

# Bias in single-step genomic evaluations attributable to unknown parent groups

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## INTRODUCTION

- Single-step genomic BLUP (ssGBLUP) works by replacing  $A^{-1}$  (numerator relationship matrix from pedigree) with  $H^{-1}$  (combining  $A^{-1}$  and genomic relationship matrix  $G^{-1}$ ).

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$

- Missing parents can be modeled by unknown parent group (UPG).
- Simple implementation of UPG in ssGBLUP is an approximation (Misztal et al., 2013 JABG).

## OBJECTIVE

- Are UPG solutions changed with ssGBLUP in large models?

## MATERIALS & METHODS

### US Holstein final score

- 10,167,604 records for 6,586,605 cows
- 9,602,031 in pedigree (34,506 genotyped bulls with 42,503 SNP)
- UPG: year of birth × sex

### Israeli Holstein 305-d milk yield

- 1,205,801 records for 713,686 cows
- 829,437 in pedigree (1305 genotyped bulls with 30,359 SNP)
- UPG: year of birth × sex × breed

### Pig 7 traits

- 2,923,141 records for 884,250 pigs
- 906,660 in pedigree (4853 genotyped animals with 63,219 SNP)
- UPG: year of birth

### Computer program

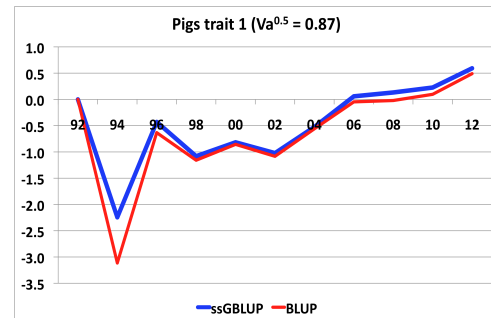
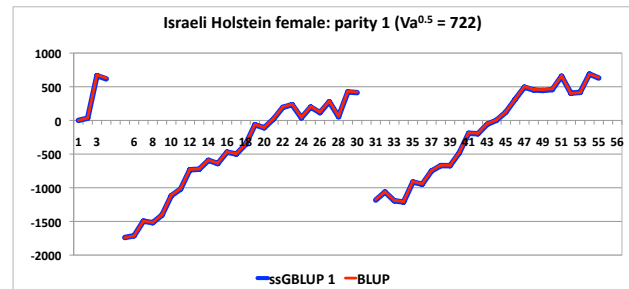
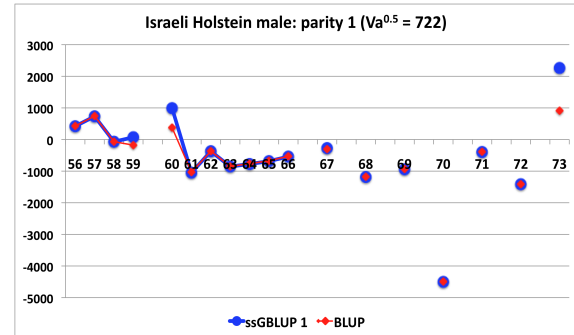
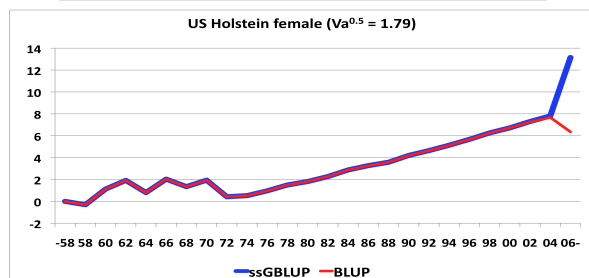
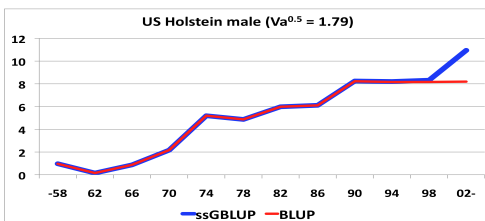
- BLUP90IOD via a single-step approach

### Options for ssGBLUP with UPG

- Keep original UPG
- Refine of UPG
- Eliminate UPG
- Two additive effects

## RESULTS

### UPG estimates with original UPGs



- Differences in UPG solutions for "very old" or "very young" groups
- UPG refinement by merging adjacent UPG
- With refinement, faster convergence by 4%, 55%, and 35% for US Holstein, Israeli Holstein, and pig data sets, respectively
- 2 to 3 times more iterations using two additive effects

## CONCLUSIONS

- Biases are mostly for very few groups with limited phenotypic information.
- Biases can be reduced or eliminated with refinement of UPG definitions.
- Refinement benefits both BLUP and ssGBLUP by improving UPG estimates and convergence rate.

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