Bayes Cπ *vs* GBLUP, PLS regression, Sparse PLS and Elastic Net: Genomic Selection in French dairy cattle

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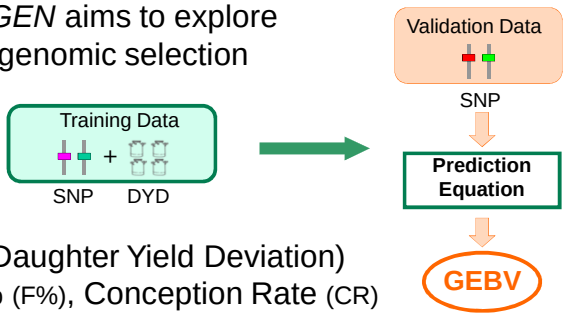
Introduction

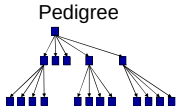
- ANR project *AMASGEN* aims to explore statistical methods of genomic selection



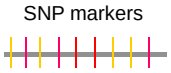
- Phenotypes: DYD (Daughter Yield Deviation) Milk Yield (MY), Fat % (F%), Conception Rate (CR)
- Two French dairy cattle breeds:

Number of bulls	Montbéliarde	Holstein
Training	950	2976
Validation	222	964

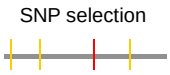
Information used in methods



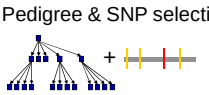
BLUP



GBLUP
PLS



Sparse PLS (sPLS)
Elastic Net (EN)
Bayes Cπ (BCπ M1)



Bayes Cπ (BCπ M2)

Conclusion

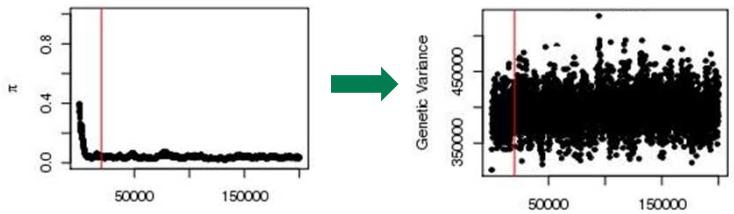
- Bayes Cπ and Elastic Net: better correlations of GEBV prediction than other methods
- Holstein: convergence quickly reached // Montbéliarde: π has to be fixed
- Pedigree information in Bayes Cπ: no increase of correlation nor regression slope

Results

Bayes Cπ M1

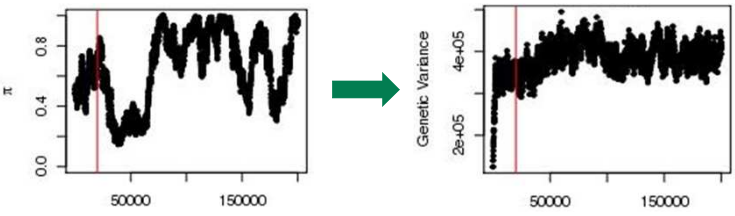
Estimation of π and genetic variance during MCMC algorithm for Milk Yield

- *Holstein*



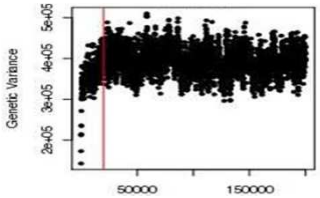
- Good convergence of π and genetic variance

- *Montbéliarde*



- π has to be fixed

π = 10%



- Similar results for F% and CR in both breeds

Bayes Cπ Models

Regression slopes b (s.e.) of observed DYD on GEBV

	Montbéliarde			Holstein		
	MY	**F%**	**CR**	**MY**	**F%**	**CR**
BCπ M1	0.74 (0.10)	0.85 (0.07)	1.35 (0.19)	0.73 (0.03)	0.90 (0.02)	0,72 (0.07)
BCπ M2	0.75 (0.10)	0.90 (0.08)	1.67 (0.26)	0.73 (0.03)	0.89 (0.02)	0.82 (0.07)

Comparison between methods

Correlations between observed DYD and GEBV

	Montbéliarde			Holstein		
	MY	**F%**	**CR**	**MY**	**F%**	**CR**
BLUP	0.28	0.40	0.43	0.38	0.44	0.28
GBLUP	0.42	0.52	0.47	0.56	0.72	**0.35**
PLS	0.44	0.58	0.43	0.53	0.70	0.33
sPLS	0.38	0.56	0.43	0.48	0.66	0.29
EN	**0.45**	0.59	**0.47**	**0.57**	**0.80**	0.33
BCπ M1	0.44	**0.62**	0.43	**0.57**	**0.80**	0.34
BCπ M2	0.44	**0.62**	0.44	**0.57**	0.78	0.34