Developments for the VikingRED

- VikingRED + NRF
- Population structure
  - Description
  - “Exploiting”

VikingRED + Norwegian Red

A "REAL" JOINT NORDIC GENOMIC EVALUATION

NORWEGIAN UNIVERSITY OF LIFE SCIENCES

geno

Genomic predictions based on a joint reference population for Scandinavian red breeds

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EAAP, Stavanger, August 29, 2011
Session 04 no 11

Joint Reference Population

- Norwegian Red
  - ~ 2800 bulls
  - 54k & 25k (imputed to 54k) SNP chip

- VikingRED
  - ~ 4,400 bulls
  - 54k SNP chip

Training & Validation

- Statistic
  - r^2(DGV,DPRF)/rel(DPFR)
- Method
  - GBLUP

Birth year = 2001

	Training	Validation
DFS	2847 < N < 3593	N = 1035
NRF	N = 2563	N = 281

Validation VikingRED

Trait	$\text{REF}_{\text{VikingRED}}$	REF_{all}	Δr^2_{DGV}
Milk	0.367	0.399	0.032
Fat	0.461	0.481	0.020
Protein	0.355	0.381	0.026
Fertility	0.289	0.282	-0.007
Birth	0.218	0.244	0.025
Calving	0.161	0.179	0.018
Udder health	0.241	0.254	0.013
Feet & Legs	0.274	0.283	0.009
Udder conform	0.328	0.342	0.014
Milking ability	0.299	0.321	0.023
Temperament	0.303	0.313	0.010
Mean	**0.305**	**0.323**	**0.018**

Min

Max

Validation Norwegian Red

Trait	**REF_{NRF}**	**REF_{all}**	**Δr^2_{DGV}**
Milk	0.36	0.38	0.02
Fat	0.38	0.45	0.07
Protein	0.28	0.39	0.11
SCC	0.37	0.40	0.03
Mastitis	0.26	0.23	-0.03
NR56 heifers	0.16	0.10	-0.06
NR56 cows	0.17	0.14	-0.03
CFI	0.11	0.10	-0.01
Calving interval	0.15	0.10	-0.05
Mean	**0.247**	**0.254**	**0.007**

Min

Max

Factors affecting genomic reliability

⇧ Larger reference population

⇩ Different traits

- Genetic correlation for production: 0.9
- Genetic correlation for fertility: 0.8

⇩ Different (but related) populations

- Larger effective population

In the pipeline …

- Revisit imputation
    - One joint imputation

- Genomic prediction models
    - Variable selection models
    - Haplotype-based models
    - Unified single-step model

EXPLORING POPULATION STRUCTURE

Characterization of Linkage disequilibrium in a Danish, Swedish and Finnish Red Breed Cattle Population

