

EFFECT OF IMPUTED MARKER GENOTYPES ON ACCURACY OF GENOMIC BLUP IN AQUACULTURE-LIKE POPULATIONS

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GENOMIC BLUP, MARKER DENSITY AND THE GENOMIC MATRICES

Genomic BLUP (GBLUP) as the simplest form of Genomic Selection.

For the implementation of GBLUP (and Genomic Selection in General), it is required a large number of markers distributed across the genome.

In order to improve genomic estimates, methods to include phenotypes from ungenotyped individuals through pedigree have been developed

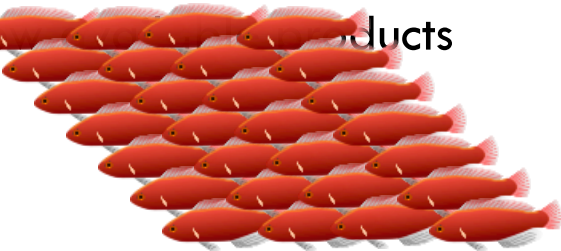
WHY TO IMPUTE?

Economical reasons

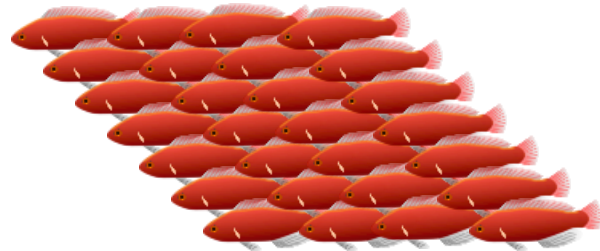
- Sparse genotypes cheaper than dense genotypes
- Increase the number of genotyped individuals

