

# Impact of preselection on subsequent ssGBLUP evaluations of pigs

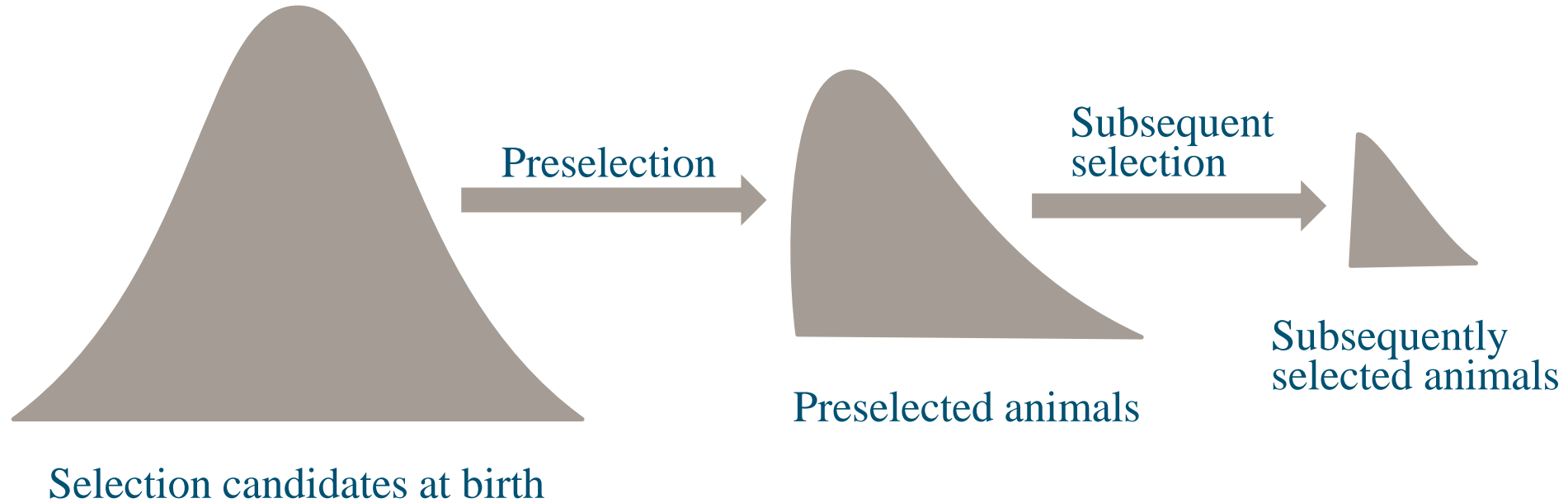
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# Acknowledgements



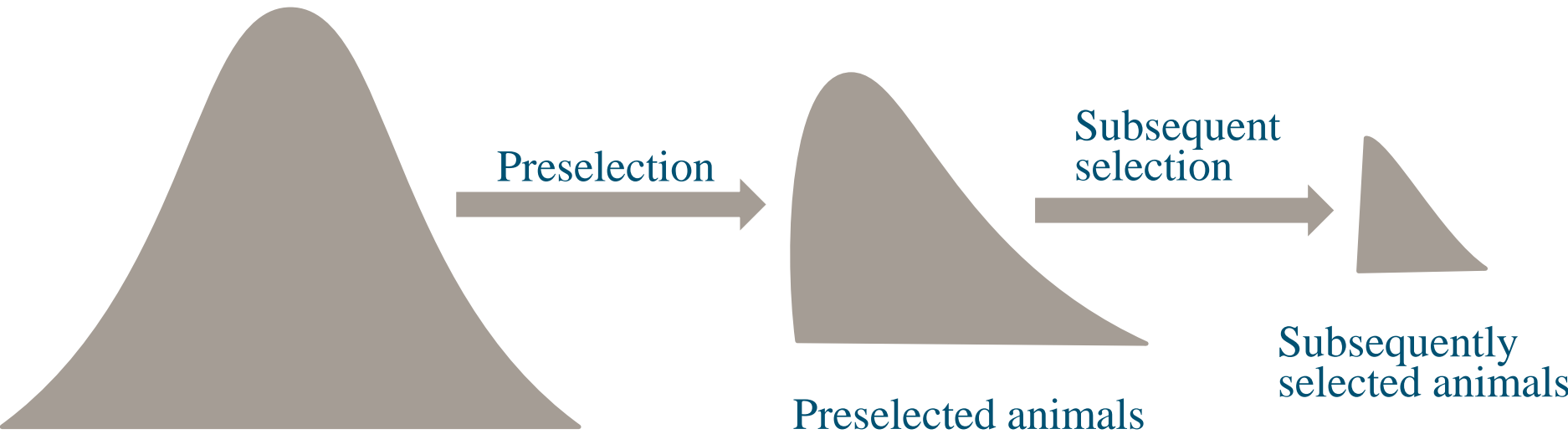
# Preselection



# Recap of our previous studies

- Our previous studies<sup>1</sup> showed no bias in ssGBLUP evaluations following preselection
- We controlled all other sources of bias except preselection
- It is difficult to control the other sources of bias with real data