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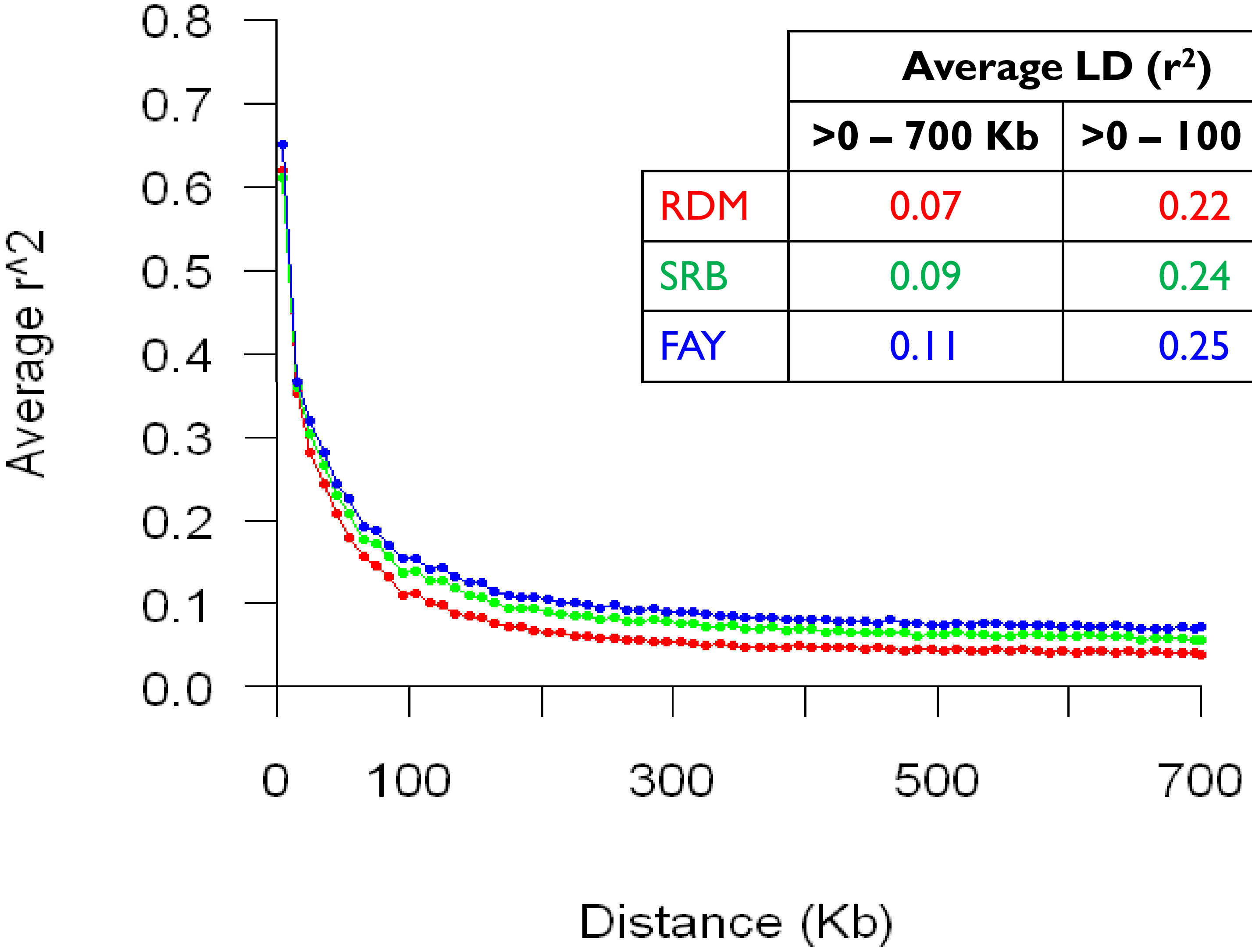
11th EAAP, 31st August 2011

