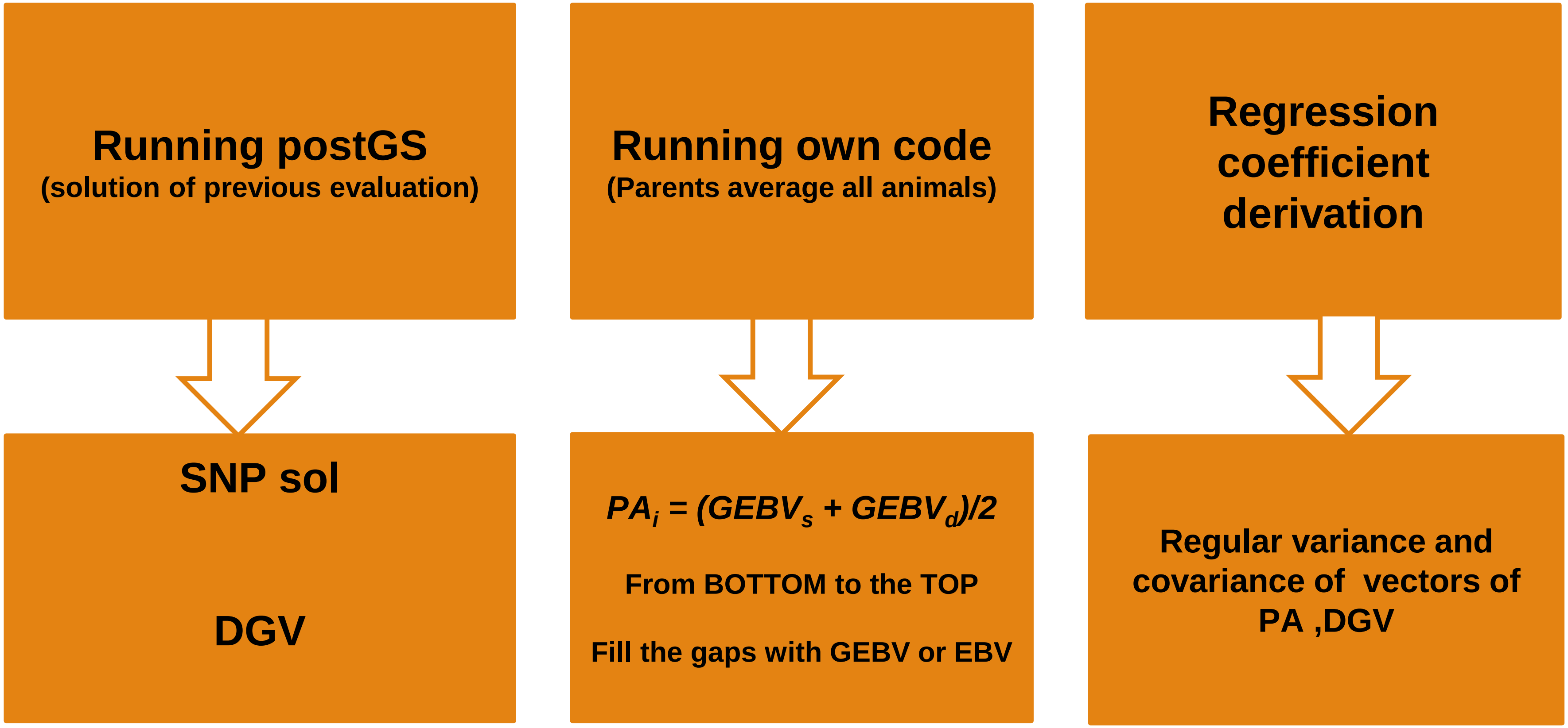
$$GEBV_i \approx w_1 PA_G + w_2 DGV_i + w_3 PA_C + w_4 EBV_i$$

$PA_i = (EBV_s + EBV_d)/2$

GEBV of ~3000 genotyped animals with progeny 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

