

Accuracy of fine mapping methods on selected populations: a simulation study

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Purpose of the study

- Factors influencing LD
 - Mutation
 - Random drift
 - Selection
- LD at larger distances in animal populations
- Sensitivity of the fine mapping methods to selection ?

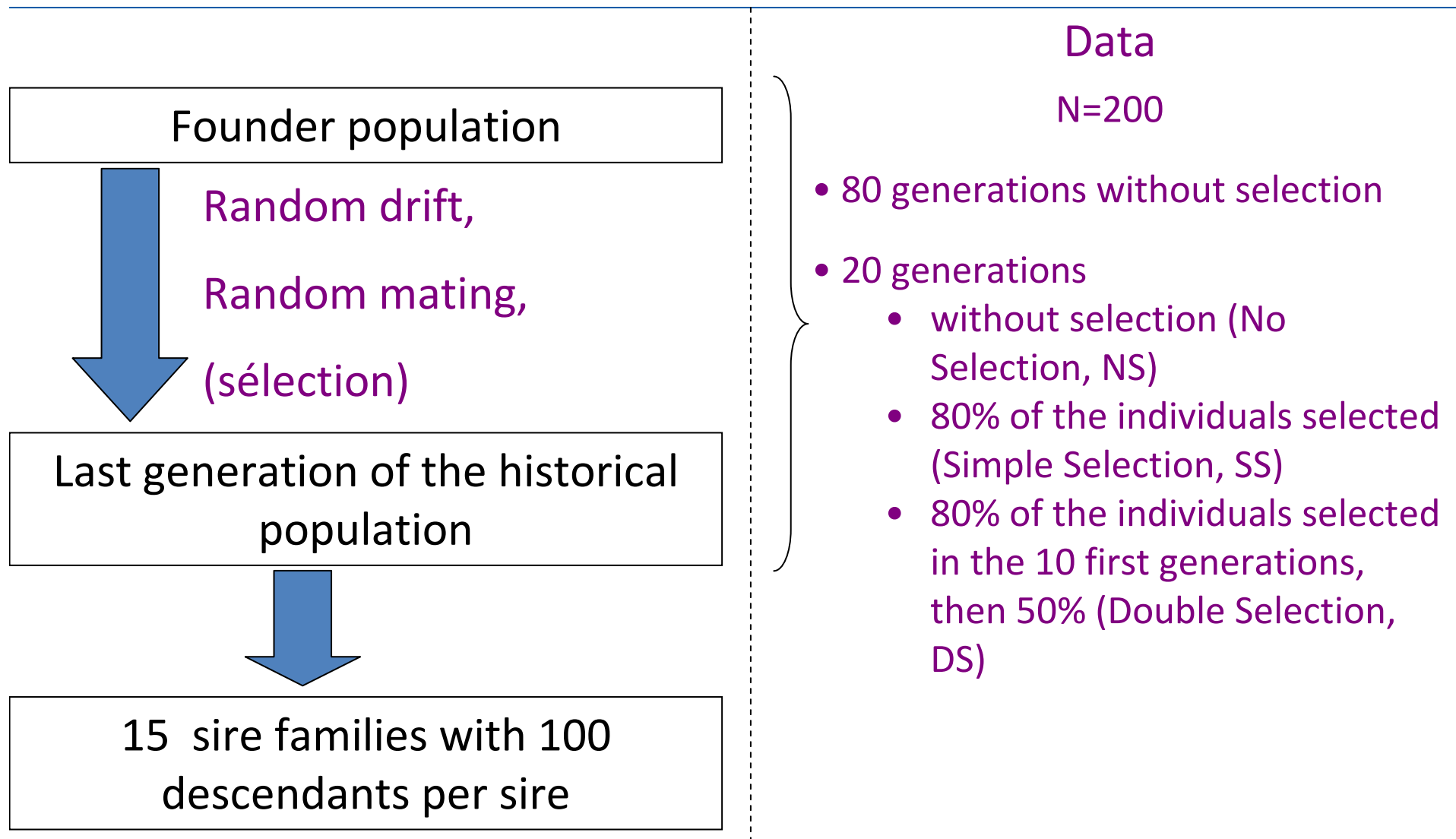
Methods

	Regression	HapIM	Terwilliger	LDLA	Cluster
Accounting for LD through ...	-	Decrease of LD with the distance		IBD probabilities	
Use of the pedigree	No	No		Yes	
Supposed origin of LD	-	Unique causal mutation		Initial population in LE	
Statistical method	Regression	Maximum likelihood		Variance components	Regression
Molecular information used	Single markers	Haplotypes of 2 markers		Haplotypes of 4 markers	

