Connecting breeding value estimation in sheep

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Today’s talk

- Sheep breeding
  - Constraints
  - Solutions
- In practice
  - Genetic means
  - Summarizing
  - Extensions
- Connectedness
  - In perspective
  - Assessment
  - Sufficiency
- Sum up

Challenges

Genetic progress limited by:

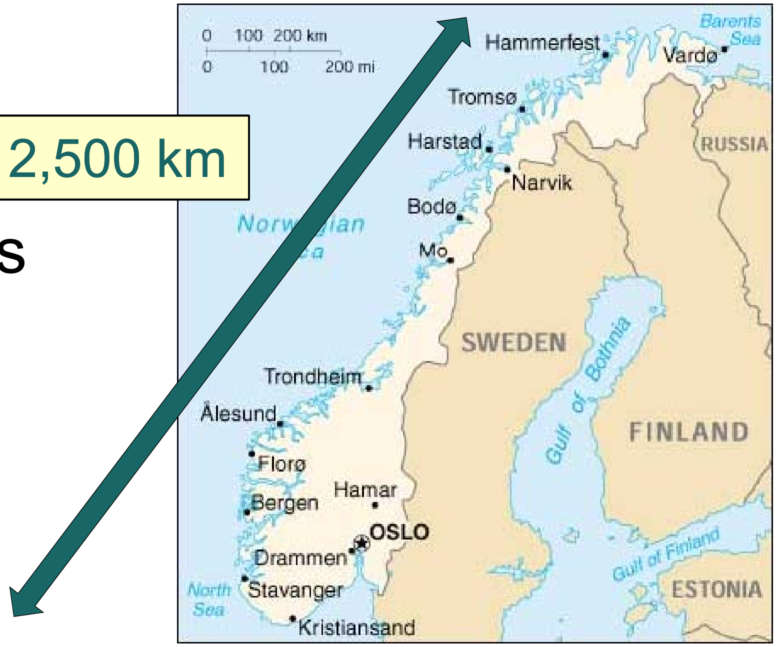
- Biological limits
  - Older age at sexual maturity
  - Produce few progeny in lifetime
- Structural constraints
  - Husbandry differences among flocks may mask genetic differences

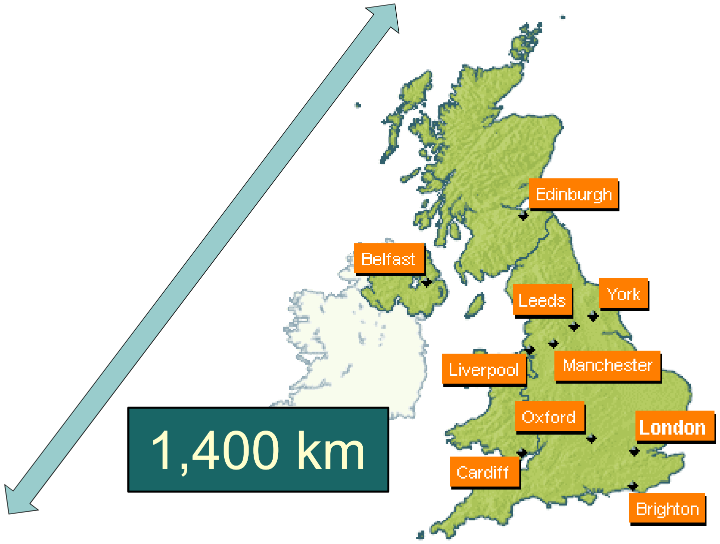
Structural constraints

- Small individual flock sizes
  - Often the case in pedigree industries
  - Few animals to choose among within flock and thus slow genetic progress
- Equitable comparison of genetic merit of animals across flocks may not be possible
- Low uptake of performance recording
  - Dairy sheep breeds an exception