Fat

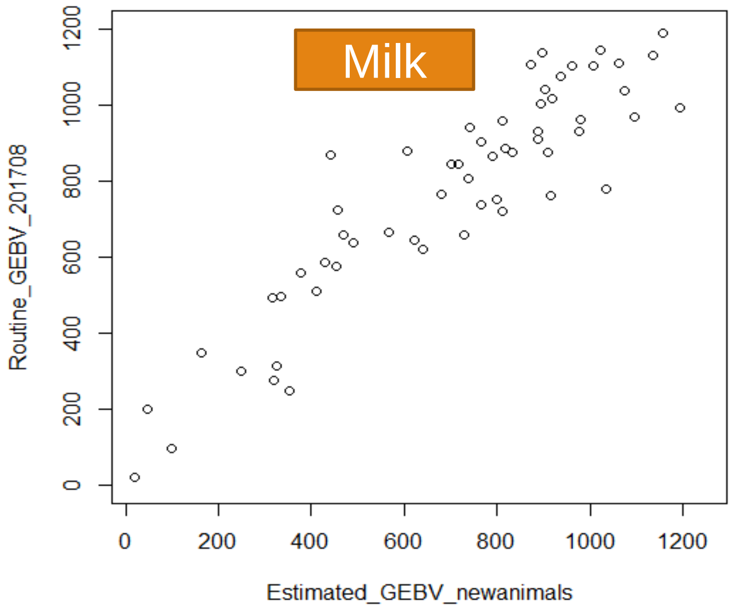
Group/ Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.95	32.57	32.77
Group I/ August 2017	23	0.84	27.42	26.42
Group II/ August 2017	120	0.88	26.46	26.04

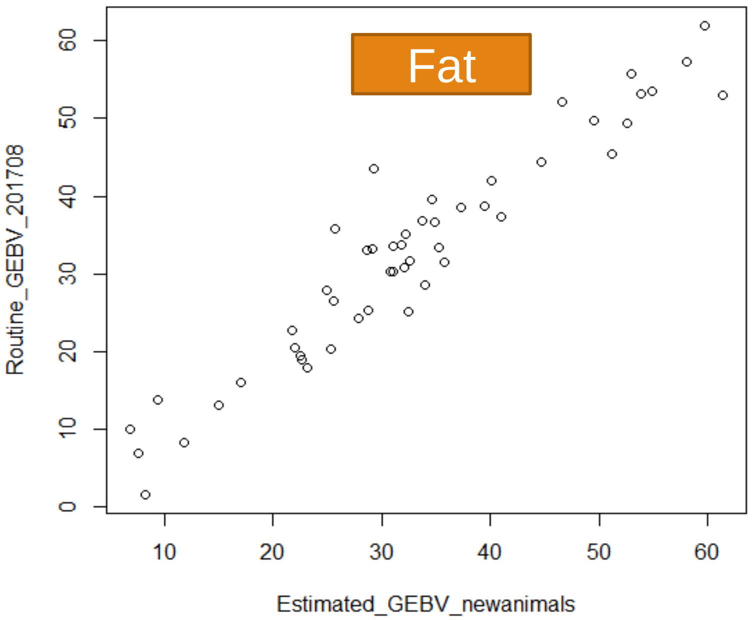
Protein

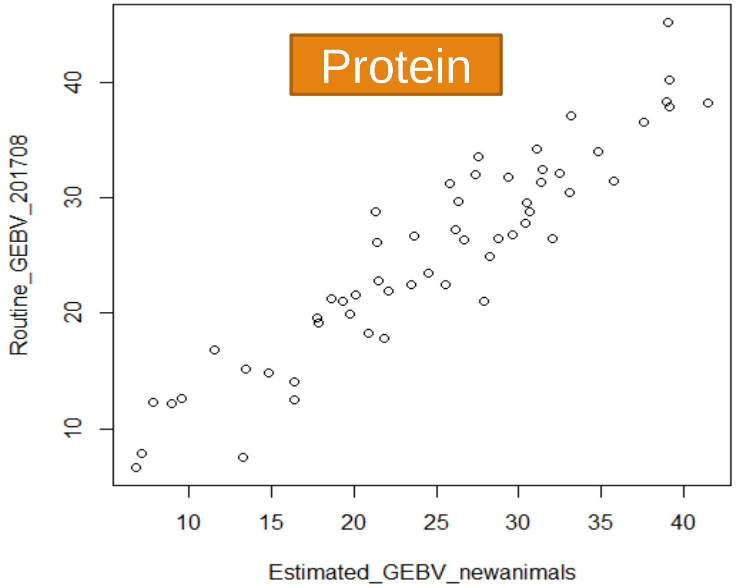
Group/ Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.93	25.15	24.86
Group I/ August 2017	23	0.89	26.17	22.56
Group II/ August 2017	120	0.95	22.22	21.34