Clustering method

- Clustering applied on IBD probabilities (Meuwissen and Goddard, 2001)
- Previously shown that no constant threshold for optimal clustering (Ytournal *et al*, 2007)
→ choice of a fuzzy clustering algorithm

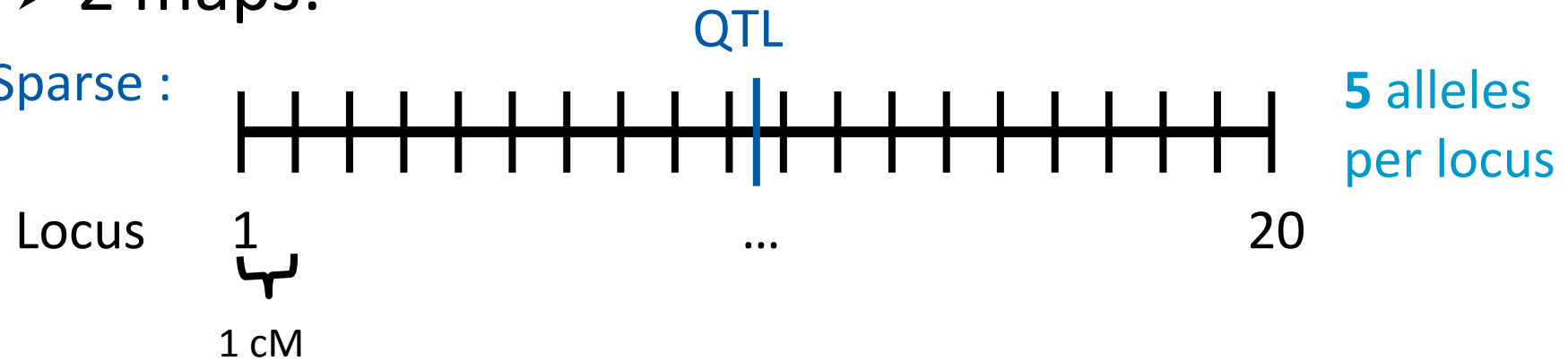
Simulated populations



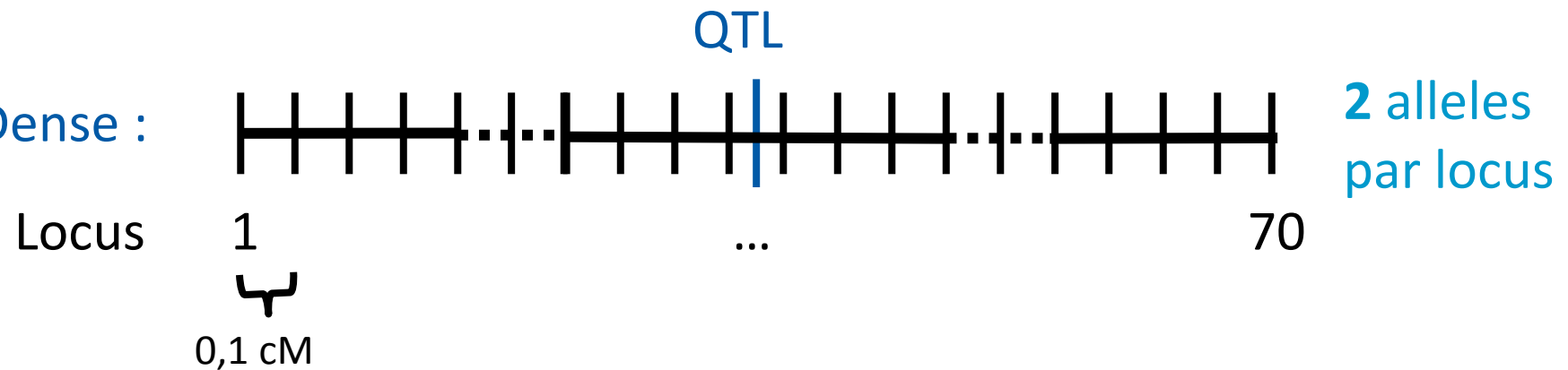
Genetic maps

➤ 2 maps:

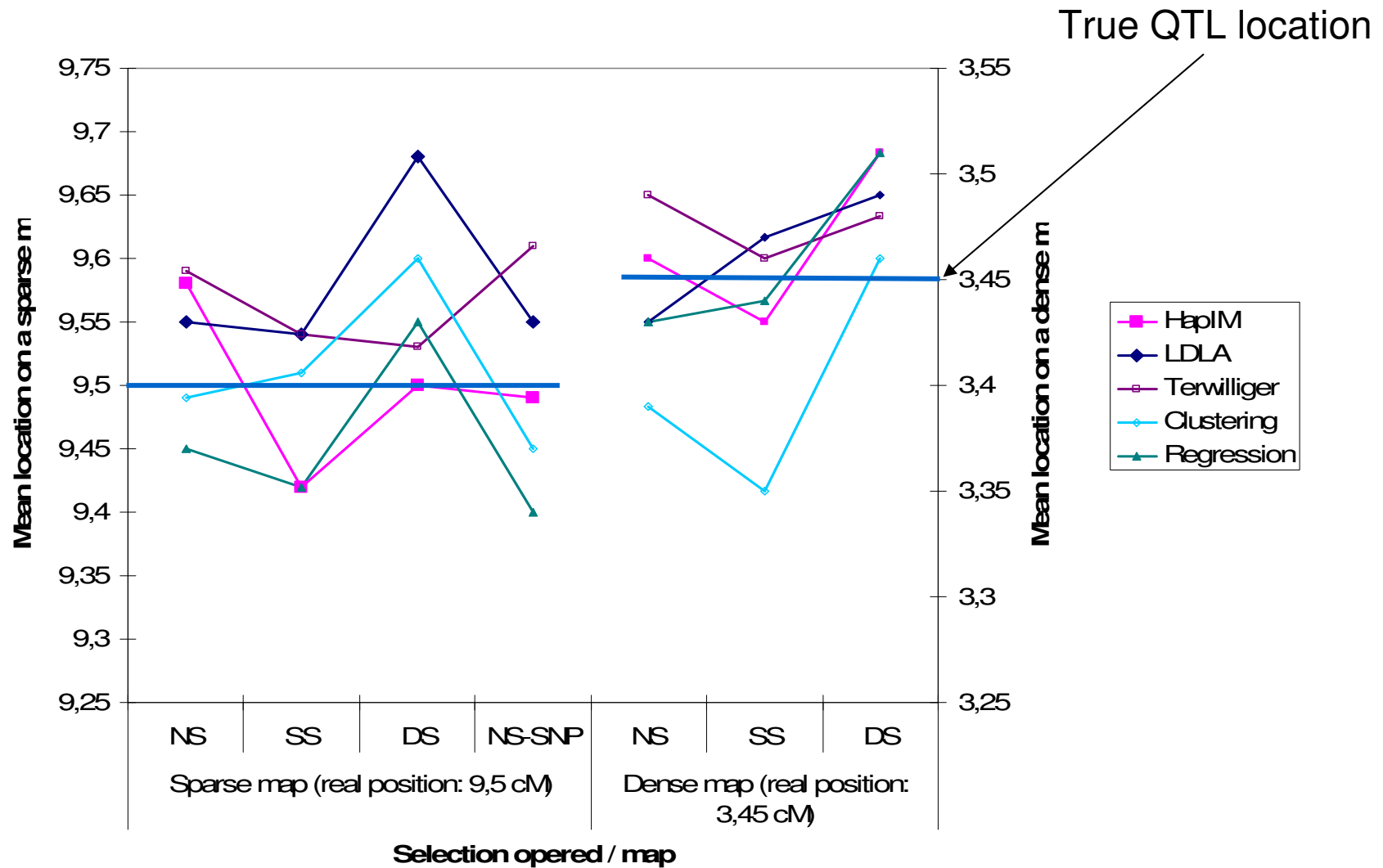
- Sparse :