Geographic distances

- Geography
  - Flocks distributed across long distances

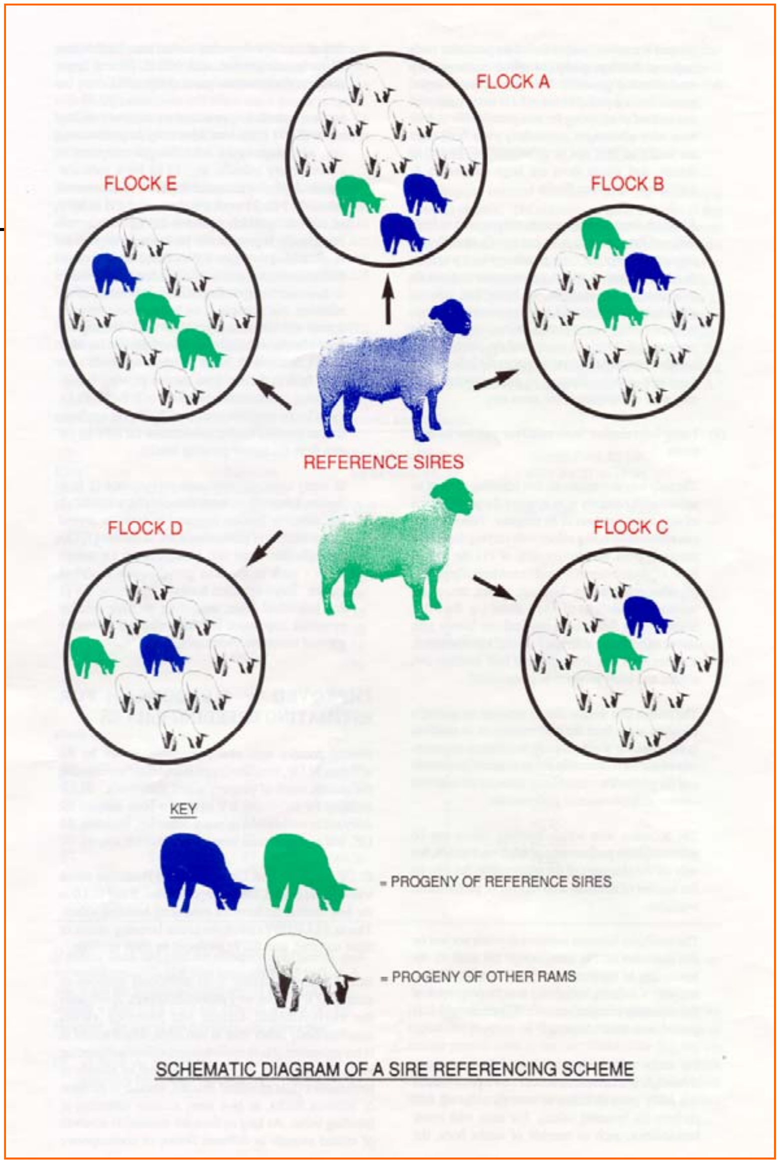

2,500 km


1,400 km

Challenge: small genetically ‘disconnected’ flocks

Solutions

Sire referencing



SCHEMATIC DIAGRAM OF A SIRE REFERENCING SCHEME

(Simm et al., 2001)

Solutions

Ram circles

- Natural service within a ram circle
- Artificial insemination among ram circles

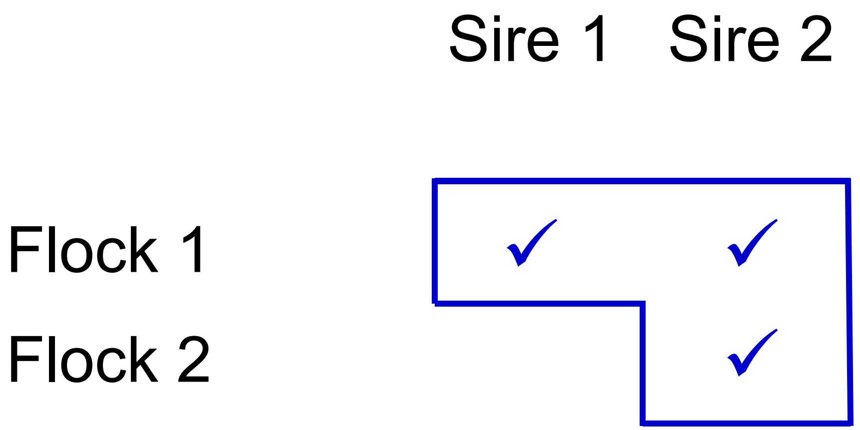
> "The main purpose of ram circles is to get the progeny of each ram spread over many farms in order to reduce the flock effect …"
>
> (Gjedrem, 1969)

(Eikje et al., 2008; Eikje et al., 2011 (this conference))

Connectedness

- In perspective
  - Connected *versus* disconnected flocks
- Assessing connectedness
- Sufficiency
  - Bias statistic