# Objective: Verify what we know so far, using real data



Selection candidates at birth

Preselected animals

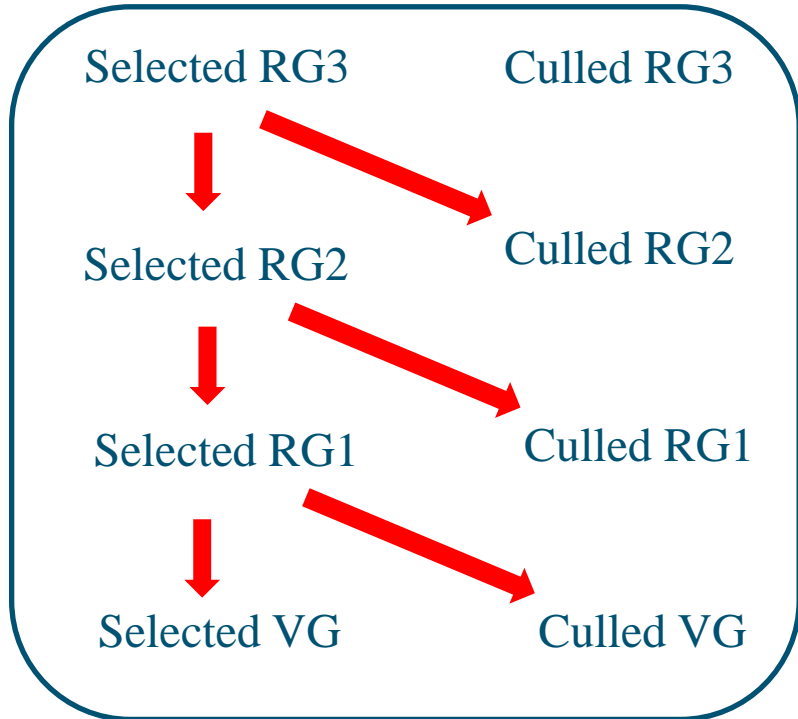
Subsequently selected animals

# Data

## Data on pig production traits, from Topigs Norsvin

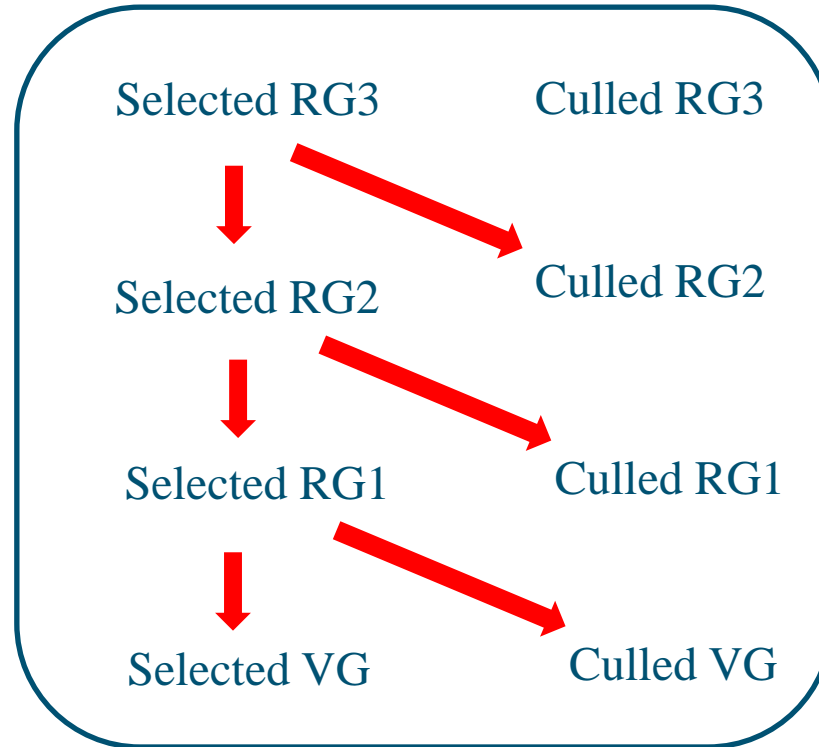
- The traits: average daily gain, backfat, loin depth
- Recorded on a sire line
- Regular genomic preselection in the data