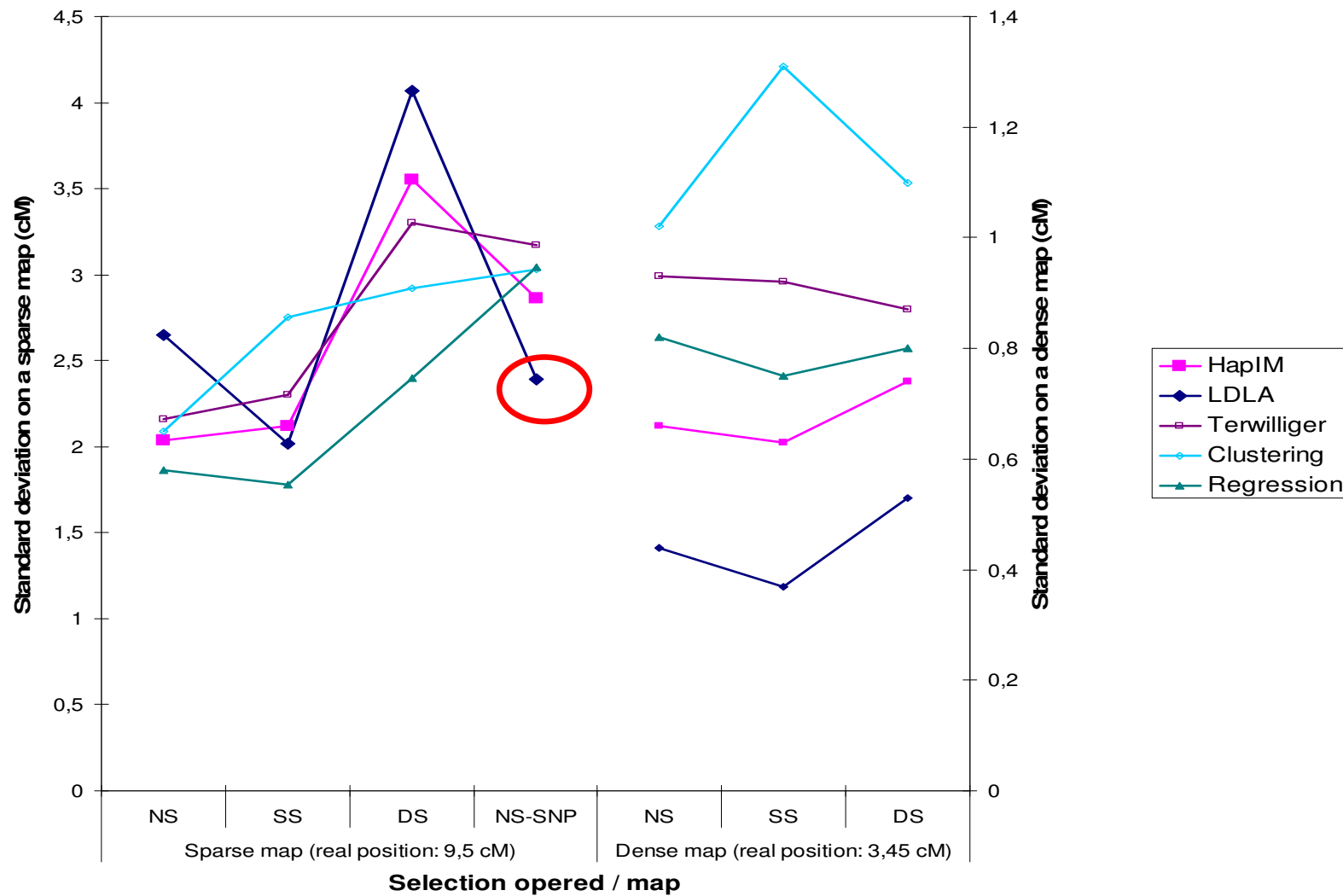
- Dense :



Results: mean location



Results: standard deviations



Discussion

- On average, QTL correctly detected
- No effect if “light” selection
- But 10 generations of “strong” selection → deleterious impact through increase of variability of the location detected

Discussion

- Regression on single markers = best on sparse map covered by multi-allelic markers
- But LDLA method = best when SNP are used, whatever the map density
- This Clustering does not have the qualities of full LDLA

Thank you
for your attention