Connected flocks

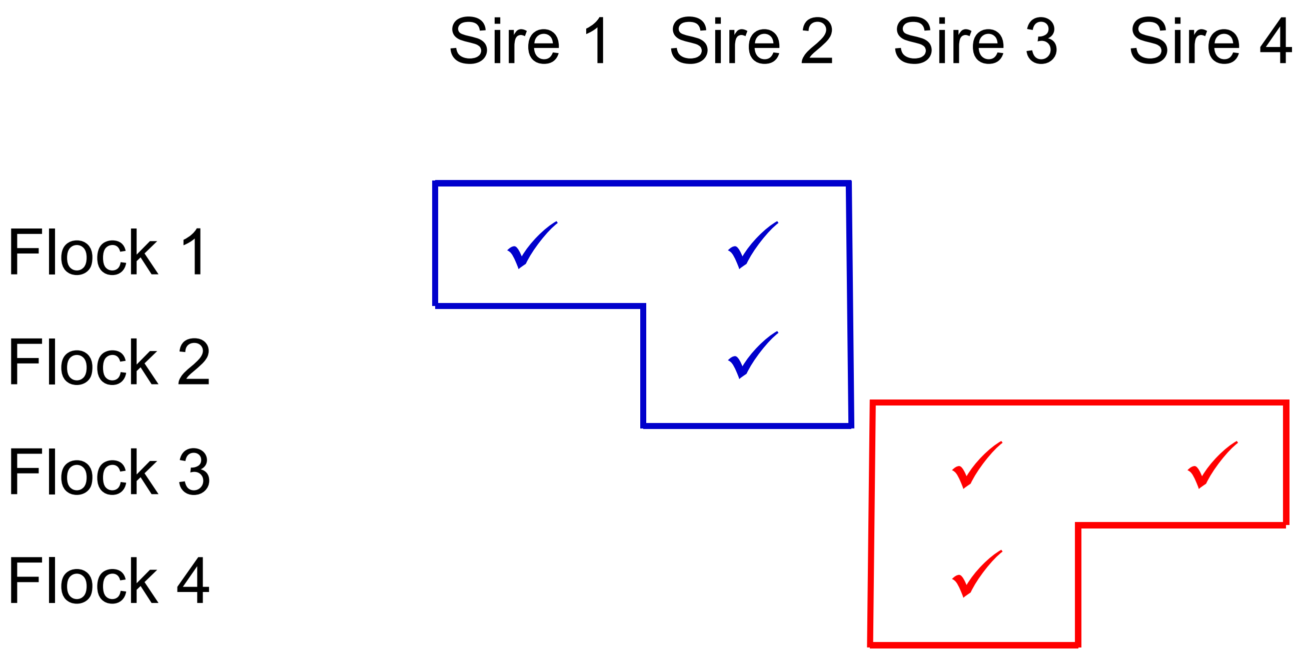


	Sire 1	Sire 2
Flock 1	✓	✓
Flock 2		✓

Model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

Disconnected flocks



	Sire 1	Sire 2	Sire 3	Sire 4
Flock 1	✓	✓		
Flock 2		✓		
Flock 3			✓	✓
Flock 4			✓	

Model

$$\mathbf{y} = \mathbf{Xb} \xcancel{+} \mathbf{Zu} + \mathbf{e}$$

Disconnected flocks

- If sires and flocks considered fixed
  - All comparisons not estimable
- If sires instead considered random
  - All comparisons estimable (BLUP)
  - Prediction error variance (PEV) of disconnected sires larger
  - Presumes average merit of sires equal
    - Biased if not so

$$\boxed{MSE = PEV + bias^2}$$

Prediction error variance (PEV)

- Increased PEV means reduced selection accuracy
  - PEV is a logical measure of connectedness (Kennedy and Trus, 1993; Kuehn et al., 2007)

Connectedness

- Quality of the comparison depends on how well flocks are linked genetically
  - Need ‘sufficient’ connectedness (Kinghorn and Shepherd, 1990; Kennedy and Trus, 1993)
  - Asymptotic (Foulley et al., 1992; Hanocq et al., 1996)