# Genomic preselection - approach



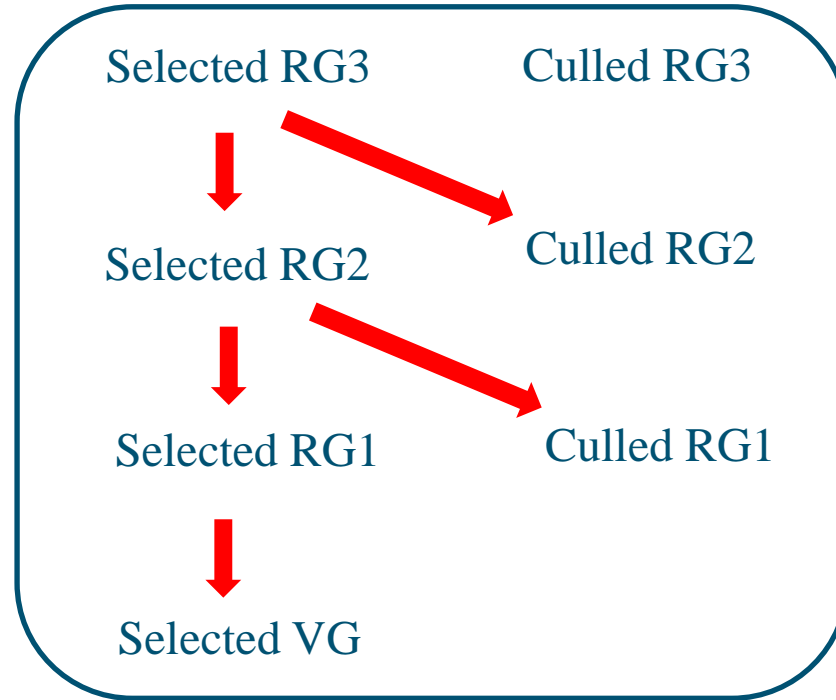
- RG: Reference generation
- VG: Validation generation
- Selected and culled RG and VG animals all have phenotypes
- Additional genomic preselection implemented in both RG and VG by excluding culled animals

# Reference scenario

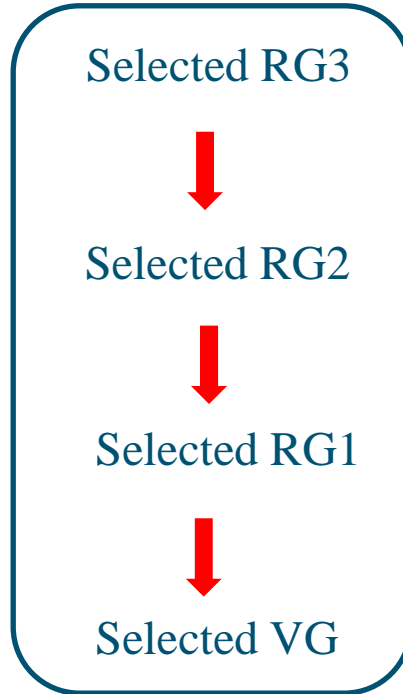




# Validation generation preselection (VGP) scenario



# Multi-generation preselection (MGP) scenario



# Subsequent evaluations

- Pre-corrected phenotypes instead of raw phenotypes
- Progeny yield deviation (PYD) used as a proxy for TBV
- Progeny of validation animals not included in the subsequent evaluations

# Measures of model performance

- Accuracy
- Level bias (mean PYD – mean GEBV)
- Dispersion bias ( $b_{\text{PYD,GEBV}}$ )
  - $E(b_{\text{PYD,GEBV}}) = 0.5$

