

- *Xijiang Yu, Peer Berg, and Theo Meuwissen (NMBU)*
- *Using alternative relationship matrices for genomic prediction and managing genetic diversity*
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Using alternative relationship matrices for genomic prediction and managing genetic diversity

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A dilemma of modern breeding

- Needs faster genetic gain to feed increasing human population
- Must maintain genetic diversity to cope with future challenges, e.g.,
 - Climate change
 - Emerging diseases
 - Societal demands

Management of population genetic structure

→ Constrain inbreeding using a relationship matrix whilst selecting for maximal genetic gain

- Optimal contribution selection

→ Before the genomic era:

- Pedigree-based relationship matrix → NRM (numerator relationship matrix)

→ In the genomic era:

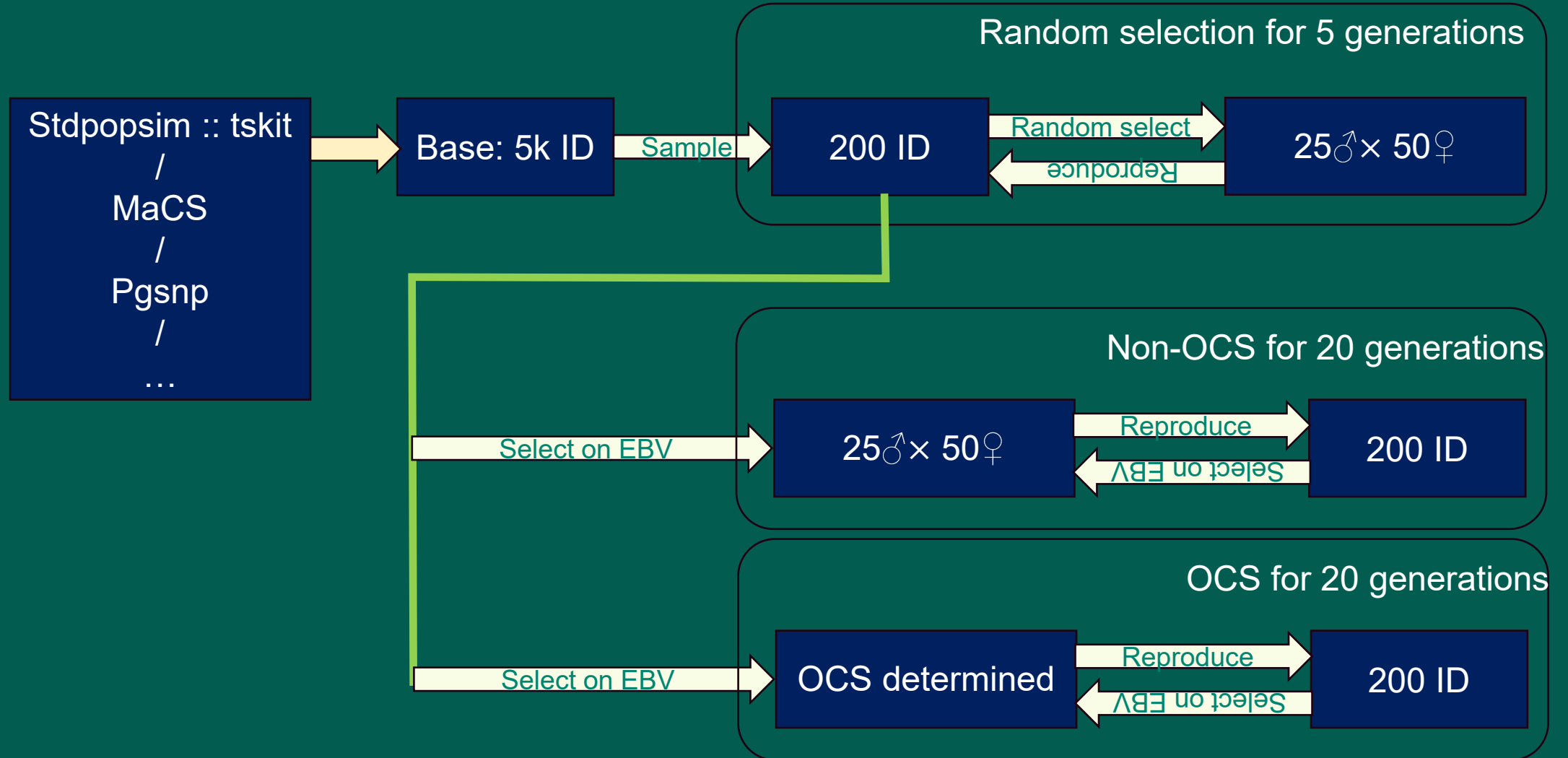
- Genomic relationship matrix → e.g., GRM, IRM (IBD RM)