Flock connectedness

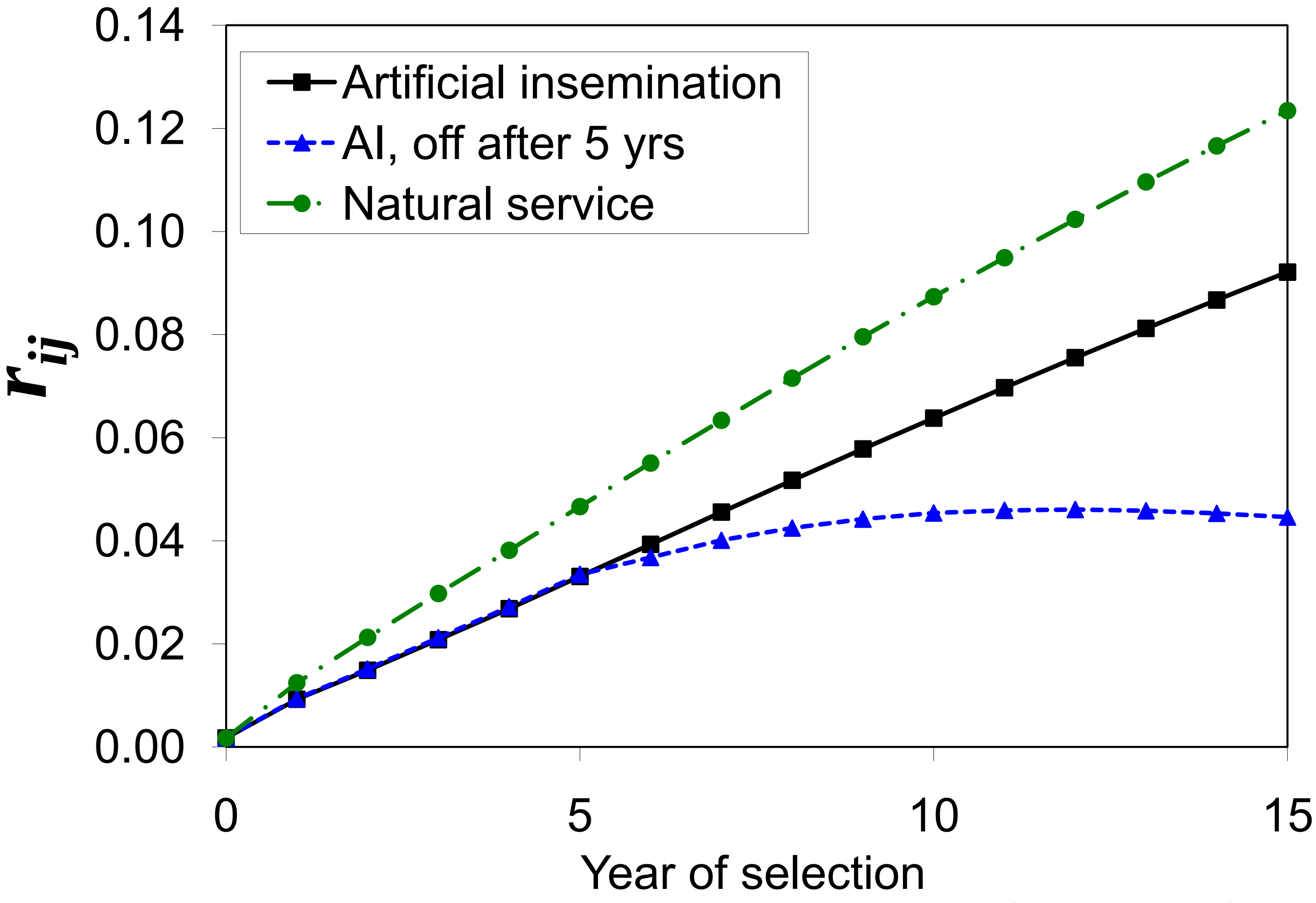
Summarized on flock basis

$$r_{ij} = \frac{\mathrm{PEC}(\hat{\bar{u}}_{i.}, \hat{\bar{u}}_{j.})}{\sqrt{\mathrm{PEV}(\hat{\bar{u}}_{i.})\mathrm{PEV}(\hat{\bar{u}}_{j.})}}$$

where $\hat{\bar{u}}_{i.(j.)}$ is the mean breeding value of all animals recorded in flock $i(j)$ since recording began

(Lewis et al., 2005)

Flock connectedness



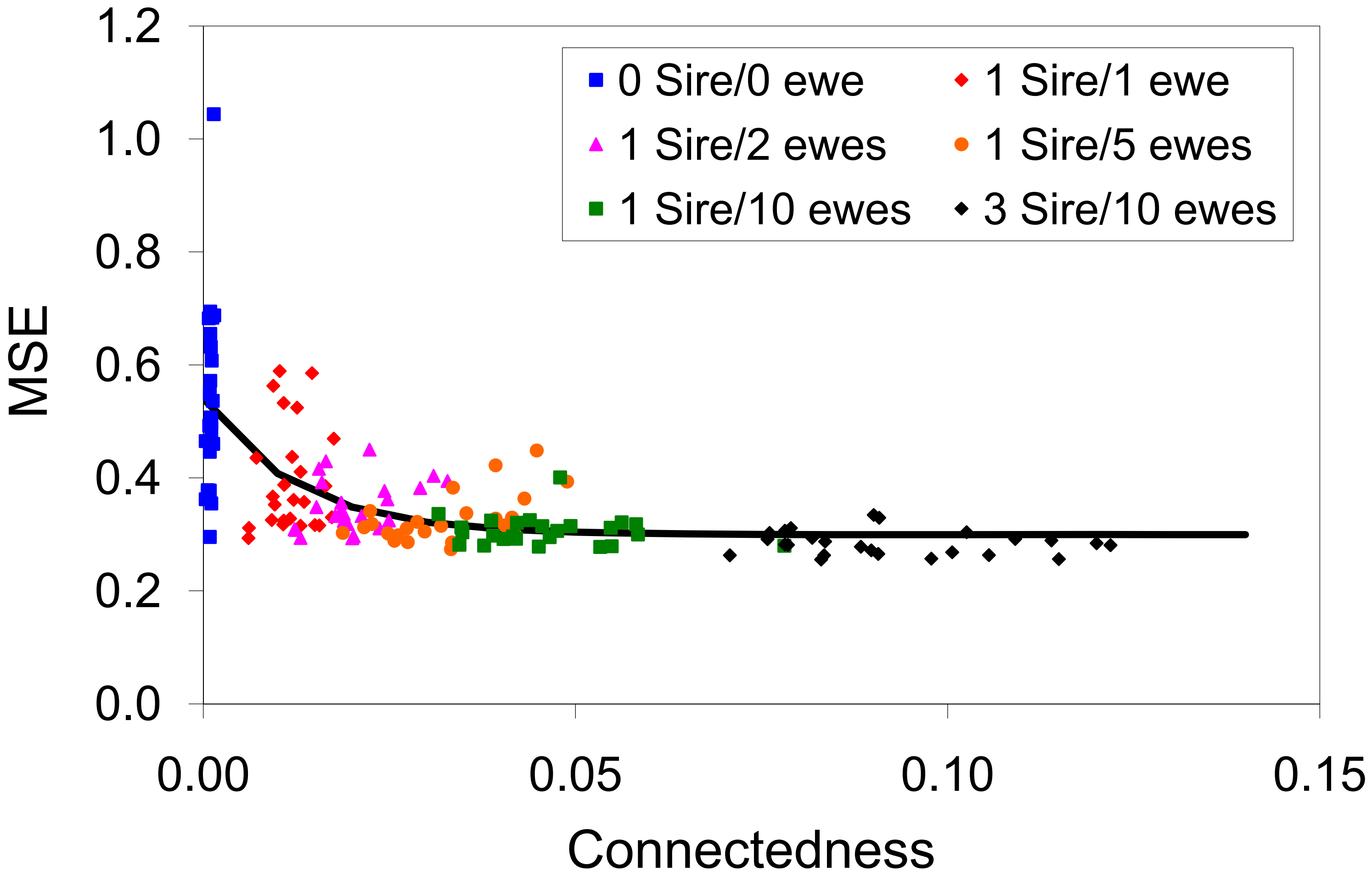
(Lewis and Simm, 2000;
Kuehn et al., 2008a,b)