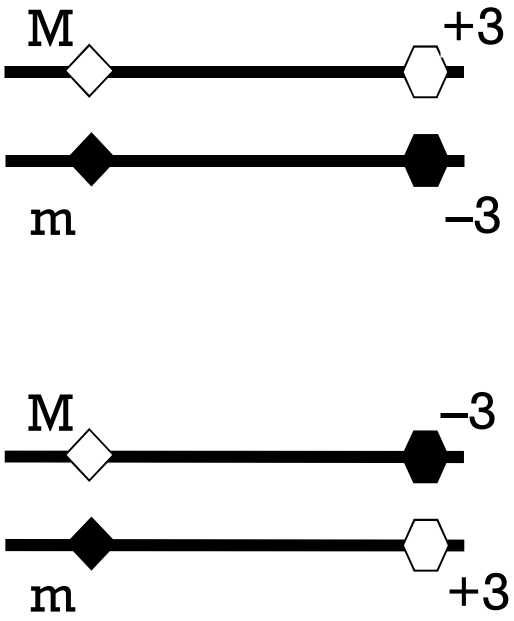
Stavanger, Norway

Average LD



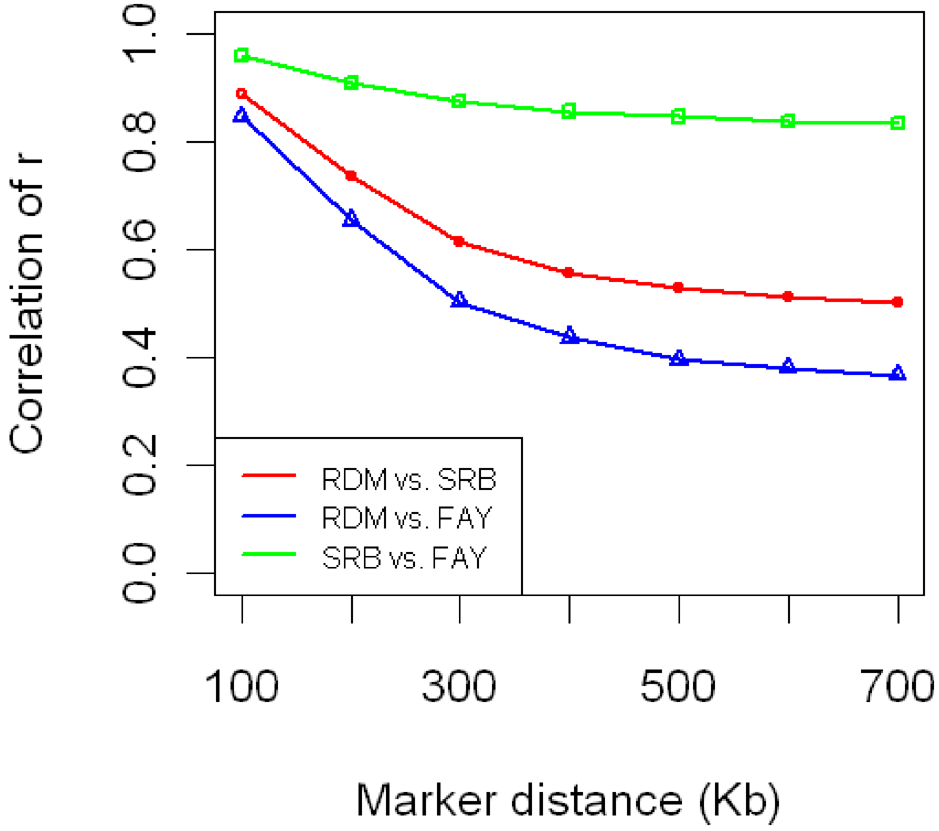
	Average LD (r^2)	
	>0 – 700 Kb	**>0 – 100 Kb**
RDM	0.07	0.22
SRB	0.09	0.24
FAY	0.11	0.25

Persistency of phase



Different association of marker allele M with QTL allele across populations?