Technological reasons

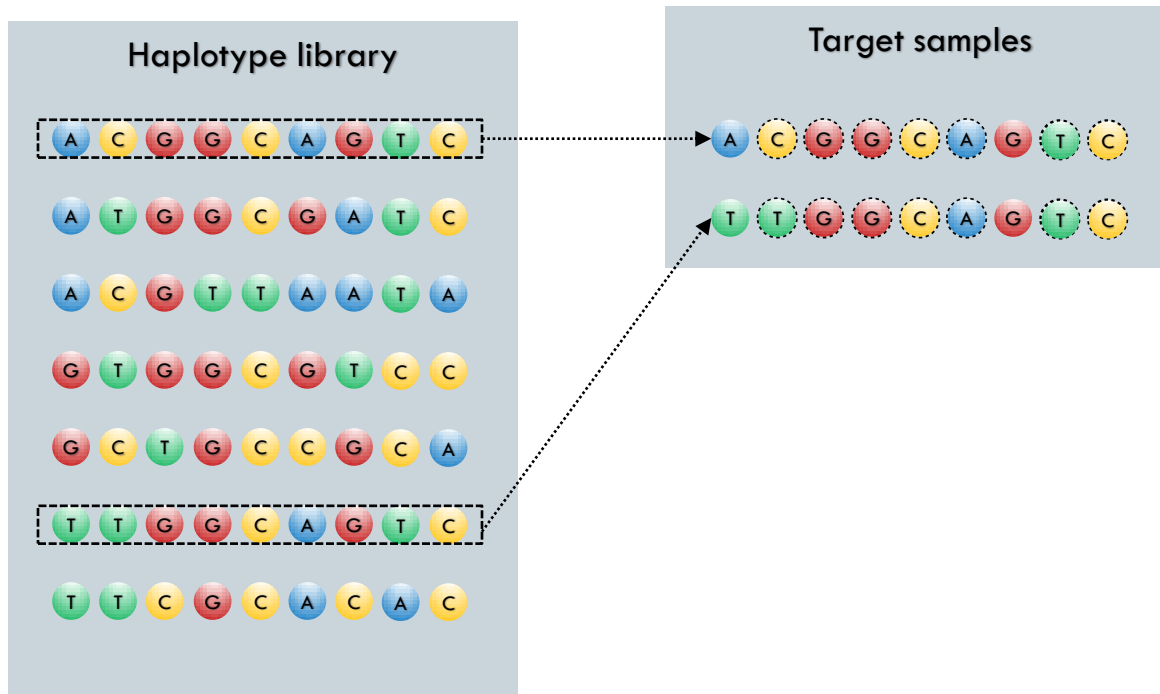
- Change of platform
- New products



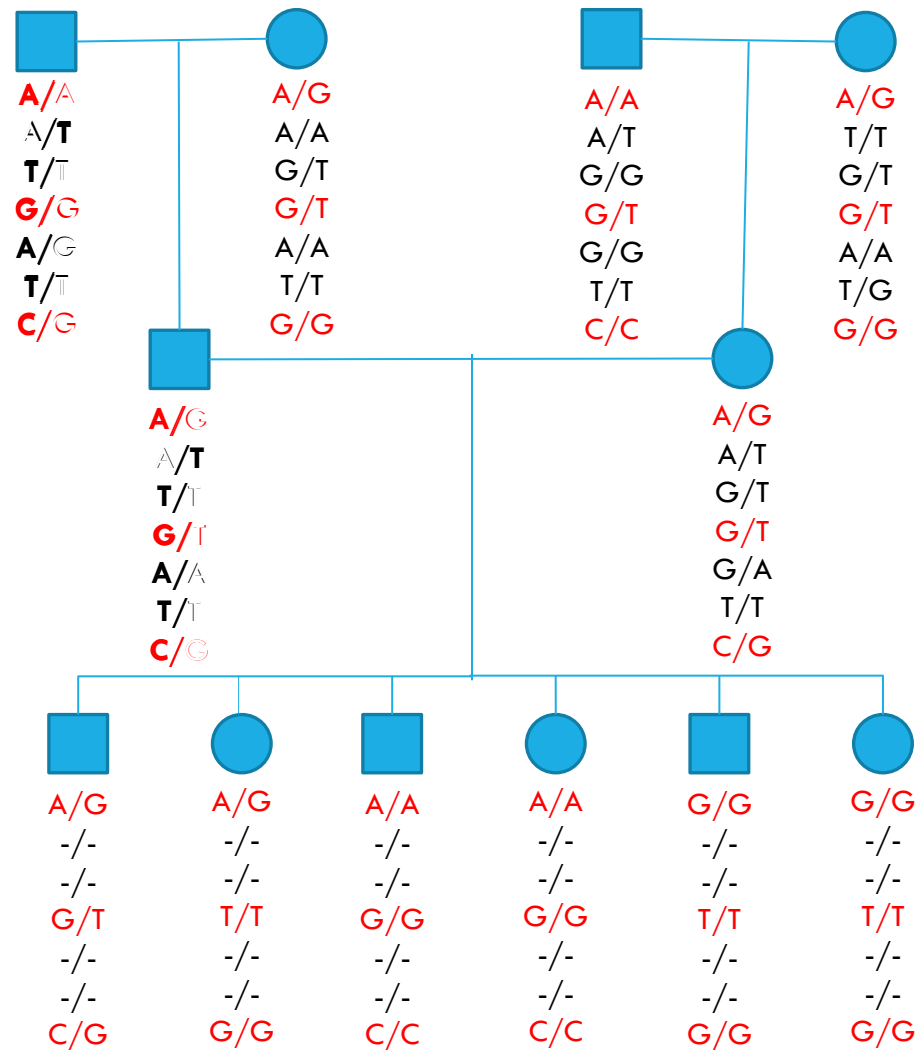
VS



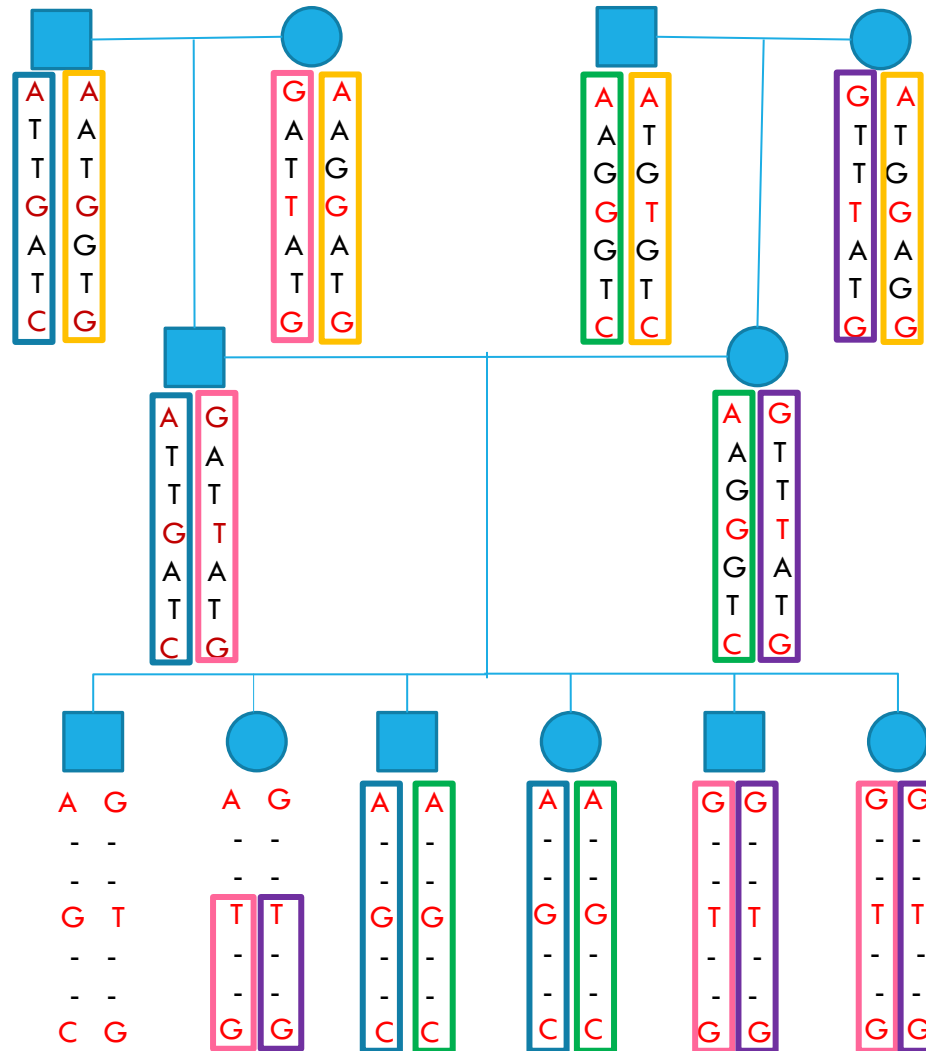
IMPUTATION: POPULATION-BASED METHODS



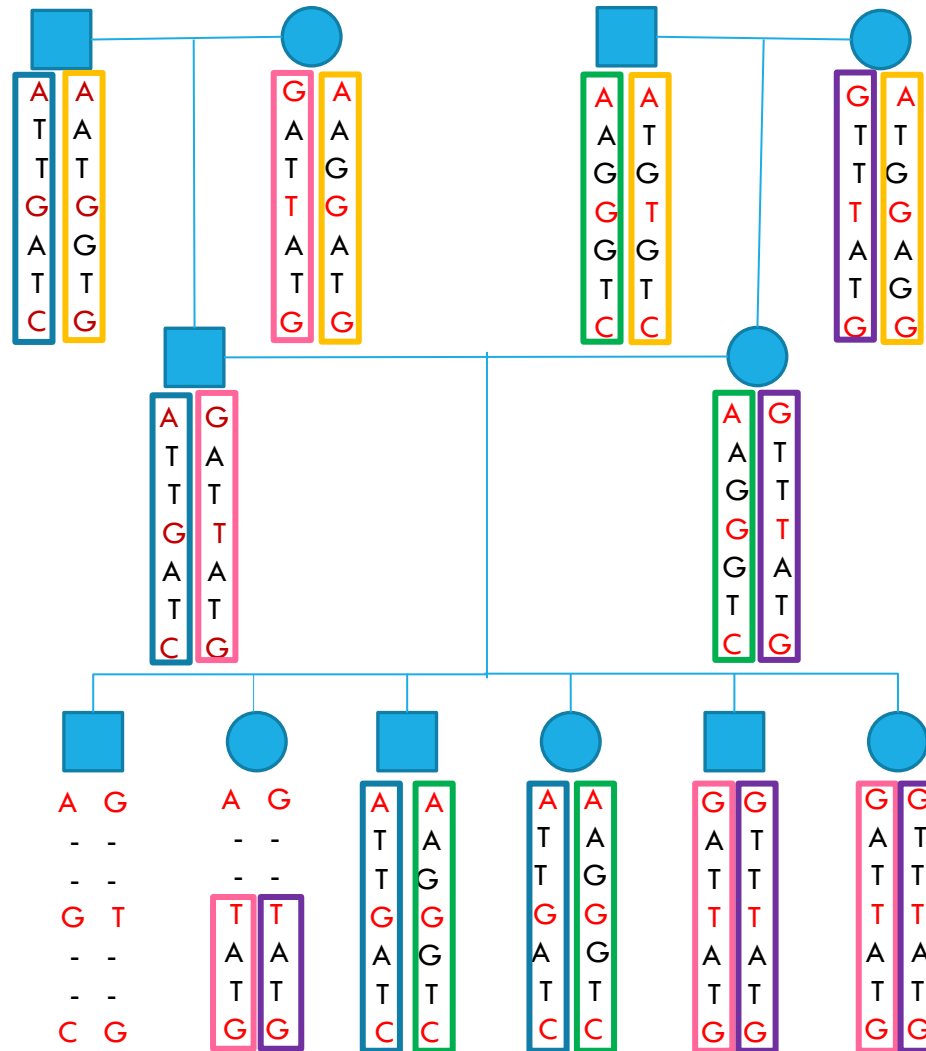
IMPUTATION FAMILY-BASED METHODS



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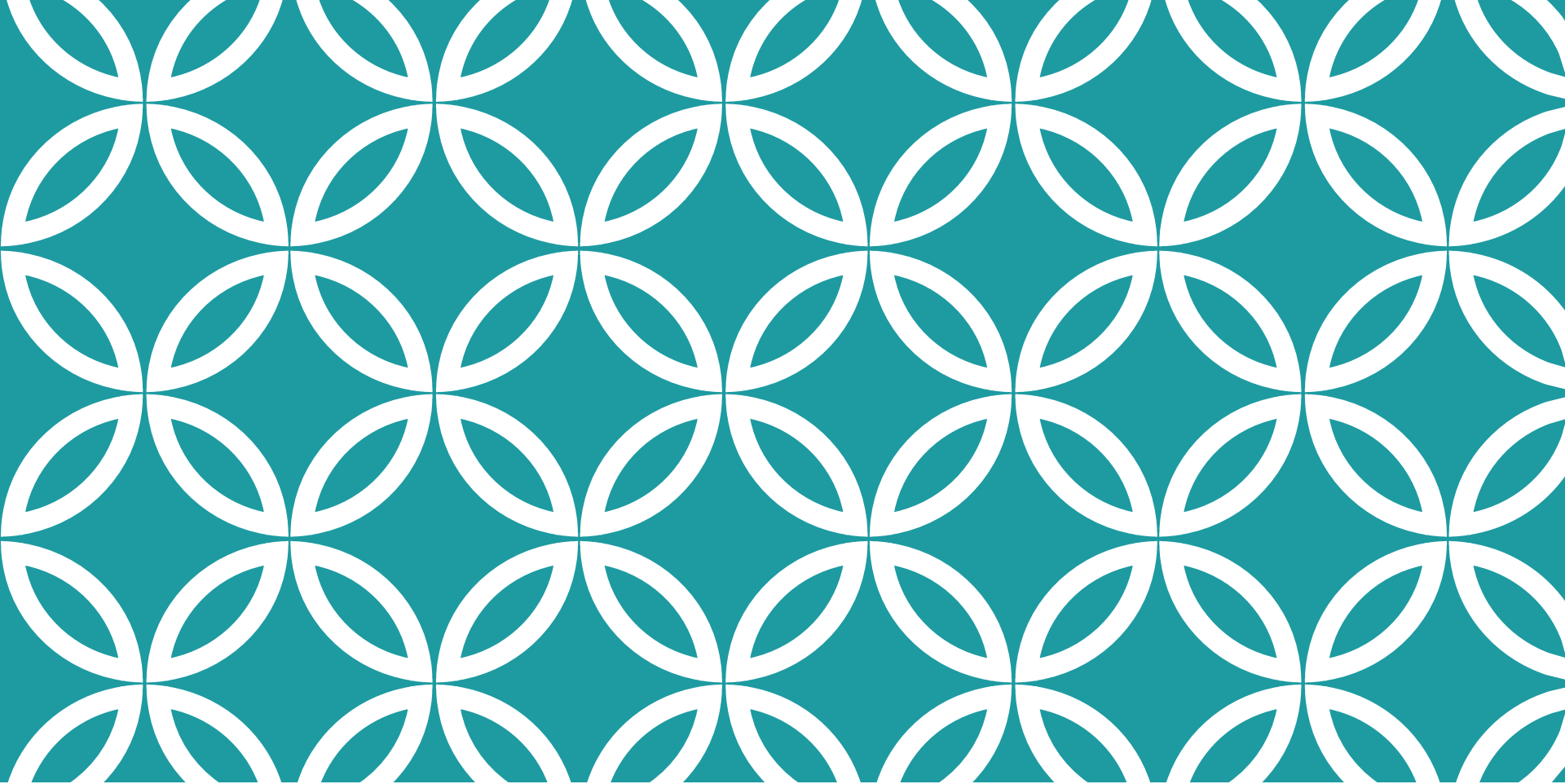


OBJECTIVE