Sufficiency: bias statistic

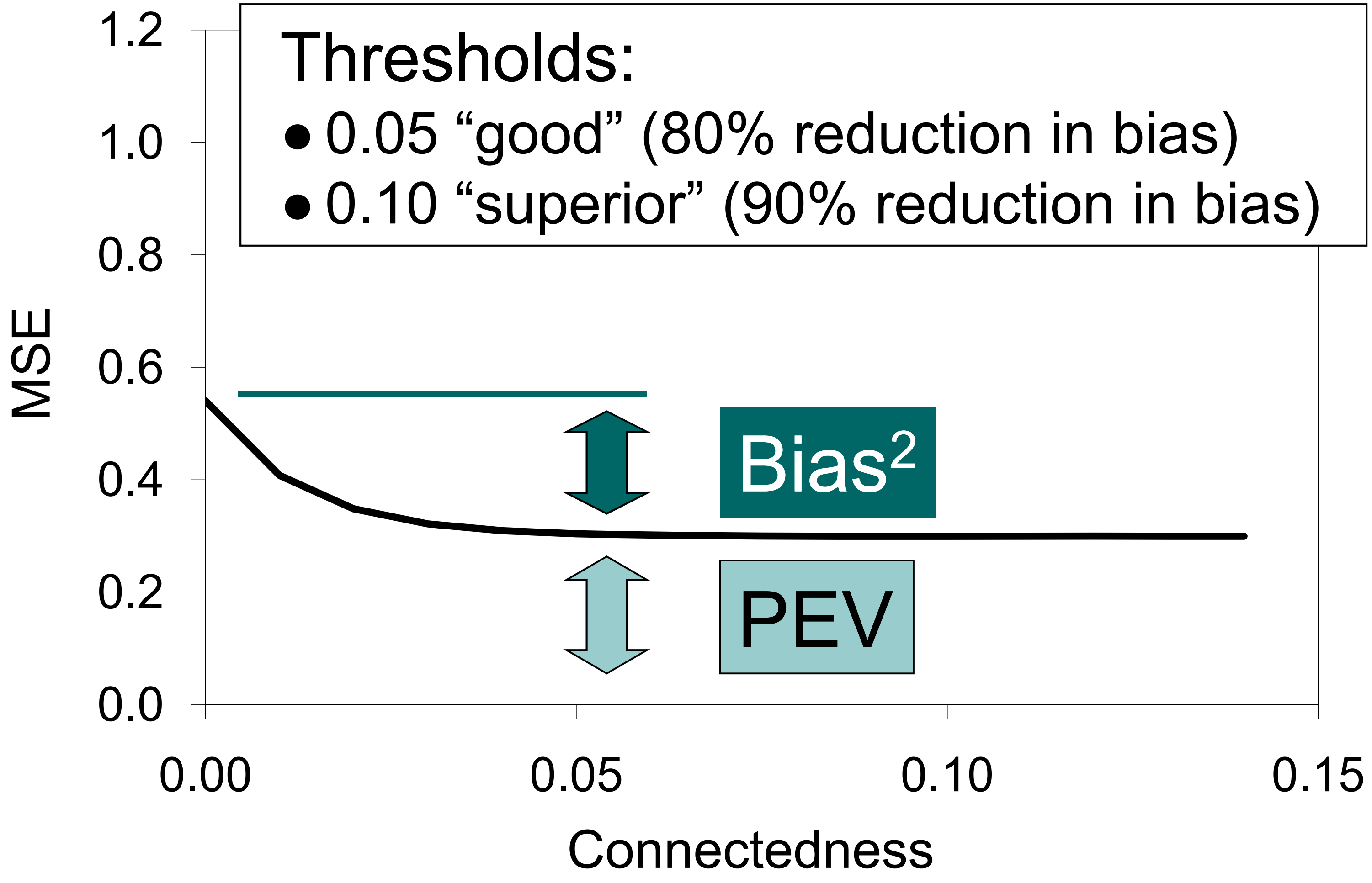
$$\hat{L}_{ij} = \left(\hat{u}_i - \hat{u}_j\right) - \left(u_i - u_j\right)$$

- Measures consistency of difference in estimated and true genetic merit
- Average squared L_{ij} measures the mean squared error (MSE)
  - Sum of PEV and squared bias