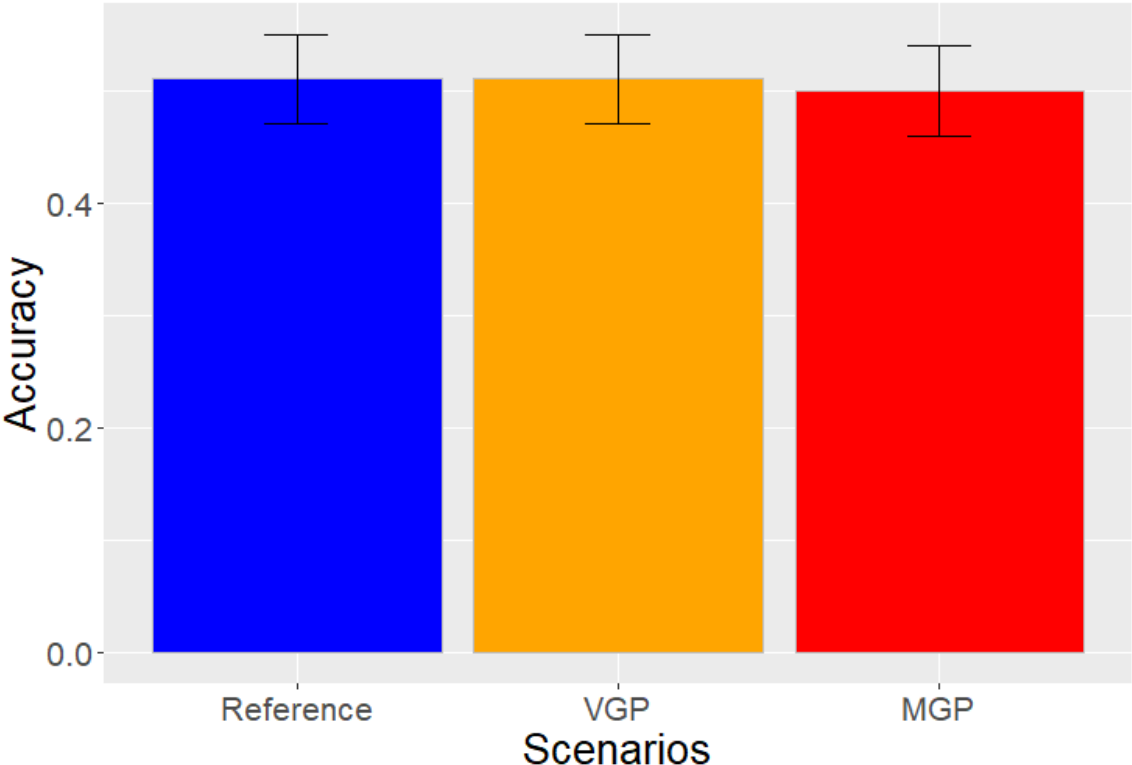
# Amount of data in the subsequent ssGBLUP

Number of animals	Preselection scenario		
	Reference	VGP	MGP
In the pedigree	81,875	60,950	12,777
With records	75,129	54,217	6,065
Genotyped	33,506	23,315	5,131

