Detecting effective starting point of genomic selection by divergent trends from BLUP and ssGBLUP

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Genotyping and genetic progress

- Extensive genotyping
- Genomic evaluation
- Various models and quality control
- Importation of “genetic progress”

- Effects of genomic preselection and selective genotyping

- Is genomic selection effective for specific organization?
Trends for Holstein cows with ssGBLUP and BLUP

Masuda et al., 2018

- 1.1 kg/yr
- 0.4 kg/yr
- 1.2 kg/yr
Goals

• Can differences in trends of ssGBLUP and BLUP identify onset of genomic selection?

• Find the theory
  • Past work: Patry and Ducrocq (2012), Tyriseva at al. (2018)

• Validate with field data sets
BLUP: \[ EBV = w_1^c PA^c + w_2^c YD^c + w_3^c PC^c \]

ssGBLUP: \[ GEBV = w_1^g PA^g + w_2^g YD^g + w_3^g PC^g + w_4 GI \]

If positive selection
+ genomic selection effective: \[ \text{avg}(GEBV) > \text{avg}(EBV) \]

PA = parent average   YD = yield deviation. PC = progeny contribution   GI = genomic index
Realized Mendelian Sampling: \[ RMS_i = (G)EBV_i - PA_i \]

If all progeny genotyped

\[ E(RMS_{BLUP}) \approx 0 \]
\[ E(RMS_{SSGBLUP}) \approx 0 \]

If selective genotyping, for “best” animals:

\[ E(RMS_{BLUP}) > 0 \]
\[ E(RMS_{SSGBLUP}) > 0 \]
\[ E(RMS_{SSGBLUP}) > E(RMS_{BLUP}) \]
US Angus national data

• 11M animals
• 9M records for birth weight and weaning weight
• 4M records for yearling weight
• 842k genotyped

• Results in genetic SD
(G)EBV trends

![Graph showing EBV trends for different breeds and years](image-url)
Mendelian sampling trends

![Graph showing Mendelian sampling trends]

Method: PBLUP, ssGBLUP

Birth Year Mean RMS/SD
Pig data

• 1.3M animals
• > 0.8M records for body weight and backfat
• 116k genotyped
(GEBV) trends

![Graph showing GEBV trends for ADG and BF over birth years 2012 to 2019. The graph compares methods PBLUP and ssGBLUP.](image)
Mendelian sampling trends
Broiler data set

• 1.2M animals
• 1M records for trait 1
• > 200k records for traits 2 and 3
• 154k genotyped
Trends of difference of GEBV and EBV
Mendelian sampling trends

Method: PBLUP, ssGBLUP

Breeding-cycle
Conclusions

• Genomic selection generally starts with divergence of BLUP and ssGBLUP trends
  • Some divergence if best animals genotyped retroactively
  • Affected by correlated traits

• Realized Mendelian sampling positive if selective genotyping even without genomic selection

• Results in agreement with practices at specific organizations
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