Connectedness *vs.* MSE



Connectedness *vs.* MSE



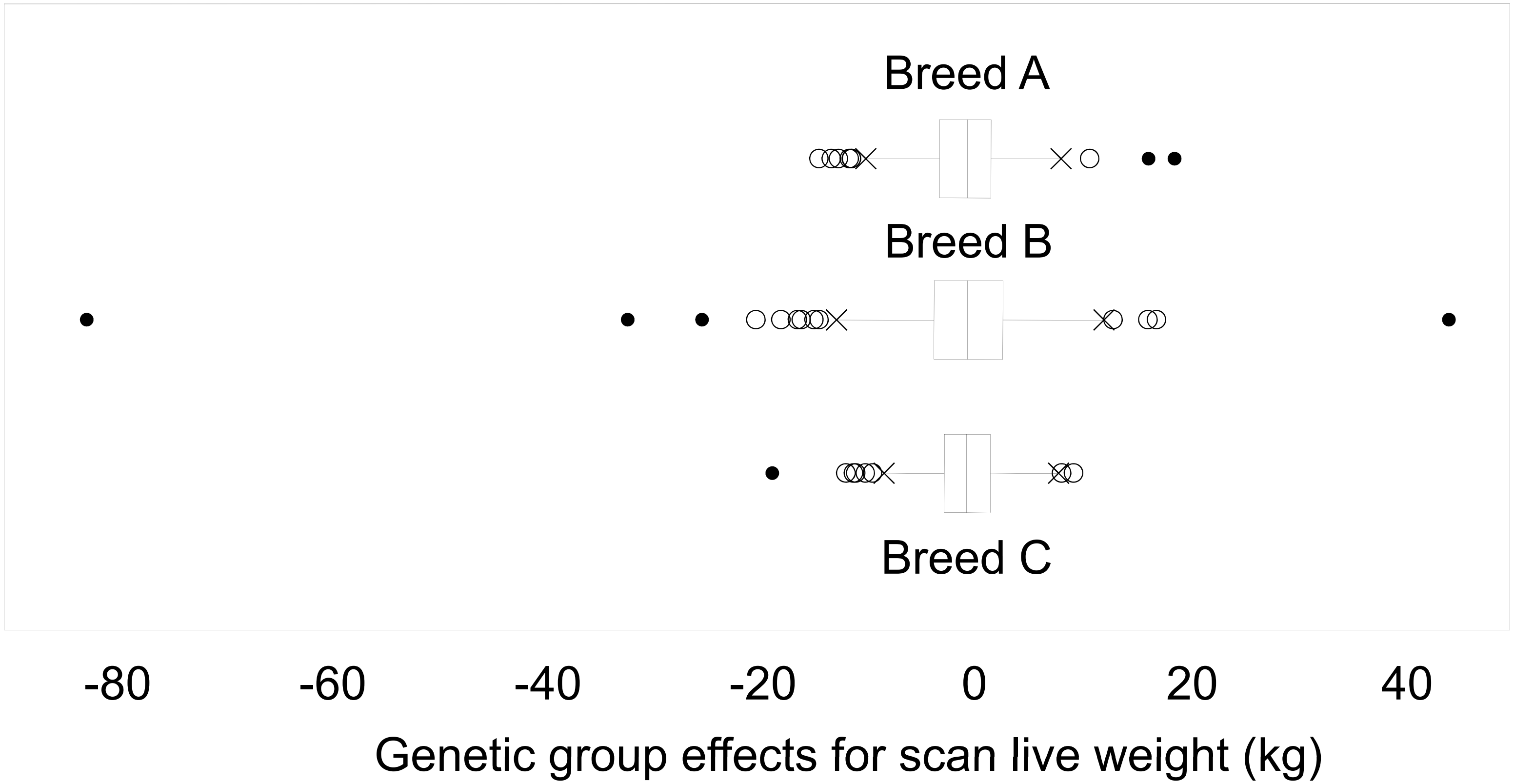
Thresholds:

- 0.05 “good” (80% reduction in bias)
- 0.10 “superior” (90% reduction in bias)