To assess the effect of imputed genotypes in the accuracy of Genomic Estimated Breeding Values (GEBVs) under different scenarios by varying:

- Number of target (dense) markers
- Number of reference (sparse) markers
- Reference (dense genotyped) population

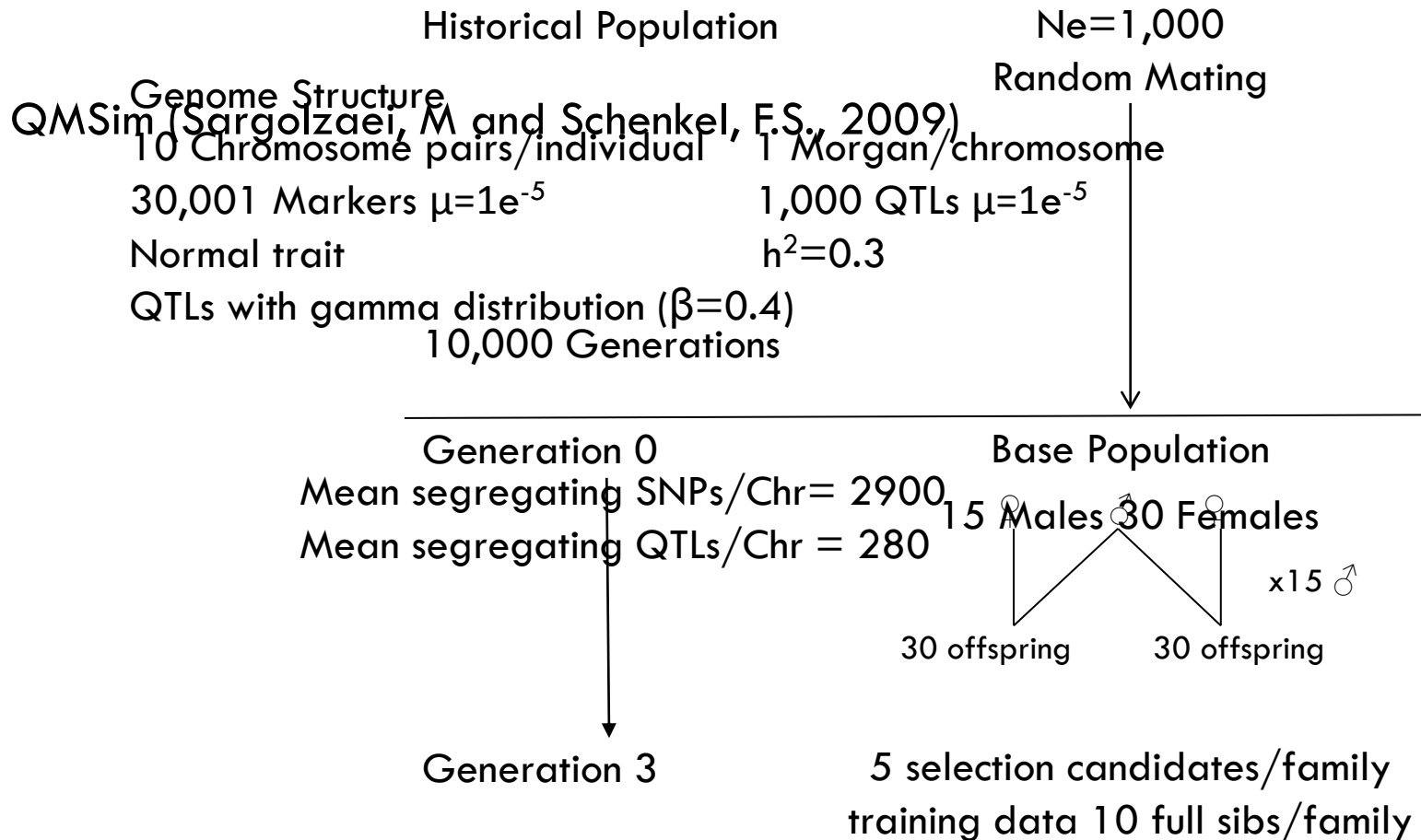
After imputation, to assess the effect of including phenotypes of ungenotyped relatives (full and half sibs of parents and grandparents) in the accuracy of GEBVs.