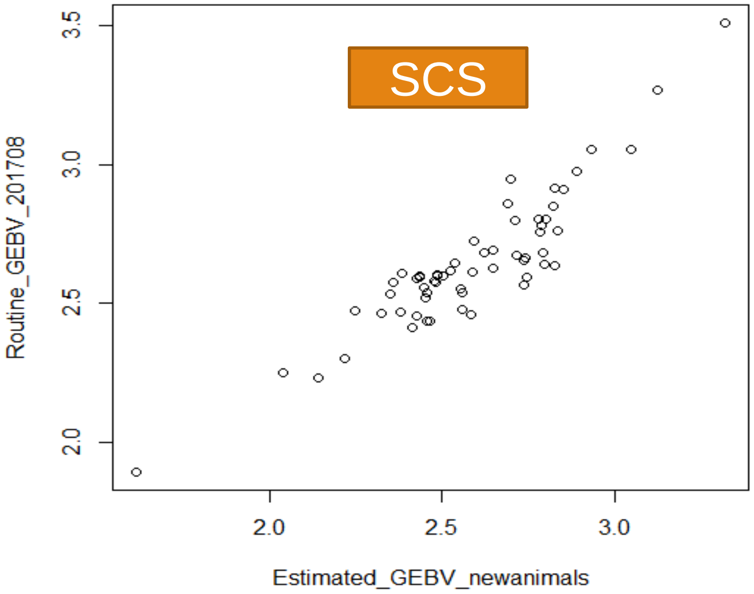
SCS

Group/ Date	Number of Animals	Cor(R_GEBV, E_GEBV)	Mean_R_GEBV	Mean_E_GEBV
Group I/ April 2017	60	0.90	2.65	2.58
Group I/ August 2017	23	0.88	2.66	2.62
Group II/ August 2017	120	0.93	2.68	2.67


Milk
Routine_GEBV_201708
0
200
400
600
800
1000
1200
Estimated_GEBV_newanimals
0
200
400
600
800
1000
1200


Fat
Routine_GEBV_201708
0
10
20
30
40
50
60
Estimated_GEBV_newanimals
10
20
30
40
50
60


Protein
Routine_GEBV_201708
10
20
30
40
Estimated_GEBV_newanimals
10
15
20
25
30
35
40


SCS
Routine_GEBV_201708
2.0
2.5
3.0
3.5
Estimated_GEBV_newanimals
2.0
2.5
3.0

Genomic selection index based methods

- **Directly proportional: selection index “H” inversion difficulty**
- **However, as shown by many researchers (e.g. Gengler et al., 1997)**
  ➔ equivalent MME

- **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)

- **New genotyped animals pedigree extraction**

- **Combining with routine pedigree**

- **GEBV from December 2017 routine evaluation as priors**
  ➔ GEBV of new genotyped animals (71 animals)