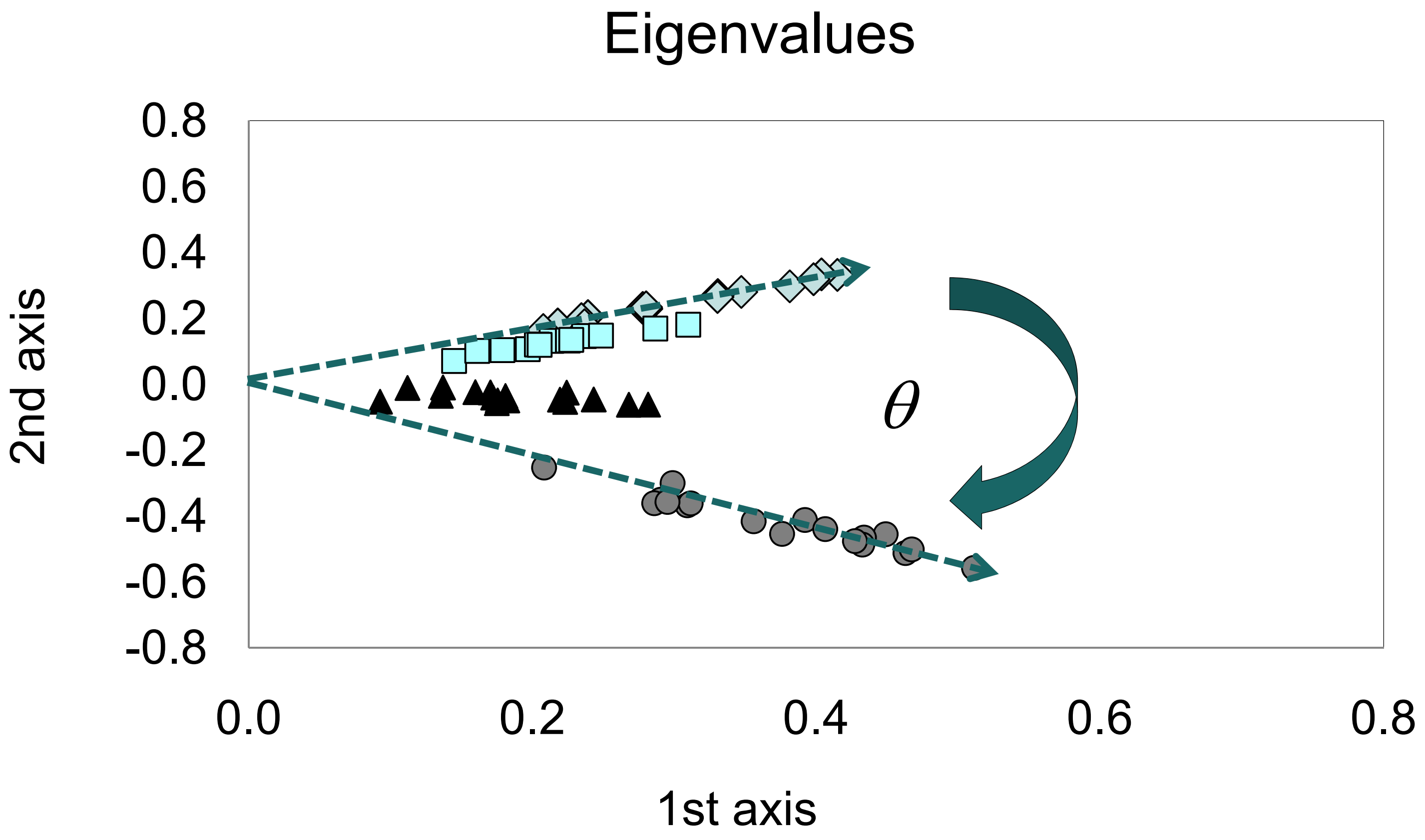
In practice

- Different genetic means
- Summarizing r_{ij}
  - Principal components
  - Clusters
- Extensions
  - Accuracy
  - Genomic information

