Faculty of Agriculture and Nutritional Science

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A Mixture Genetic Model for whole genome analyses

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Animal Breeding & Genetics

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Motivation

Genomic Selection (GS)

- Accuracy decreases rapidly after training
  - Use of linkage disequilibrium (LD) and co-segregation
- Model dominance and epistasis
  - Difficult to accommodate with linear models

→ Mixture genetic model

Objectives

- To present an approximate Bayesian approach feasible for whole genome analyses using a mixture genetic model
- To study the consequences of the approximations with a simulated fine mapping scenario

Fine-mapping scenario

Genome segment

- Length 1 cM
- 20 SNPs (Spacing 0.05 cM)
- 1 QTL ($h^2 = 0.05$)
- SNPs and QTL were in LD

Task: Find the SNP interval that contains the QTL

Mixture Genetic Model

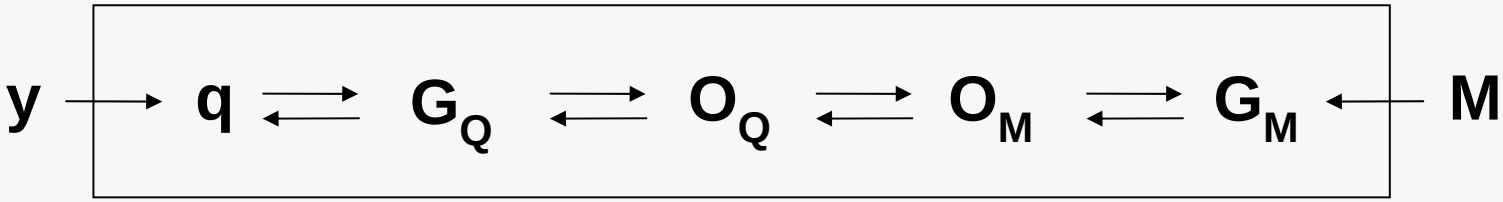
Additive QTL model for each SNP interval k

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{q}_k\alpha + \mathbf{e}_k$$

$\mathbf{q}_k$ is the vector of unobservable QTL genotypes (0,1 or 2)