METHODS

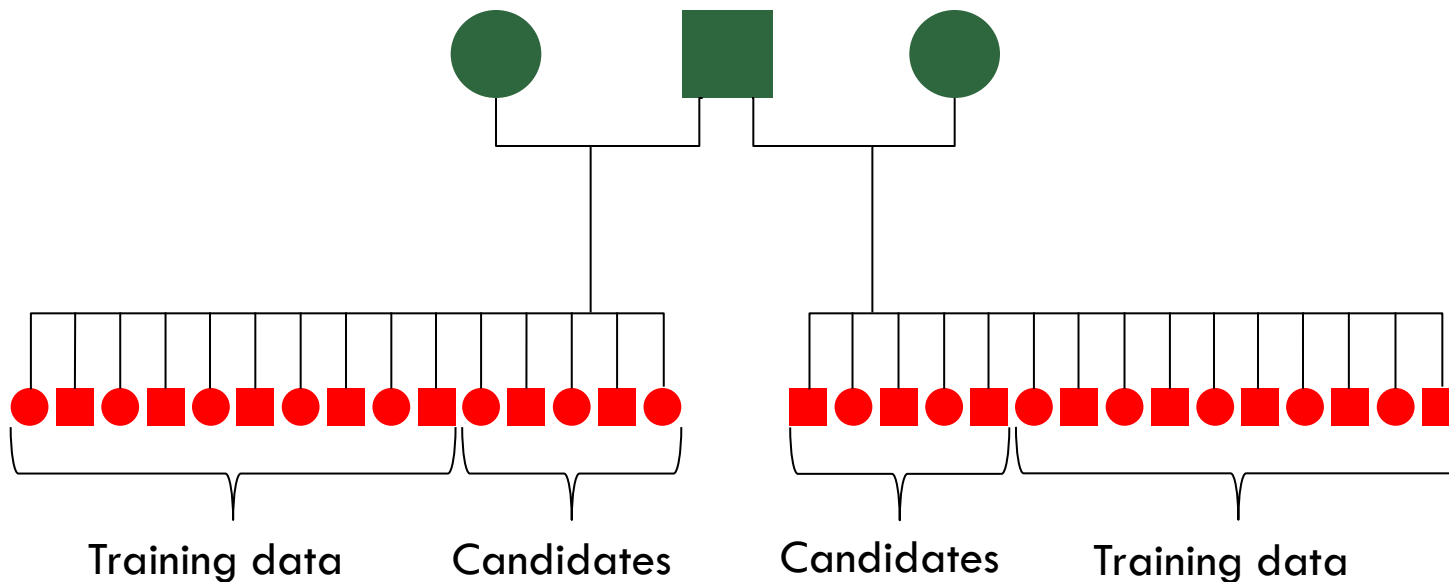




SIMULATED DATA



IMPUTATION: STRATEGIES

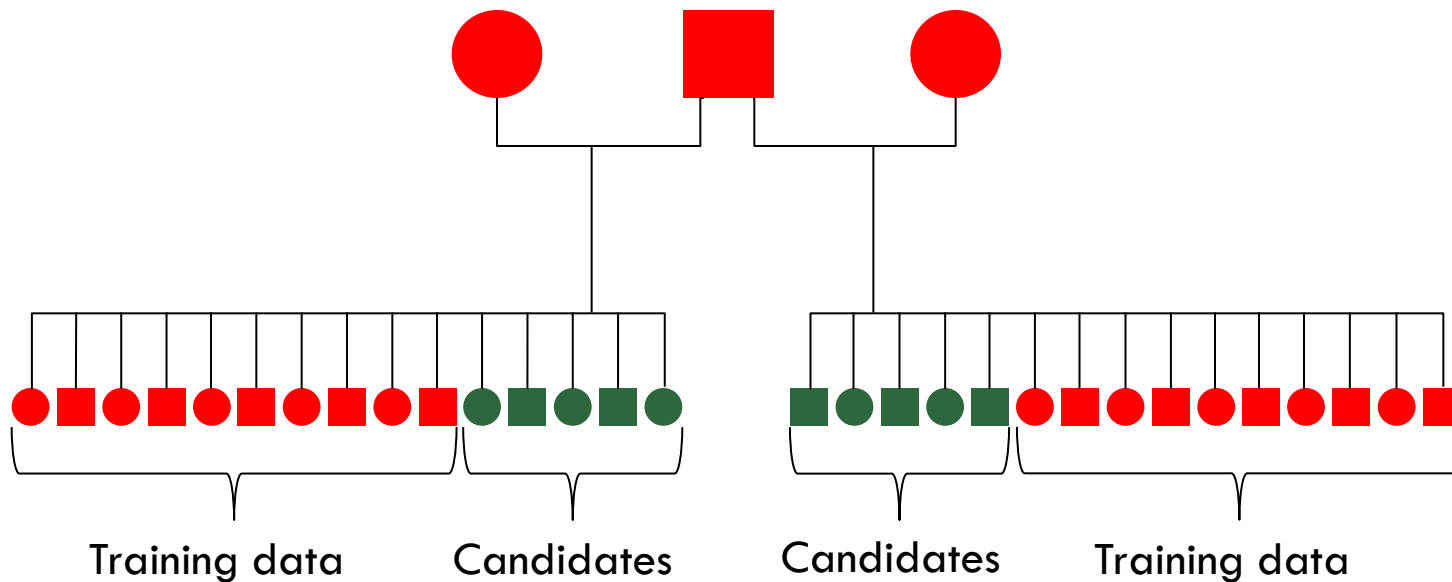
Imputing down the pedigree





-  Dense genotyped (reference individuals)
-  Sparse genotyped (target individuals)

IMPUTATION: STRATEGIES

Imputing up the pedigree



-  Dense genotyped (reference individuals)
-  Sparse genotyped (target individuals)

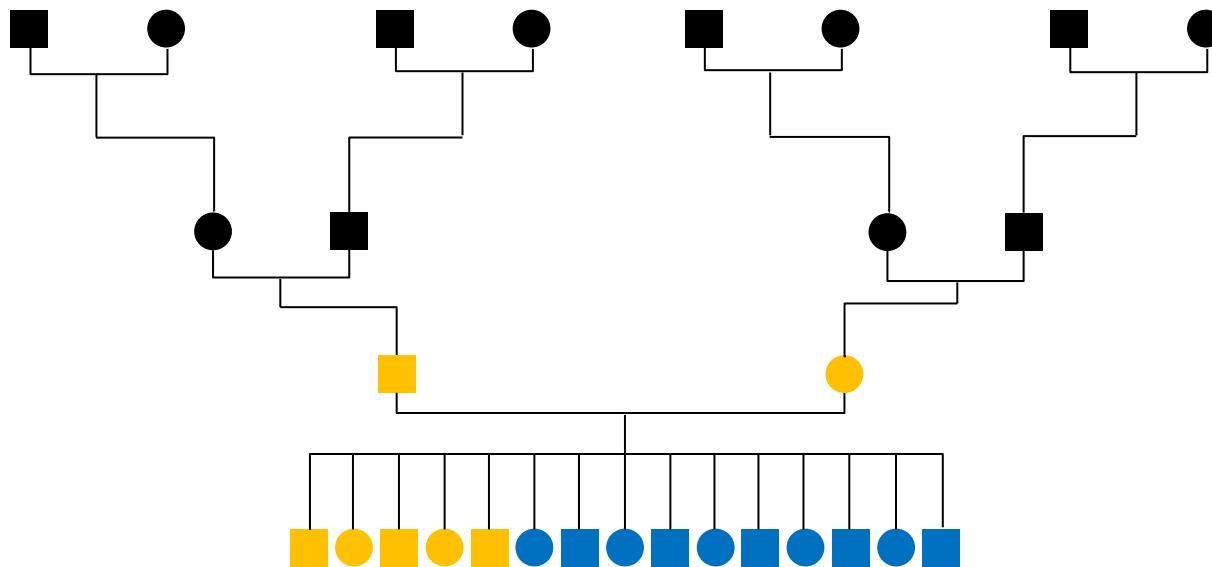
DENSITIES

All the imputations were made using one of the densities combinations as follow:

