

Reconstruction of 777k SNP genotypes of founders using information from genotyped Progeny

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Objective

To reconstruct the 777k SNP genotypes of non-genotyped founders in a population

Results

Table 1. Imputation accuracy (% Correct call) using the whole population as done in conventional approaches

Flmpute	AlphaImpute
90.4 ± 4.3	89.1 ± 5.2

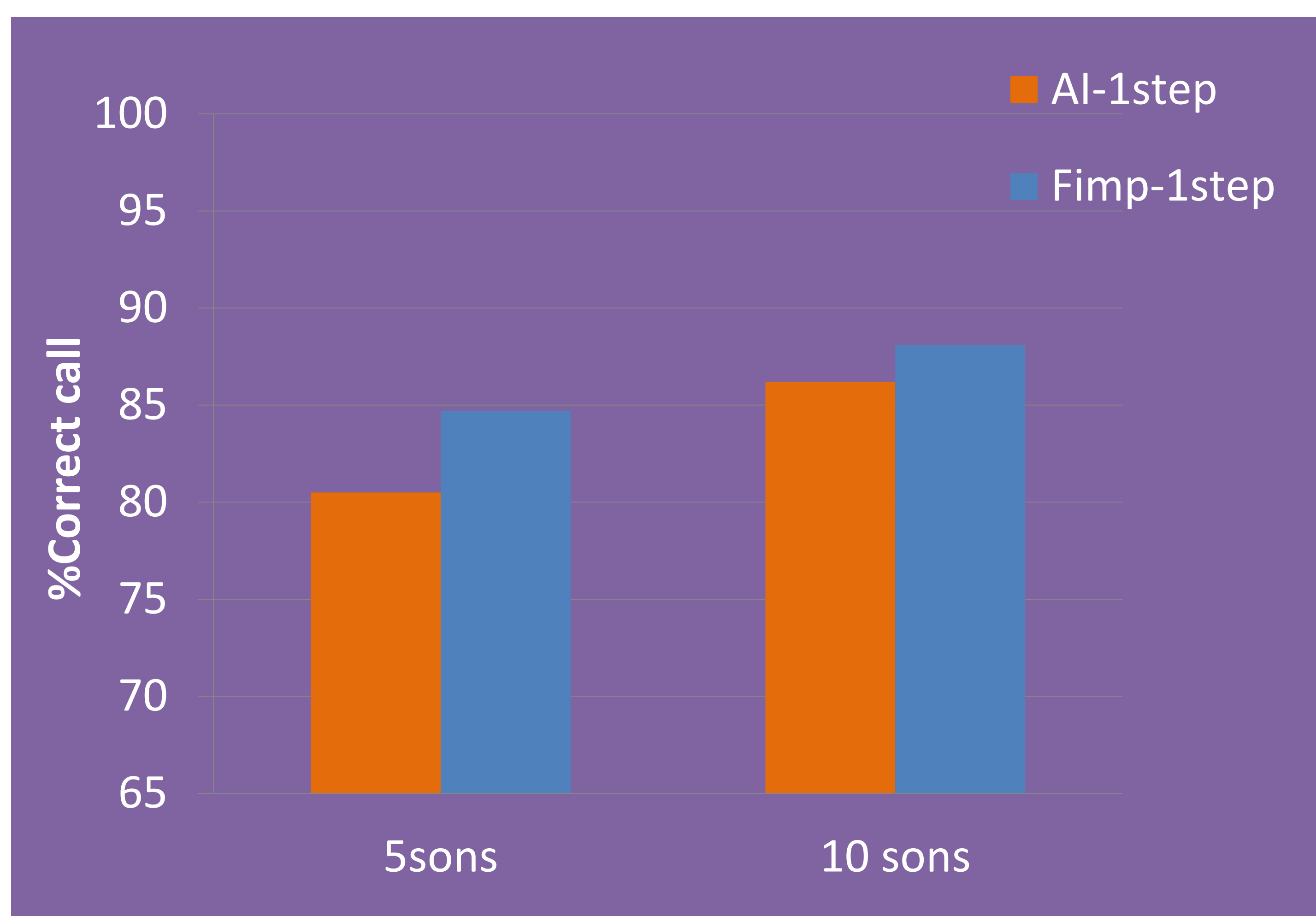


Figure 1. Accuracy of un-genotyped sires using single step approach

Background

Imputing founder genotypes that contribute to current population could be used for estimating identity-by-descent, genomic relationships and for imputing genomes of descendent

However some livestock population don't have access to genotypes of these important founders due to non availability of DNA samples and or lack of access to genotypes from other countries especially when sires are used in multiple countries