Objectives

→ Effects of alternative relationship matrices on

- Genetic progresses
- Diversity, inbreeding, and future selection potentials

Breeding schemes



Optimum contribution selection (OCS)

Maximize:	$\Delta G = \mathbf{c}'\mathbf{EBV}$
Subject to:	$\mathbf{c}'\mathbf{X}\mathbf{c}/2 \leq F_{t+1}$
	$\mathbf{c}'\mathbf{s} = 0.5$
	$\mathbf{c}'\mathbf{d} = 0.5$
	$c_i \geq 0$

- Non-OCS uses
 - relationship matrix (RM) for EBVs
 - A: numerical RM
 - G: genomic RM
 - I: IBD RM (by counting uniquely coded alleles)
 - GBLUP, ABLUP or IBLUP
- xyOCS
 - RM = y for EBVs
 - For constraint x = A, G, or I
 - E.g.: AGOCS:
 - Uses A for constraint,
 - Uses G for EBV

Data recording

→ Genotypes of 29 cattle chromosomes

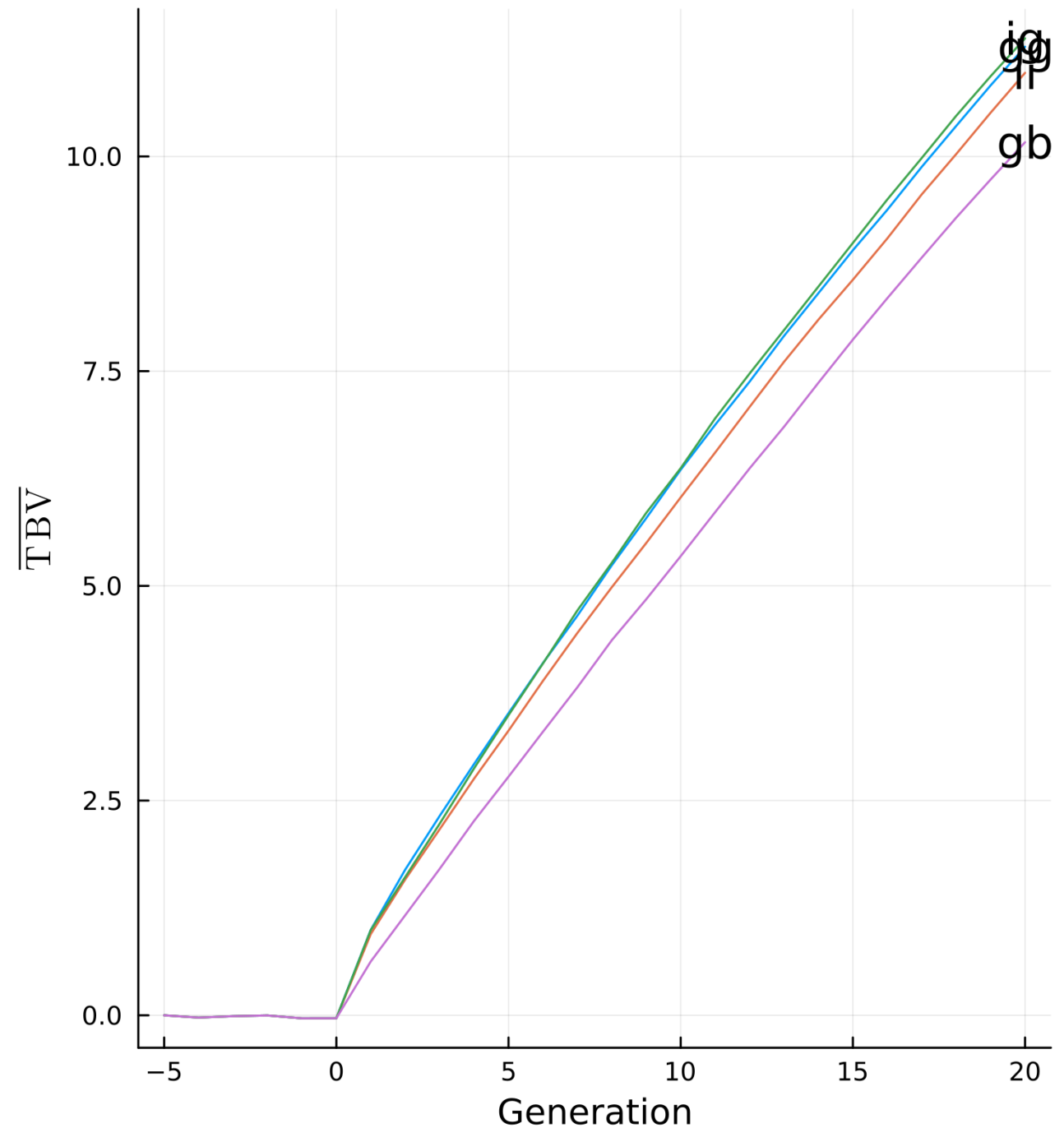
- Linkage map
- 50k (visible) chip SNP
- 10k (invisible) reference SNP
- 10k QTL
- All uniquely coded to trace every allele