	Sparse	Target (Dense)
Density 10-950	10 SNPs/Morgan	~950 SNPs/Morgan
Density 10-2.9k	10 SNPs/Morgan	All Markers (~2900 SNPs/Morgan)
Density 100-950	100 SNPs/Morgan	~950 SNPs/Morgan
Density 100-2.9k	100 SNPs/Morgan	All Markers (~2900 SNPs/Morgan)

GENOMIC AND PHENOTYPIC DATA

Scenario 1

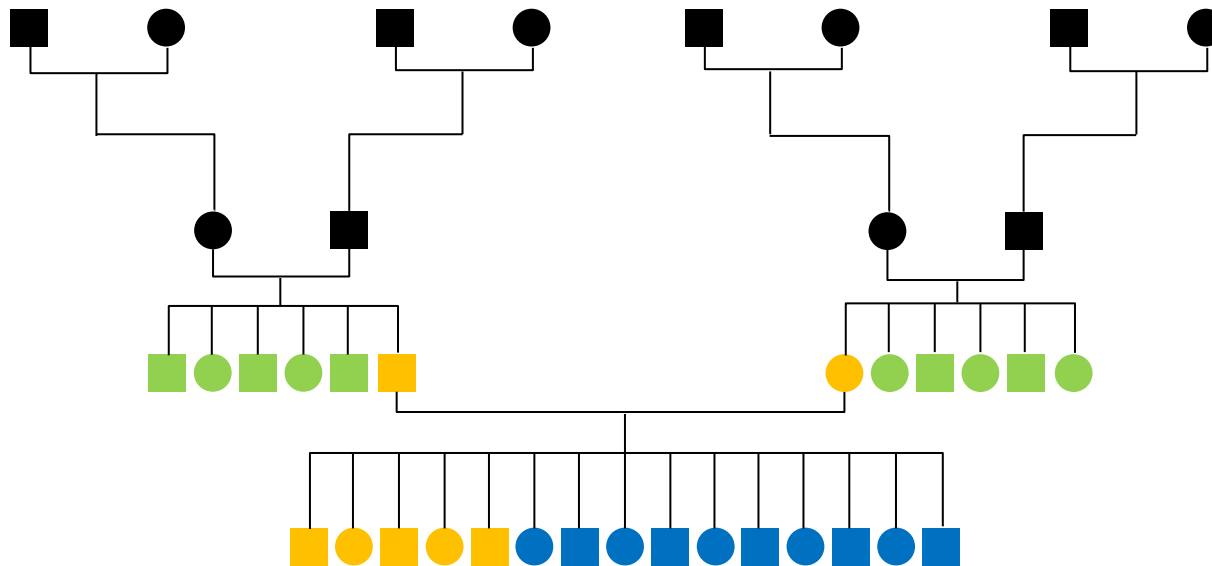


Phenotype
Genotype

No genotype or phenotype
Genotype + phenotype

GENOMIC AND PHENOTYPIC DATA

Scenario 2

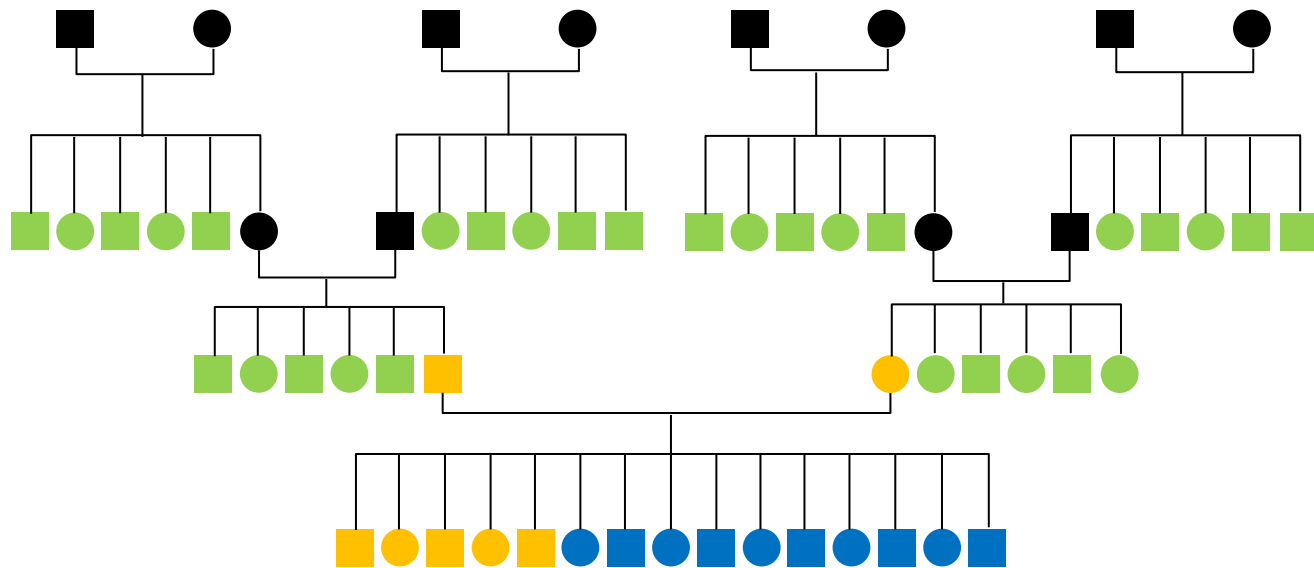


■ Phenotype
■ Genotype

■ No genotype or phenotype
■ Genotype + phenotype

GENOMIC AND PHENOTYPIC DATA

Scenario 3



■ Phenotype
■ Genotype

■ No genotype or phenotype
■ Genotype + phenotype

IMPUTATION: METHOD

Population-based method:

- Beagle V4 (S. R. Browning and B. L. Browning., 2007)

Family-based method:

- Fimpute (Sargolzaei et al., 2014)