Conclusions

- ✓ 2-step imputation approach gives higher accuracies than using 1-step pedigree + population based and current conventional approaches
- ✓ Flmpute and MaCH gives higher accuracies compared to BEAGLE and AlphaImpute

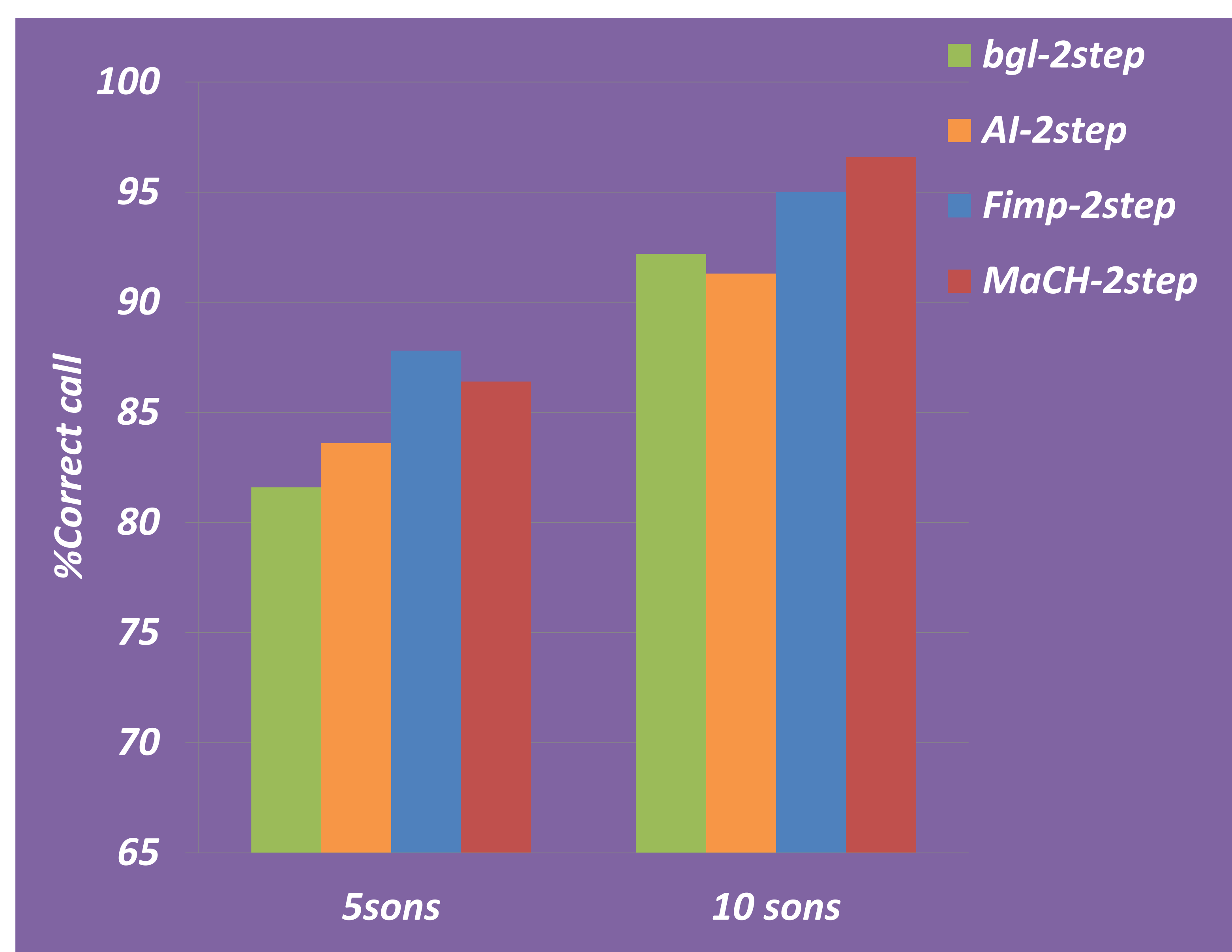


Figure 2. Accuracy of un-genotyped sires using proposed 2-step approach

Data and Methods

- 23 sires with 777k Bovine HD genotypes were masked as missing out of 996 sires of a Nelore population
- Reconstruct un-genotyped sire using 5 sons or 10 sons
- Impute un-genotyped sire with pedigree + population based methods; AlphaImpute and Flmpute (1-step approach)
- Impute un-genotyped sire in two steps (2-step approach)
 1. Only pedigree based method (MERLIN)
 2. Fill in the non-imputed part from step 1 with population based methods; BEAGLE (bgl), modified MaCH, Flmpute (Fimp), AlphaImpute (AI)

Accuracy of Imputation was calculated as % correctly called genotype