→ Pedigrees

→ Summary DataFrame with 30+ indices

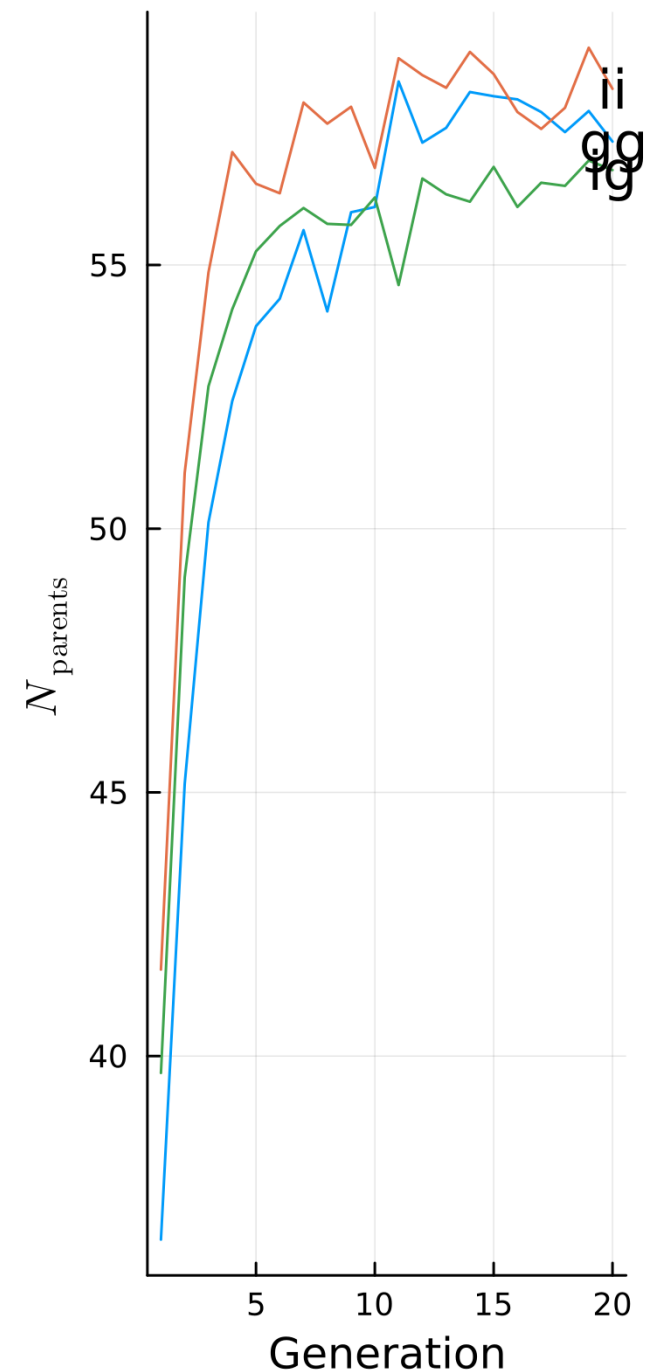
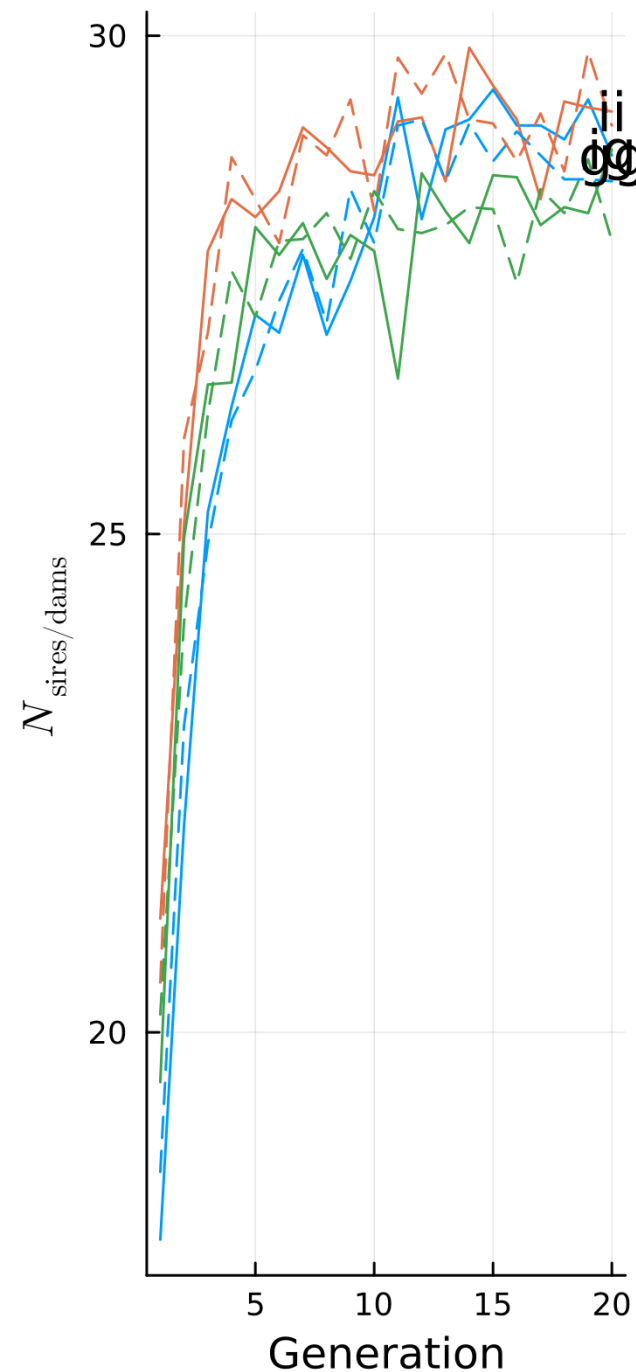
TBV improvements