Combined family-and population-based

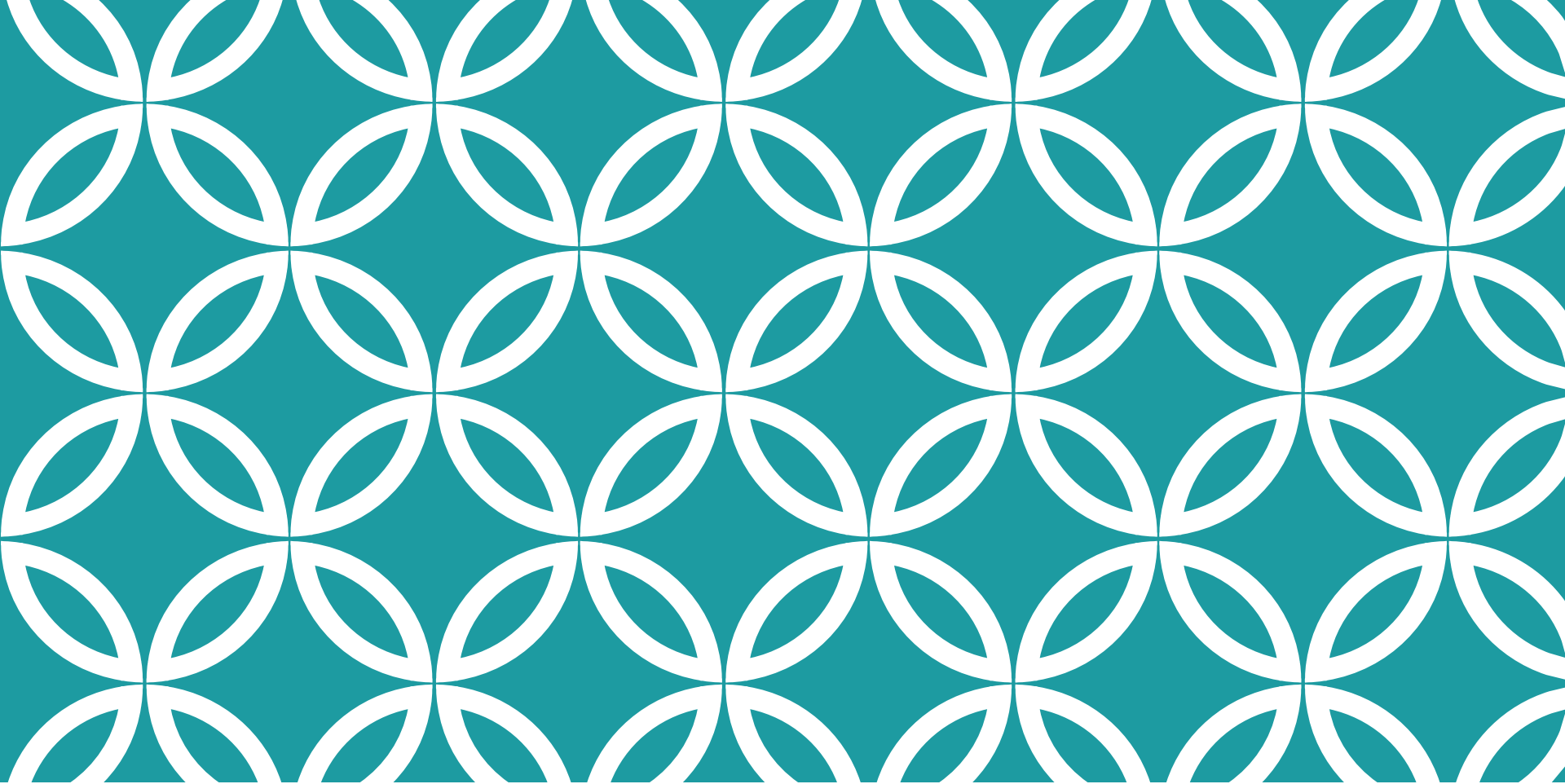
- AlphaImpute (Hickey et al., 2011)

GENOMIC RELATIONSHIP MATRICES AND GENOMIC BLUP

Genomic Relationships after imputation were constructed for each method using the software Gmatrix (version 2) (Guosheng Su and Per Madsen)

Genomic BLUP was carried out using DMU (version 6 release 5.2) (Per Madsen & Just Jensen). Genomic and Pedigree relationship matrices were merged using the PGMIX option in DMU in order to include phenotypic information from ungenotyped relatives from previous generations.

Accuracies of EBVs and G-EBVs were estimated as correlation between true (TBVs) and estimated breeding values (EBVs or G-EBVs)

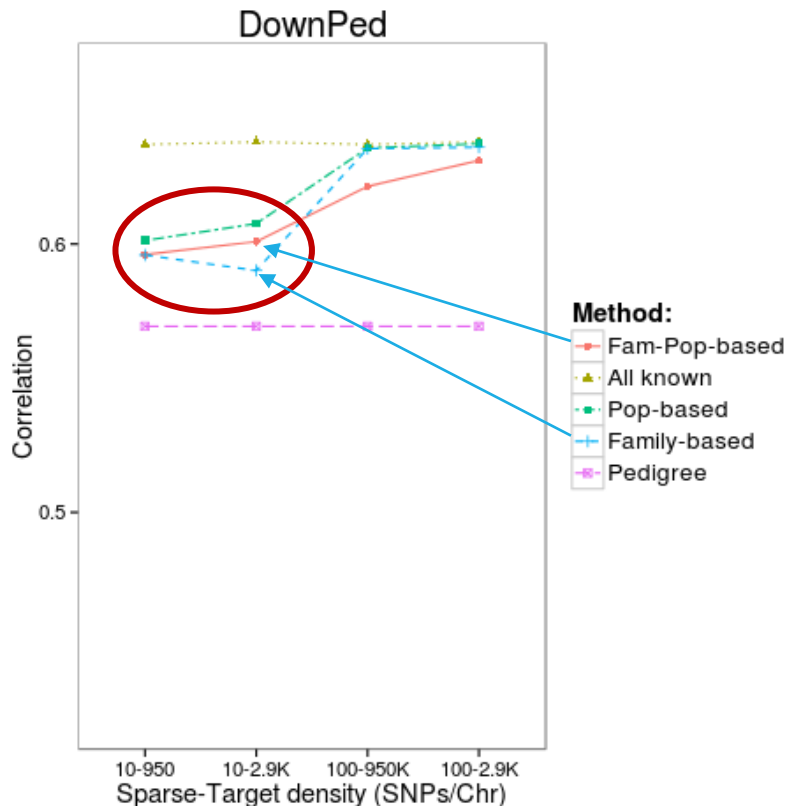


RESULTS



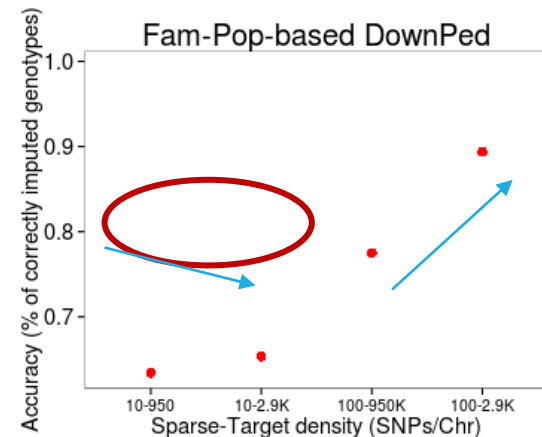
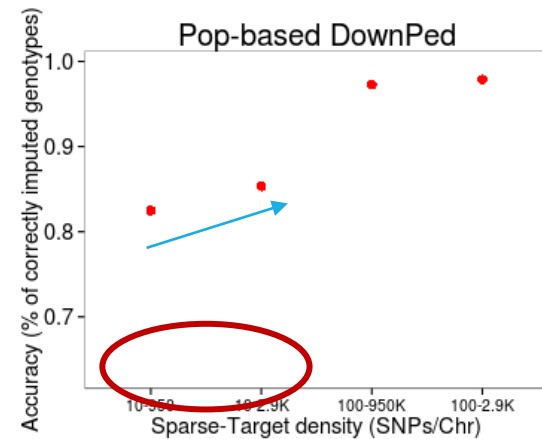
RESULTS IMPUTING DOWN THE PEDIGREE