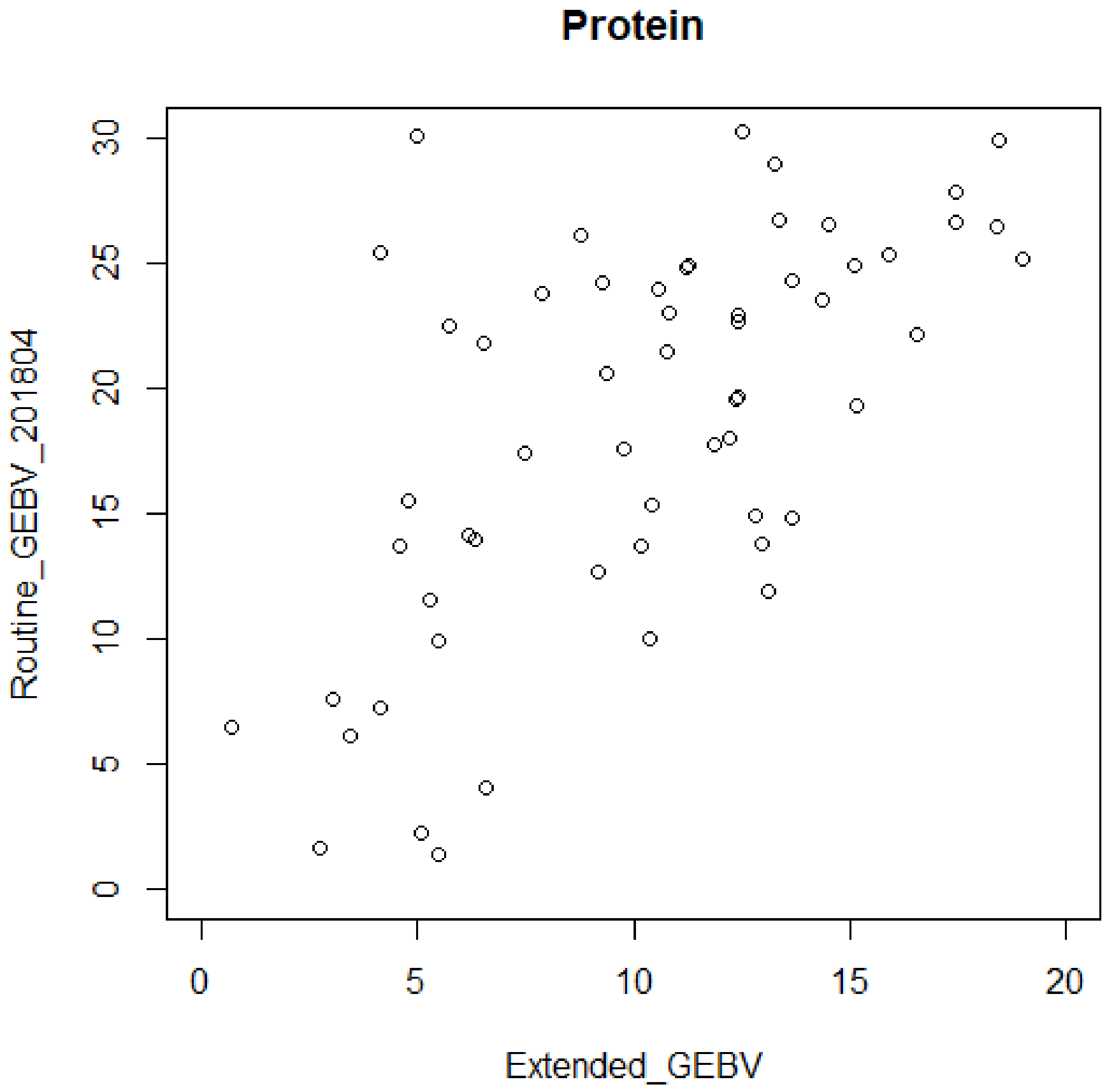
Overlapping and relationship of new genotyped animals with animal in routine evaluation

New Genotyped animals	Sire	P.G.S	Ancestors	M.G.S.	P. G.G.S.	M.G.G.S.
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	c	EST	Mean R
Milk		0	796.30
Fat		0	34.10
Protein		0	18.90



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 may 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 generating 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 SNP estimates
- The proportion of residual polygenic variance in total additive genetic variance (approach B)

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Thank you for your attention

Cor (R_GEBV, E_GEBV) for other traits (April 2017)

Trait	Number of Animals	Cor(R_GEBV, E_GEBV)
BCS	60	0.86
Calving_ Ease	60	0.87
Longevity	60	0.89
Fertility	60	0.91
Stature	60	0.90
Chest width	60	0.89

Regression (de-regression) coefficient used for Protein

Data	Genomic PA	DGV	Pedigree prediction based	EBV	Conventional PA
Young bulls without progeny	0.62	0.72	-0.34	-	-
EST_GEBV	0.6236	0.7223	-0.3449	-	-
EXT_GEBV	0.6673	0.4492	-0.3242	-	-
Animals with progeny	0.44	0.63	-	0.43	-0.50

- Used to estimate GEBV for new genotyped animals
- Used to estimate GEBV for animals with Progeny