- OCS schemes have greater ΔG
- They also have lower cost of genetic variance and inbreeding as shown later.



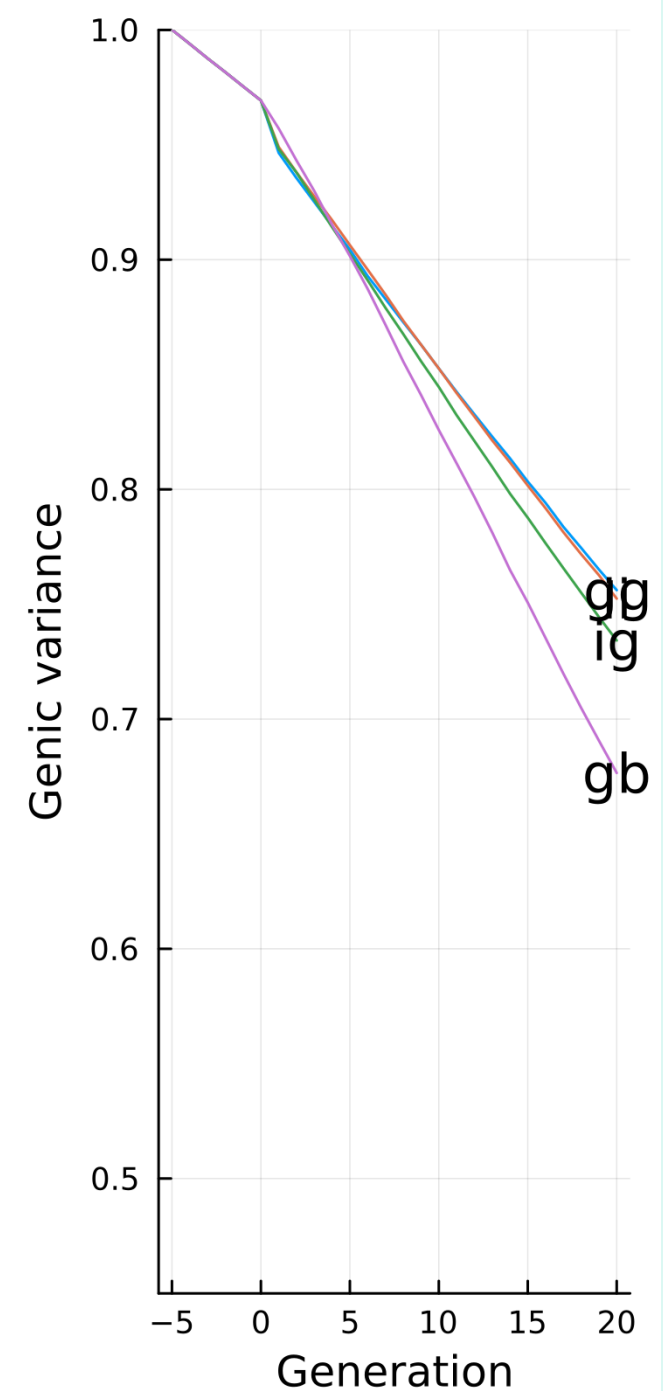
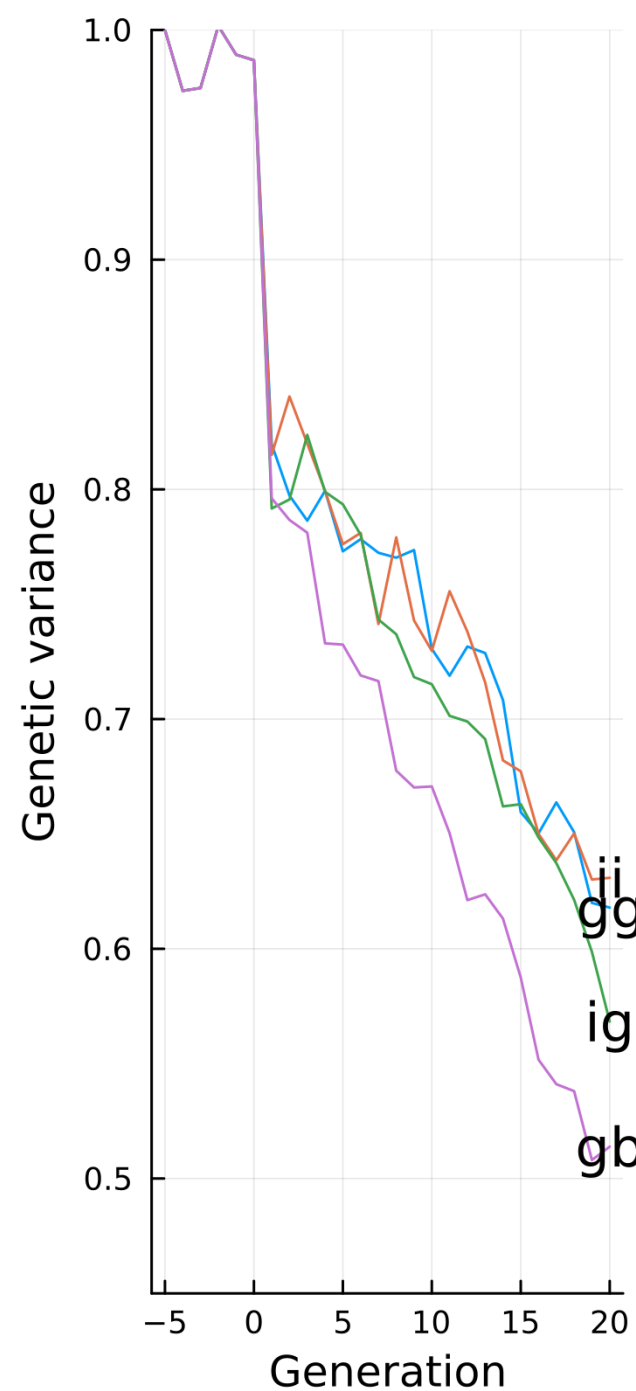
Number of parents

- Numbers are for the OCS scheme II-, GG-, and IG-.
- Solid lines are for sires
- Dash lines are for dams
- In random selection stages, and ordinary cull selection the number of sires is 25, that of dams is 50.



