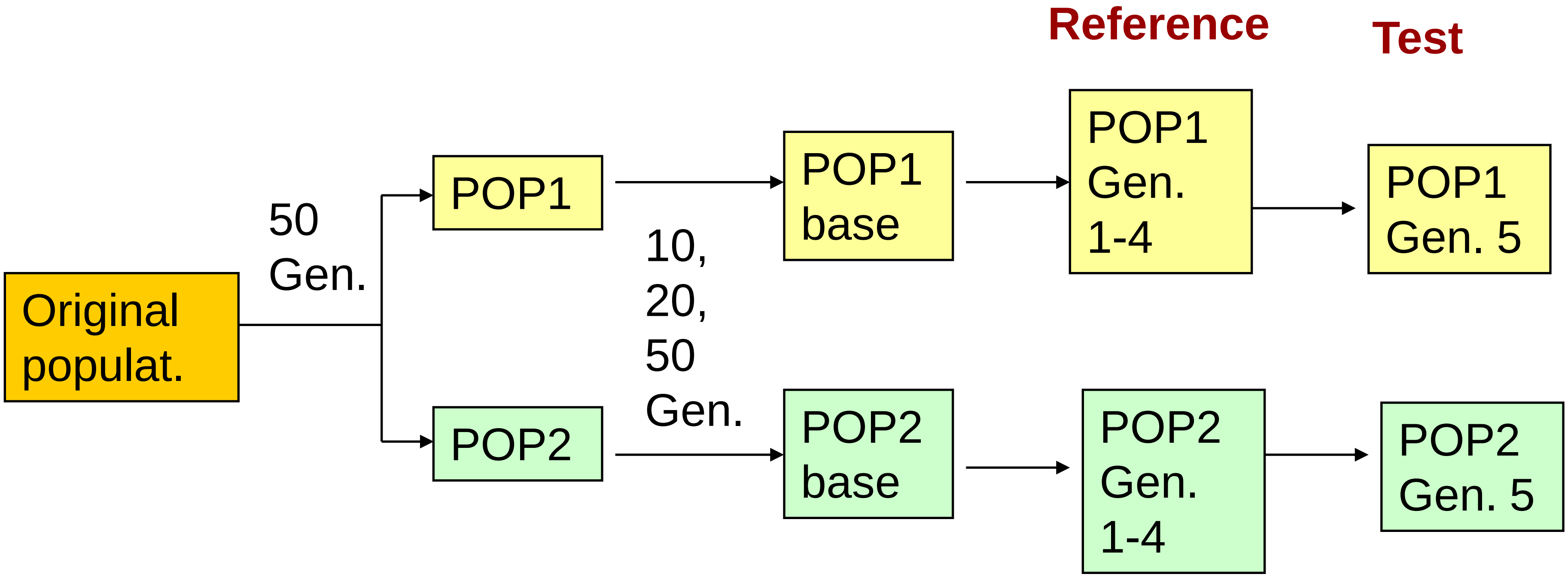
Nordic collaboration
Some of the work in 2010

Across breed GEBVs (simulations by Guosheng Su)



50 sires
50 dams

50 sires, 50 dams per gen.

500 sires, 25000 dams per gen.

Across breed GEBVs (simulations by Guosheng Su)

Reference	Pop 1	Pop 2	Pop1 + Pop 2
Test	Pop 1	Pop1	Pop1
10 generations	**0.70**	**0.44**	**0.77**
20 generations	**0.67**	**0.32**	**0.74**
50 generations	**0.69**	**0.13**	**0.75**

Across FAY/SRB/RDM GEBVs

- Higher accuracy due to larger reference
- Lower accuracy due to opposite phase
- Haplotype structure (within and between red breeds)
- Genomic model with haplotype effects
- IBD based models

Across Red/Jersey/HF GEBVs

- Potential Red/Jersey/Holstein reference of 21000 bulls

More SNPs (600K)

- Imputation by double genotyping some bulls
- Which and how many bulls to genotype with 600 K
- Biggest advantage for across breeds evaluations

Genomic multitrait models (Udder health)

- Genomic model directly on index - can we do better?
- Estimate SNP effects on component traits (multitrait)
- Value of indicator traits?
- Estimate SNP effects on clinical mastitis and blend with index?
- Comparison of multitrait methods (Bayesian vs. GBLUP)

Summary – another busy year

- Joint HF analyses (DSF / DEU / FR / NL)
- Blended GEBV
  - Method developments
  - Routine evaluations / Interbull
- Multi breed analyses
  - FAY/SRB/RDM
  - Red/Jersey/HF
- Dense SNP chips (600 K)
- Multi trait analyses
  - Method comparison
  - Udder health

Summary – another busy year

- What is the best cross validation method?
  - Compare different studies
  - Choose best method for future comparisons
- Breeding plans
- Genomic test day model (method development)
- QTL mapping