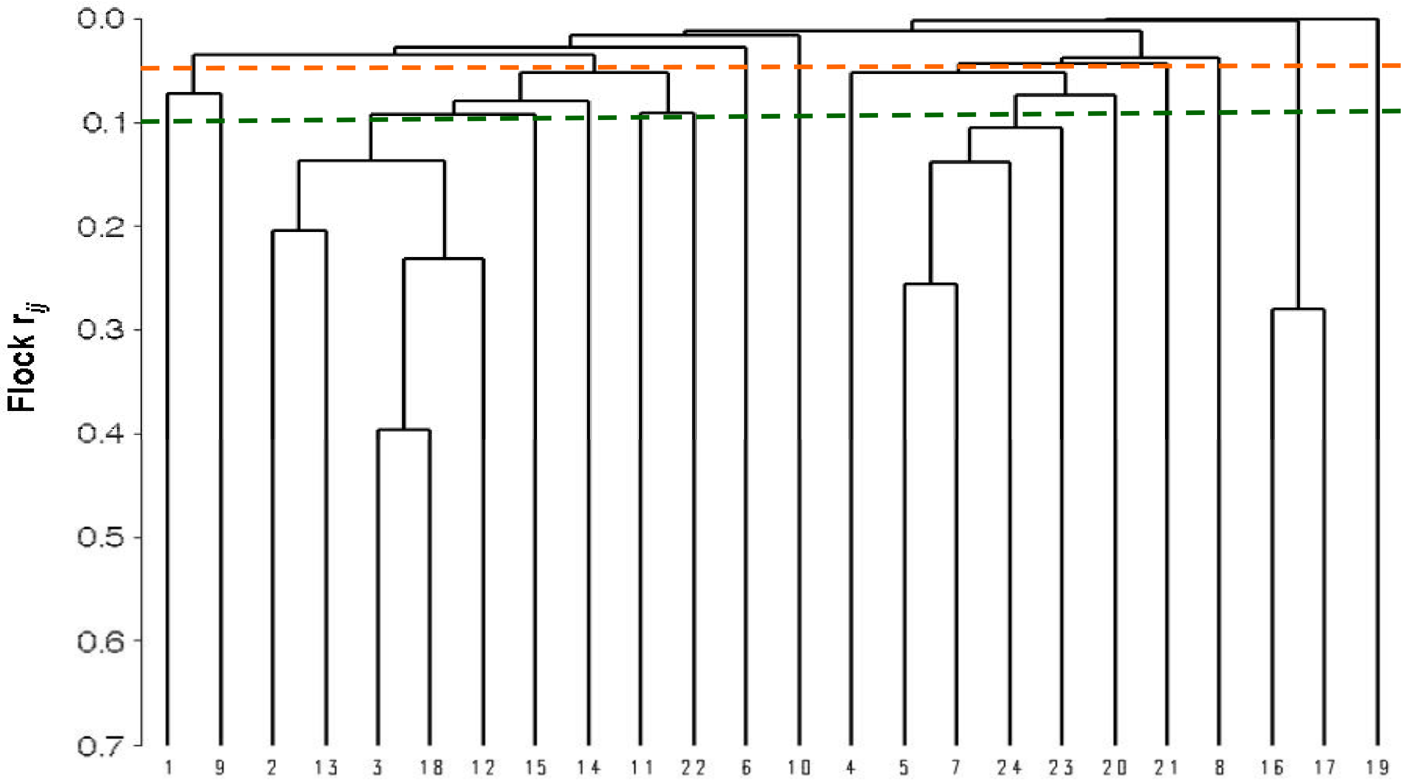
Different genetic means



Summarizing r_{ij}



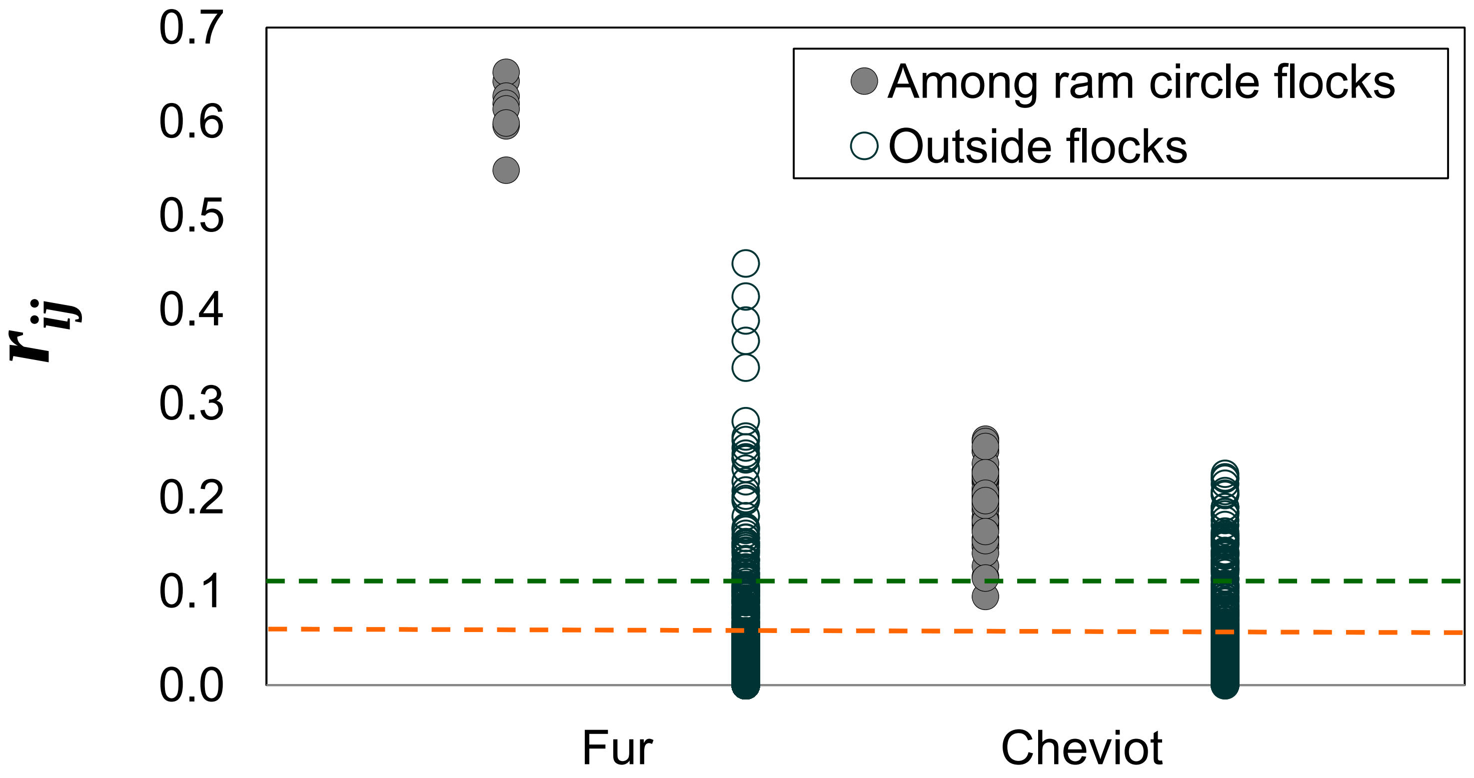
Summarizing r_{ij}



(Kuehn et al, 2009)

Extensions

- Connected set



(Eikje et al., 2011 (this conference))

Extensions

- Impact on accuracy ($\sqrt{1-PEV}$)

Breed	Measure	RC alone	$r_{ij} \geq 0.1$	All
Fur	No. weights	15,472 (1.0)	55,103 (3.6)	110,955 (7.2)
	Accuracy	0.564 (1.00)	0.577 (1.02)	0.580 (1.03)
Cheviot	No. weights	50,193 (1.0)	84,796 (1.7)	131,012 (2.6)
	Accuracy	0.555 (1.00)	0.561 (1.01)	0.563 (1.01)

Extensions

- Genomic information
  - Genomic selection (Baloche et al., 2011; Larroque et al., 2011; Robert-Graine et al., 2011 (this conference))
  - Augmented $\mathbf{A}^{-1}$

$$PEV = \left(\mathbf{Z'MZ} + \mathbf{A}^{-1}\lambda \right)^{-1} \sigma_e^2$$

$$\uparrow$$

$$\begin{bmatrix} A^{11} & A^{12} \\ A^{21} & G^{22} \end{bmatrix}$$

Summing up

- Connectedness matters in across-flock genetic evaluations
  - Genetic means vary among flocks
  - Evaluations biased if connectedness among flocks ‘insufficient’

Summing up

- Connectedness can be evaluated in large data
  - In illustrations shown (Eikje et al., 2011 (this conference))
  - Norwegian White
    - Pedigree: 3,522,302
    - Wean wt.: 2,763,746

Summing up

- Connectedness can be used to define the dynamics of breeding systems
    - Delineate differences among breeding objectives
    - Define performance data to include or exclude in genetic evaluation
        - Balance between unbiasedness and accuracy

Thanks for listening, and to …

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  - Thor Blichfeldt

NSG
Norsk Sau og Geit