G-EBVs accuracy

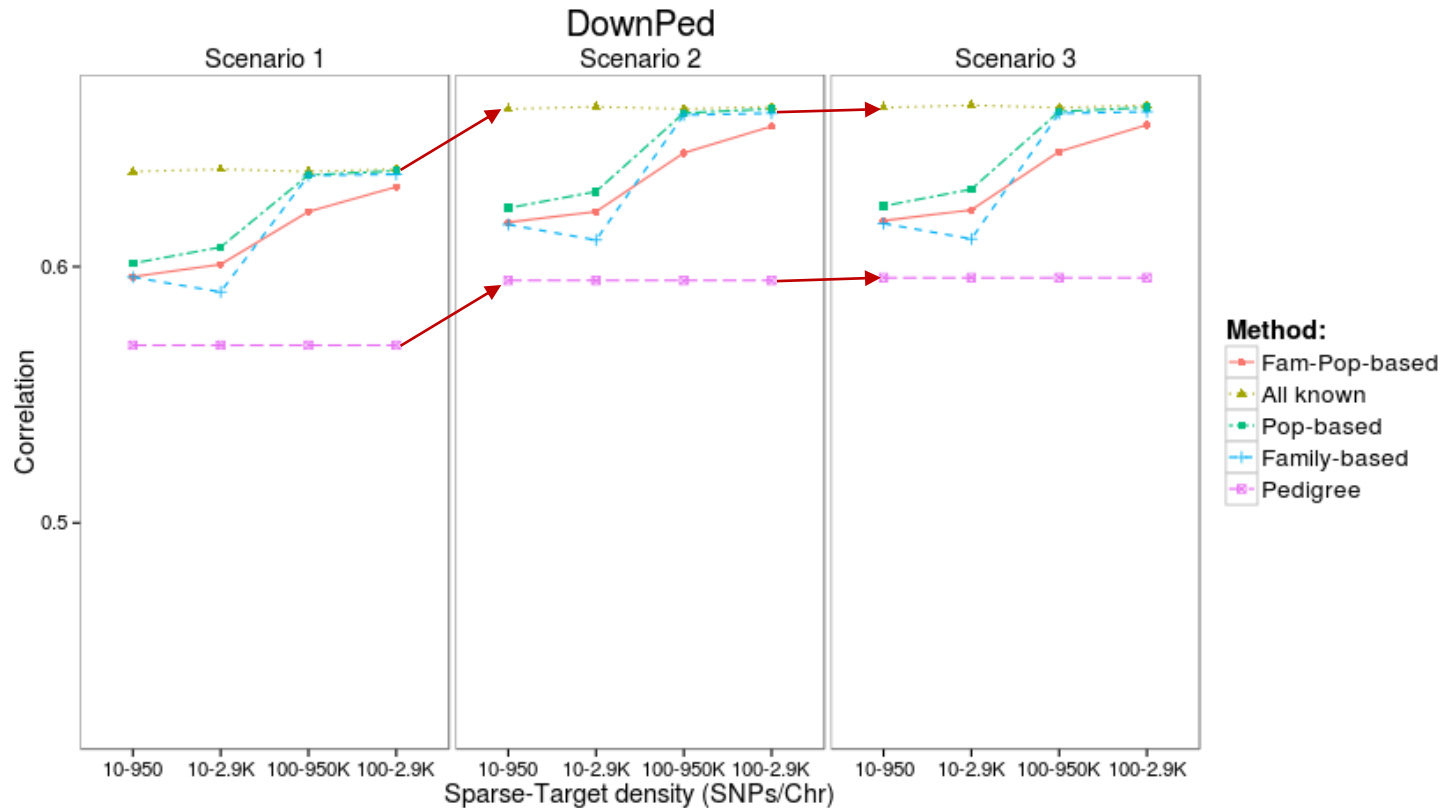


All methods better than traditional pedigree method

Imputation accuracy

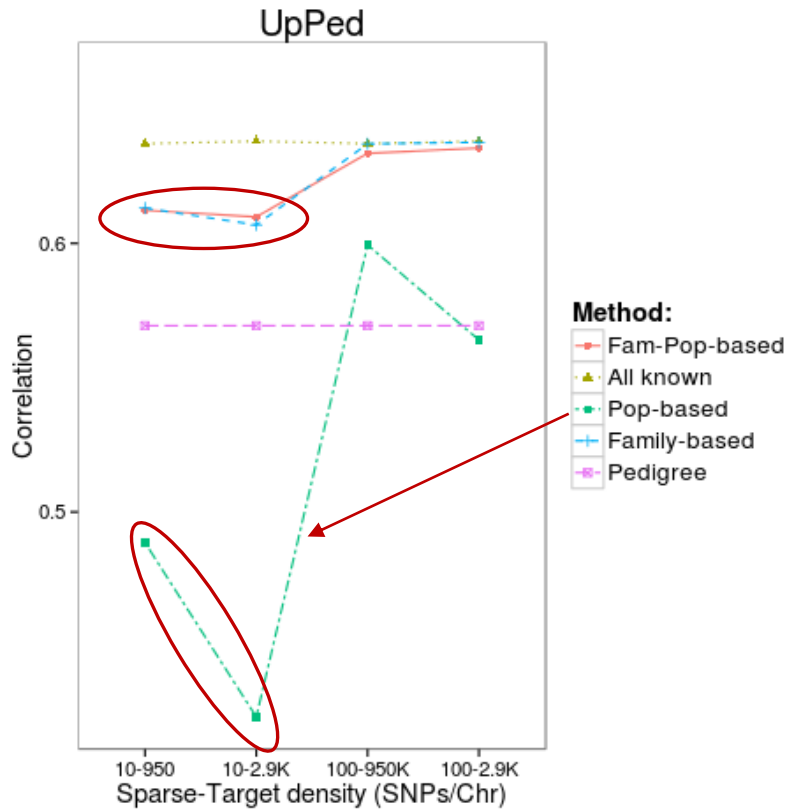


RESULTS IMPUTING DOWN THE PEDIGREE

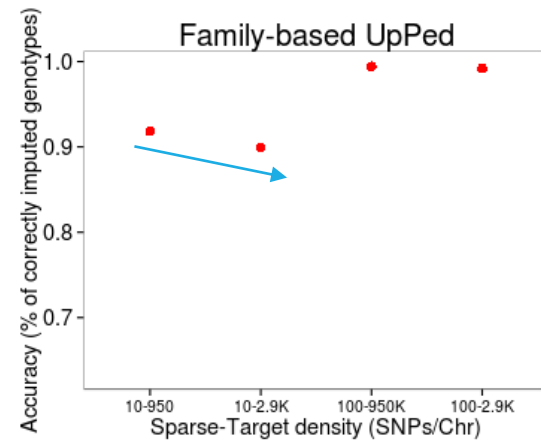
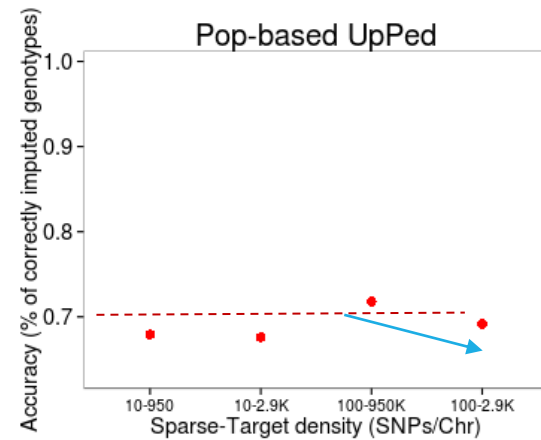