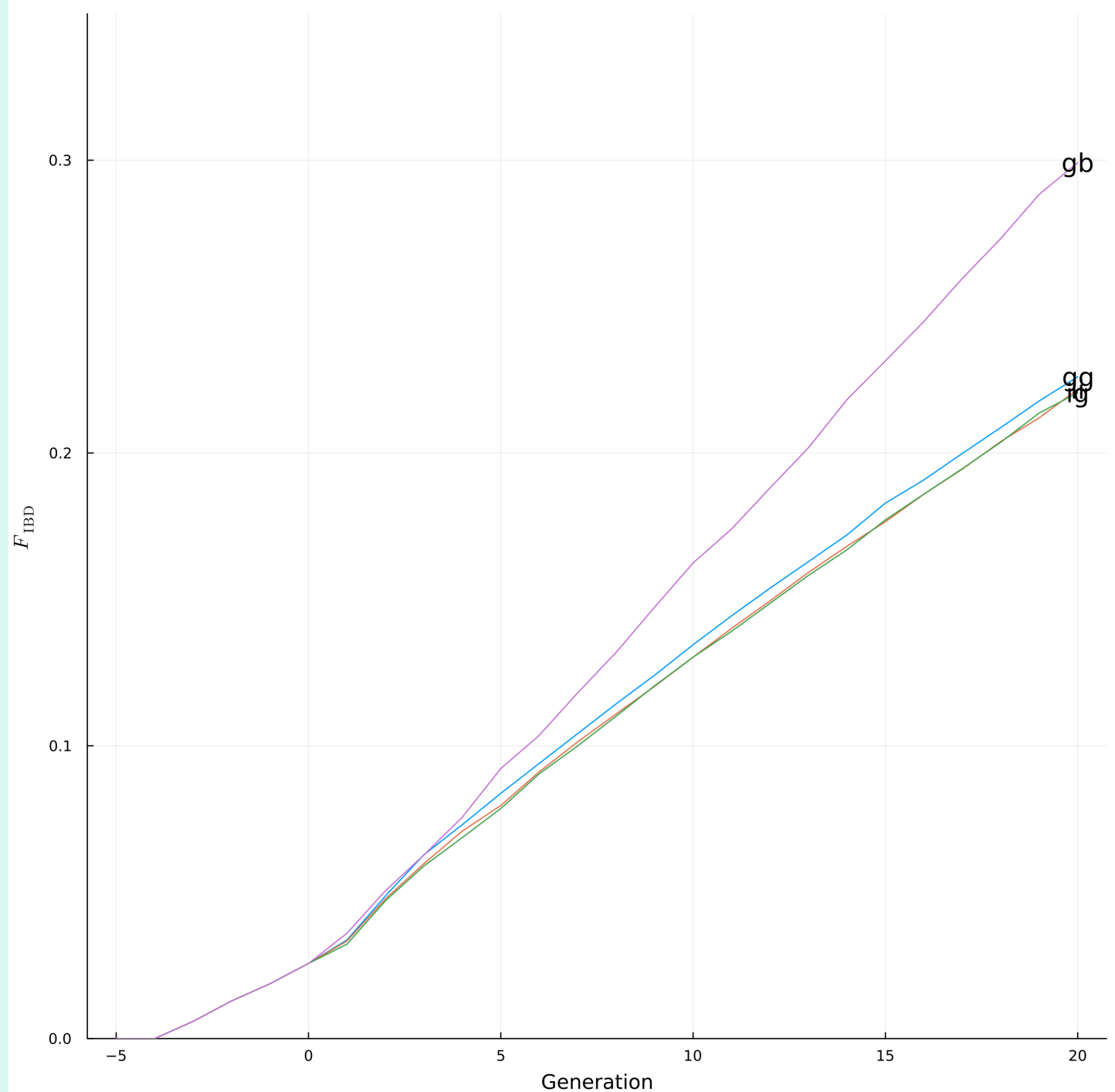
Genetic & genic var

- Genetic variance = $\text{Var}(\text{mean TBV})$
- Genic variance = $2 \sum_i p_i q_i a^2$



Mean inbreeding

- F-ibd, -grm, and -ped are from IRM, GRM and NRM, respectively
- F-het of t generation = $(H_0 - H_t) / H_0$
- Only F-IBD are shown here



Conclusions

- OCS schemes have higher genetic gain over non-OCS ones
- They (except AG-) have maintained more diversity
 - Higher ceiling, lower floor
 - More genetic/genic variance
 - Less allele fixation
 - Flatter QTL allele freq. distribution
- Selection without constraints (traditional methods) are not only slow
 - but also costly
- Constraints about ΔF may not be constant
- GGOCS is as good as IIOCS
 - The latter uses perfectly known relationships

We thank the RUMIGEN project supported by ERC



Thank you for your attention (<https://www.rumigen.eu>).