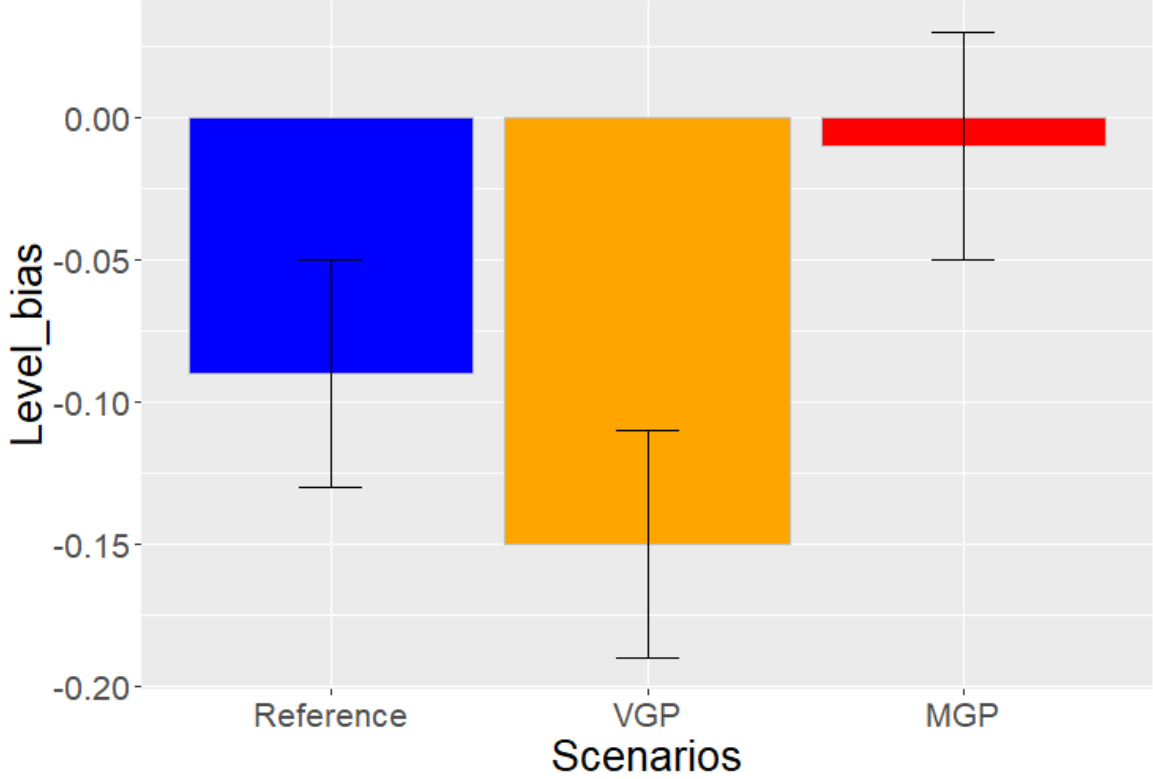
# Results

- Similar trends across all traits
- Only shown for average daily gain during performance testing

# Accuracy

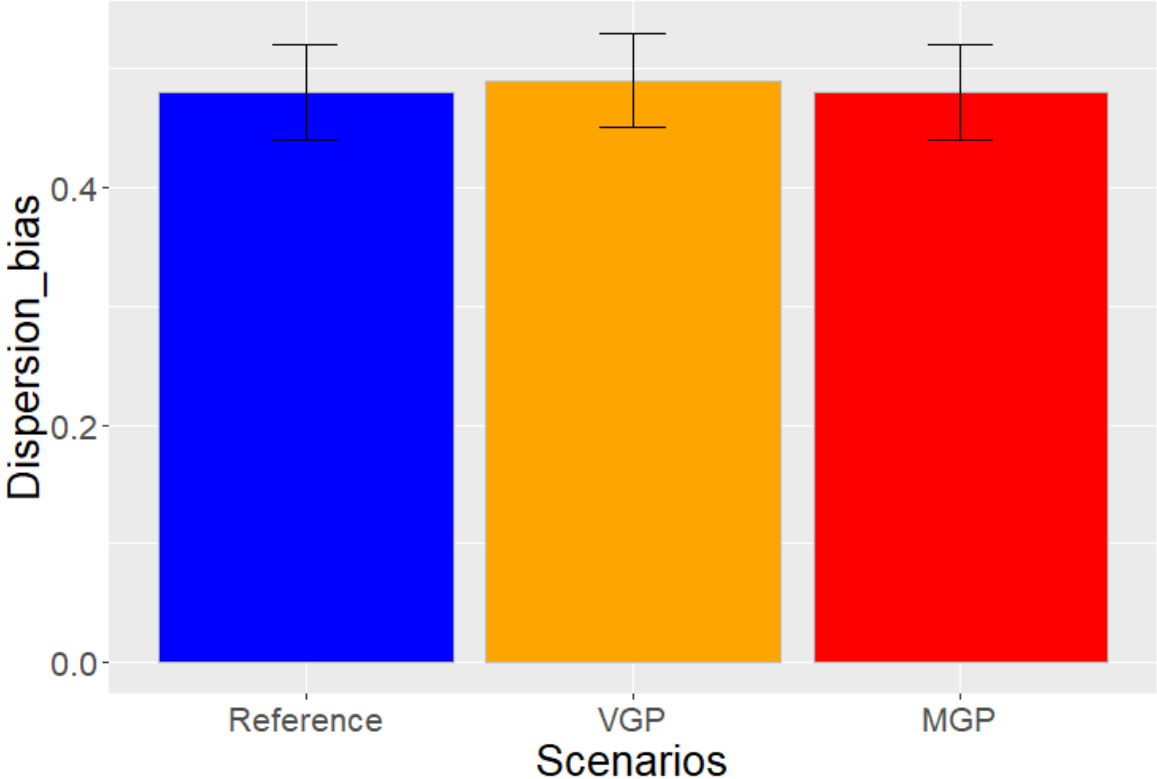


# Level bias





# Dispersion bias



# Summary, conclusion and discussion

- Accuracy did not differ
- Level bias always minimal
- Dispersion bias always absent
- Impact of genomic preselection minimal
- Biases in real life due to other sources