RESULTS IMPUTING UP THE PEDIGREE

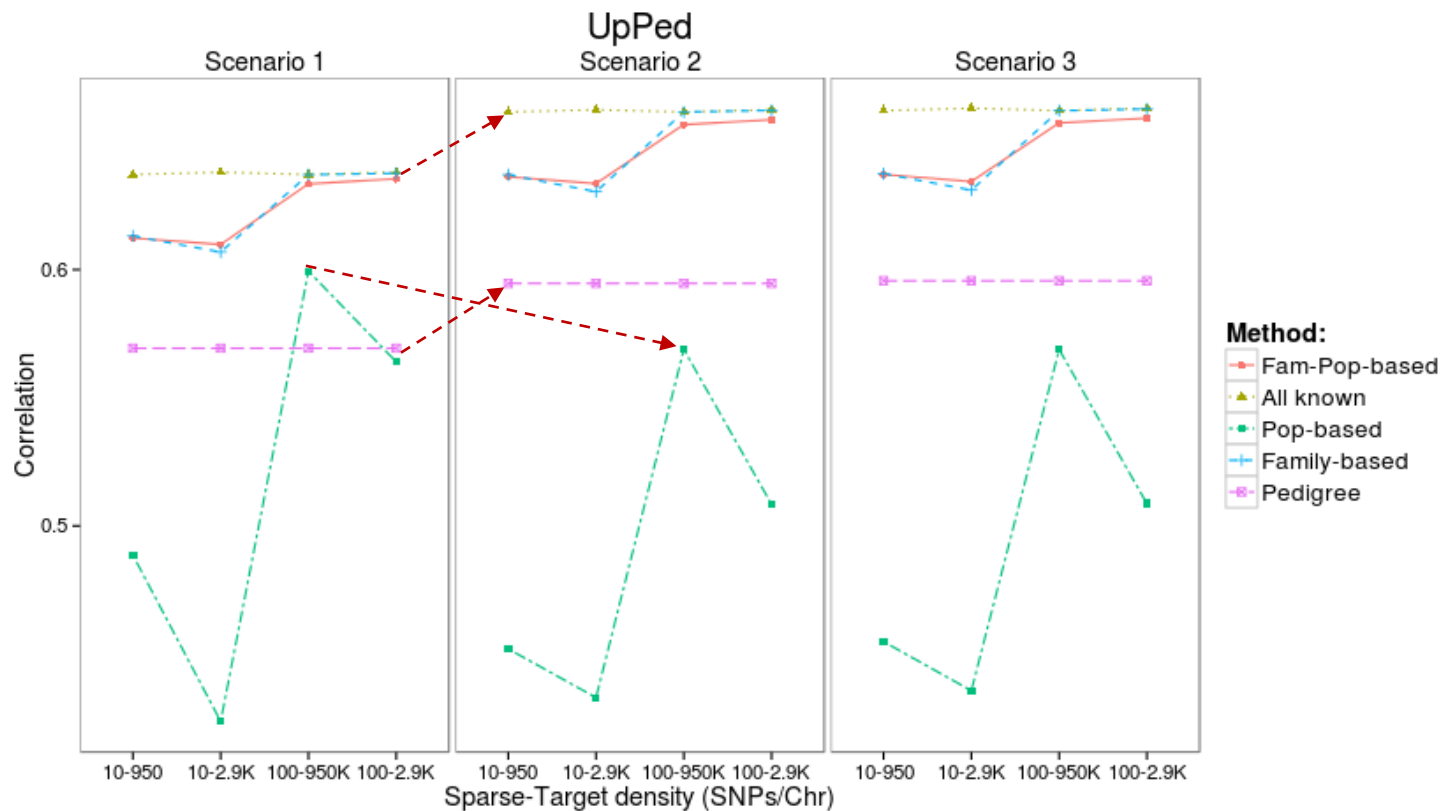
G-EBVs accuracy



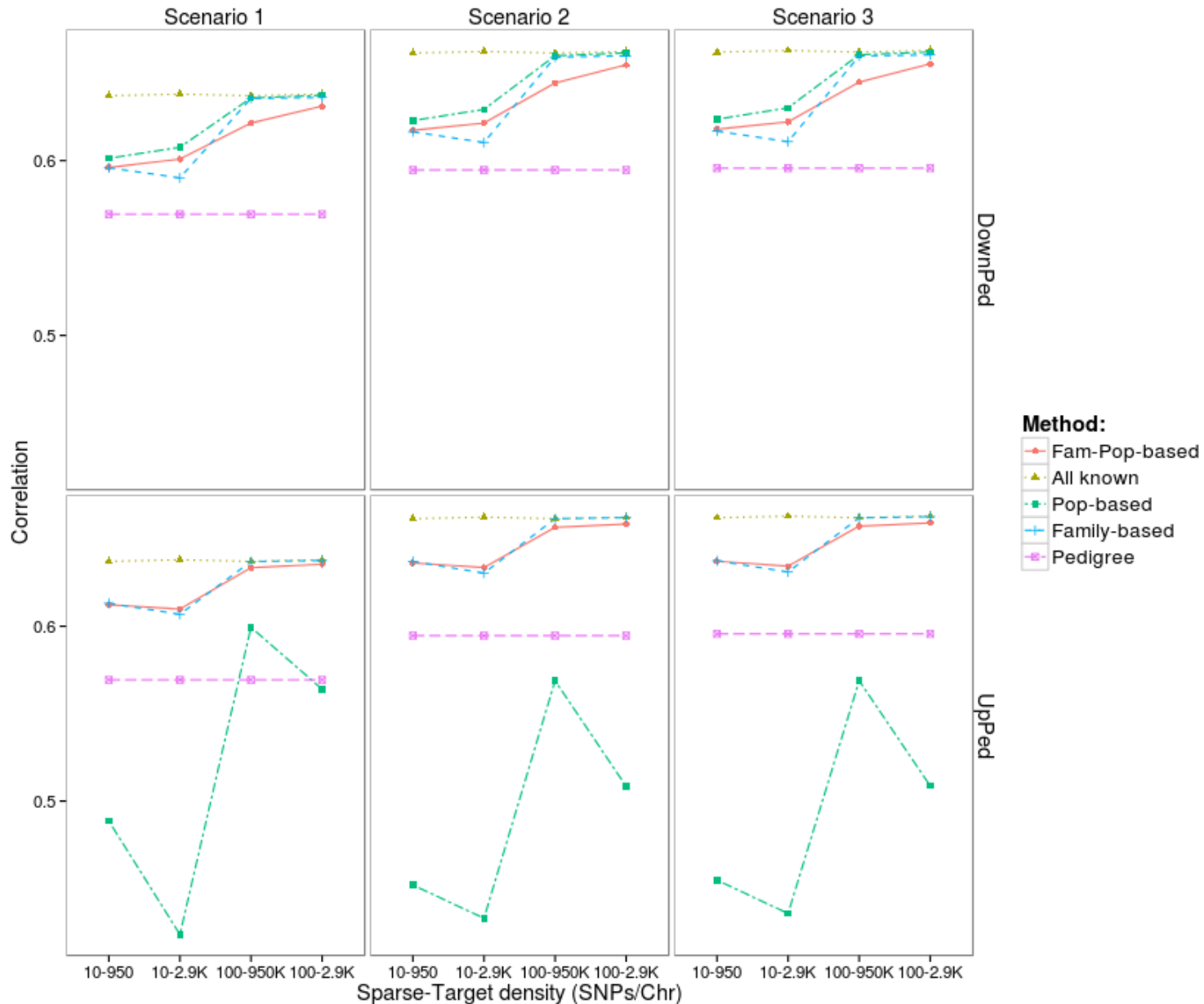
Imputation accuracy



RESULTS IMPUTING UP THE PEDIGREE



G-EBVS ACCURACY OVERVIEW



THANK YOU



0,00 K.M.