Exact Bayesian Approach

Exact MCMC-Sampler



G - ordered genotypes

O - segregation indicators

M - unordered SNP genotypes

$\theta_{il} = (\mathbf{O}_{Mil}, \mathbf{G}_{Mil})$ individual i, locus l

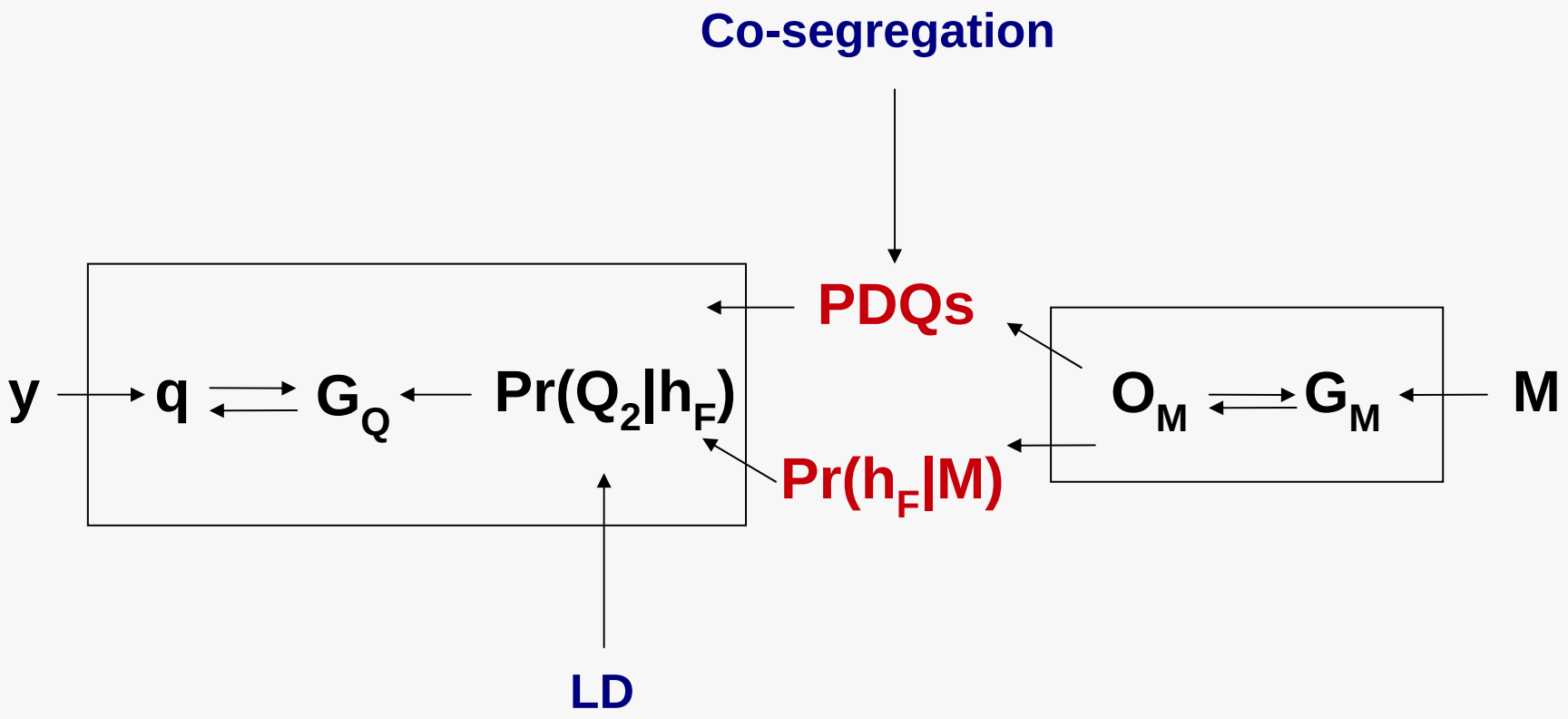
Overlapping blocks for peeling

Locus block

Pedigree block

θ_{11}	θ_{12}	θ_{12}	θ_{14}	θ_{15}	θ_{16}	…	θ_{1M}
θ_{21}	θ_{22}	θ_{23}	θ_{24}	θ_{25}	θ_{26}	…	θ_{2M}
θ_{31}	θ_{32}	θ_{33}	θ_{34}	θ_{35}	θ_{36}	…	θ_{3M}
θ_{41}	θ_{42}	θ_{43}	θ_{44}	θ_{45}	θ_{46}	…	θ_{4M}
…	…						…
…			…				…
…					…		…
…							…
θ_{N1}	θ_{N2}	θ_{N3}	θ_{N4}	θ_{N4}	θ_{N4}	…	θ_{NM}

Approximate 2-step approach



Simulation

Simple pedigree

- 810 individuals in 5 generations
- 10 males are mated to 100 founder females each generation

Complex pedigree with loops

- 1000 individuals in 5 generations
- 25 males are mated to 100 females each discrete generation

Results: Simple pedigree

- 16 replicates
- No pedigree blocks
- Locus block: 8 SNP, 3 overlapping

		Mean absolute difference for QTL		
	Accuracy of qα	**Position (cM)**	**Effect**	**Genotype**
Method/Range	0-1	0-1	0.325	0, 1 or 2
Exact	0.865	0.09	0.10	0.31
Approximate	0.830	0.11	0.09	0.38

Results: Complex pedigree

- 16 replicates
- SNP-Pedigree block: sire, its mates, their parents and offspring
- Locus block: 8 SNP, 3 overlapping
- QTL-Pedigree blocks

		Mean absolute difference for QTL		
	Accuracy of qα	**Position (cM)**	**Effect**	**Genotype**
Method/Range	0-1	0-1	0.325	0, 1 or 2
Approximate	0.95	0.08	0.07	0.23

Discussion and Conclusions

- Pedigree and locus blocking was not feasible with the exact approach

Approximate 2-step approach

- Large complex pedigrees and high-density SNPs feasible
- Limited loss of accuracy of genotypic values
- Limited loss of precision to locate QTL
- Markers are sampled once for all traits
- Reduction of computing time

Thank you for your attention!