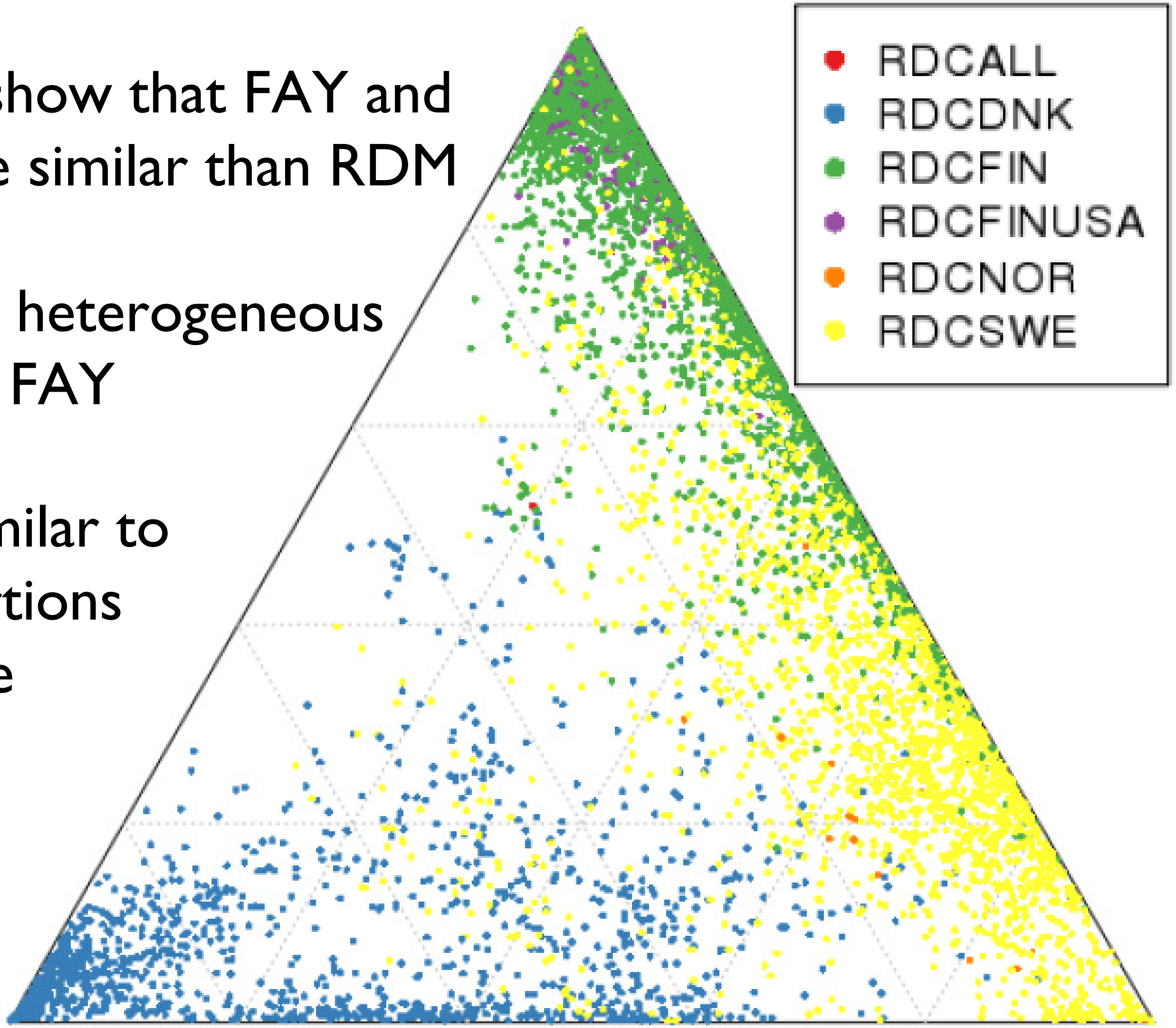
Persistency of marker phase



	RDM-SRB	RDM-FAY	SRB-FAY
P. Phase (0-100kb)	29.1% (16.5%)	33.2% (19.0%)	15.6% (9.1%)
Corr. of r (0-100kb)	0.68 (0.89)	0.58 (0.85)	0.89 (0.96)

Genotyped-based grouping of animals

- All methods show that FAY and SRB are more similar than RDM
- RDM is more heterogeneous than SRB and FAY
- Groupings similar to breed proportions from pedigree



EXPLOITING POPULATION STRUCTURE

Across breed multi-trait random regression genomic predictions in the Nordic Red dairy cattle

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M.J. Sillanpää[1], U.S. Nielsen[3] & J. Juga[1]

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[3]*Danish Agricultural Advisory Service, Udkaersvej 15, 8200 Aarhus, Denmark*

Use of breed proportions

- GBLUP with random regression on breed proportions
- Difficult to estimate variance components

- Slight improvement in reliability

In the pipeline …

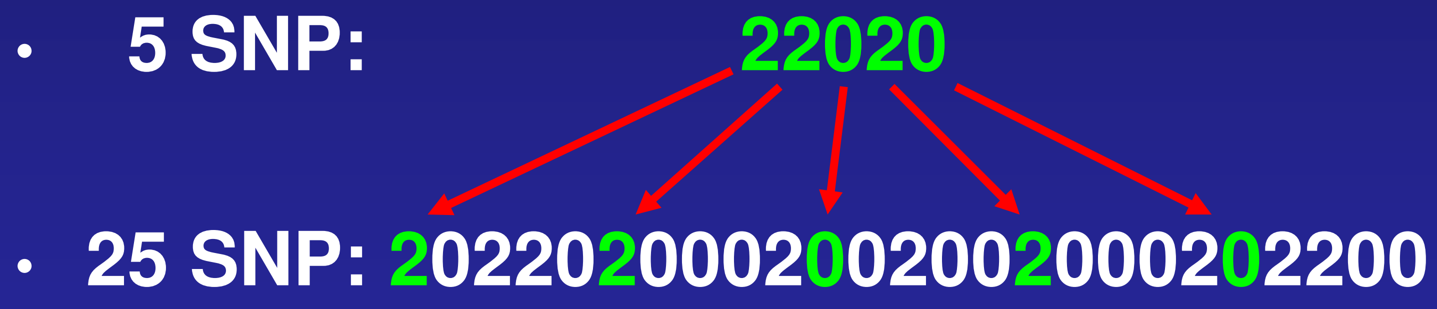
- Use genotype-based ”breed”-proportions
- Haplotype blocks
    - Structuring haplotypes according to breed
    - QTL-assisted genomic prediction
- Use by-products of imputation

VikingRED + Nordic Holsteins

IMPUTATION AND HD

How does imputation work?

- **Identify** haplotypes in population using many markers
- **Track** haplotypes with fewer markers
- e.g., use 5 SNP to track 25 SNP



  - 5 SNP: 22020
  - 25 SNP: 2022020002002002000202200

Genomic prediction using high-density SNP markers in Nordic Holstein and Red (RDC)

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Bernt Guldbrandtsen[1], Gert P. Aamand[2], Mogens S. Lund[1]

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Joint Reference Population

- VikingRed
  - ~ 4,400 bulls
  - HD SNP chip for 706 bulls
  - Rest 54k SNP chip imputed to HD

- Nordic Holstein
  - ~ 4,500 bulls
  - HD SNP chip for 557
  - Rest 54k SNP chip imputed to HD

Allele error rate of imputation

	Training	Test	%error
VikingRED	556	100	0.96
Holstein	457	100	0.77

RDM: 1.75%, SRB: 0.59%, FIN: 0.54%

Training & Validation

- Statistic
  - r^2(DGV,DPRF)/rel(DPFR)
- Method
  - GBLUP
  - Bayesian mixture model

Training & Validation

YoB = Oct 2001

	Training	Validation
Hol	N = ~ 3,100	N = ~1,400
VRed	N = ~ 3,500	N = ~ 900

Cross-validation Reliability

Viking RED	**GBLUP**			**Bayesian Mixture**		
	54k	HD	Δr^2_{DGV}	54k	HD	Δr^2_{DGV}
Protein	0.346	0.358	0.012	0.346	0.359	0.013
Fertility	0.297	0.304	0.007	0.299	0.307	0.008
Udder health	0.244	0.257	0.013	0.243	0.259	0.016
Average	**0.296**	**0.306**	**0.010**	**0.296**	**0.308**	**0.012**

Cross-validation Reliability

Holstein	**GBLUP**			**Bayesian Mixture**		
	54k	HD	Δr^2_{DGV}	54k	HD	Δr^2_{DGV}
Protein	0.425	0.429	0.004	0.435	0.440	0.005
Fertility	0.404	0.413	0.007	0.406	0.416	0.010
Udder health	0.370	0.370	0.000	0.375	0.376	0.001
Average	**0.400**	**0.404**	**0.004**	**0.405**	**0.410**	**0.005**

Factors affecting genomic reliability

⇧ Larger reference population

⇩ More (SNP) effects to estimate

Summary

- Marginal increases in reliability
- Short horizon in validation