

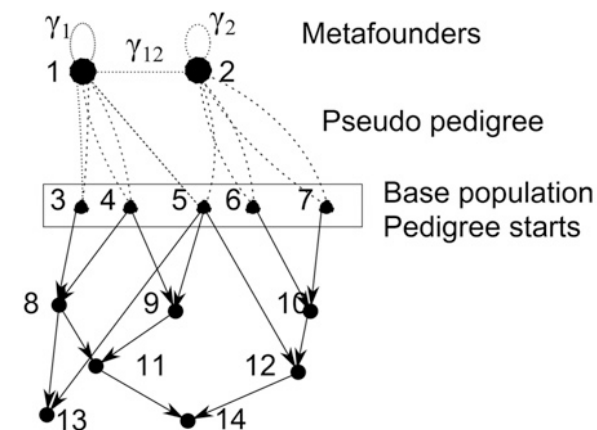
CAN METAFFOUNDERS IMPROVE INBREEDING ESTIMATION?

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Motivation

- In sheep natural mating is (usually) not recorded
 - Only AI offspring has known parents
- This incomplete pedigree information underestimates inbreeding

• *Metafounders*: pseudo-animals that represent relationship across and within base populations

$$\Gamma = \begin{pmatrix} \gamma_{11} & \gamma_{12} & & \\ & \gamma_{22} & & \\ & & & \dots \end{pmatrix}$$

Ancestral relationships in matrix Γ

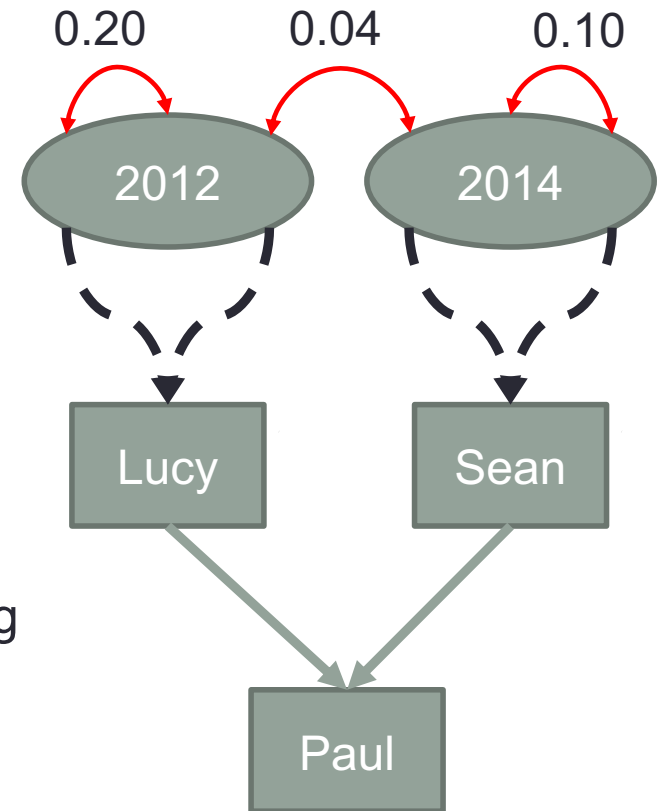
- Unknown parents of an animal born in 2000 are offspring of animals born in 1996, but this relationship is lost if metafounders are not used

Inbreeding with metafounders

$$\Gamma = \begin{pmatrix} \mathcal{Y}_{2012,2012} & \mathcal{Y}_{2012,2014} \\ \mathcal{Y}_{2014,2014} & \mathcal{Y}_{2014,2014} \end{pmatrix} = \begin{pmatrix} 0.20 & 0.04 \\ 0.10 & 0.10 \end{pmatrix}$$

By repeated application of the Tabular Method

- “Lucy” born in 2012 with unknown parents has $F=0.1$
- “Sean” born in 2014 with unknown parents has $F=0.05$
- Relationship of Sean and Lucy is 0.04
- “Paul” offspring of Sean and Lucy has inbreeding 0.02
- This shows that we compensate for missing pedigrees

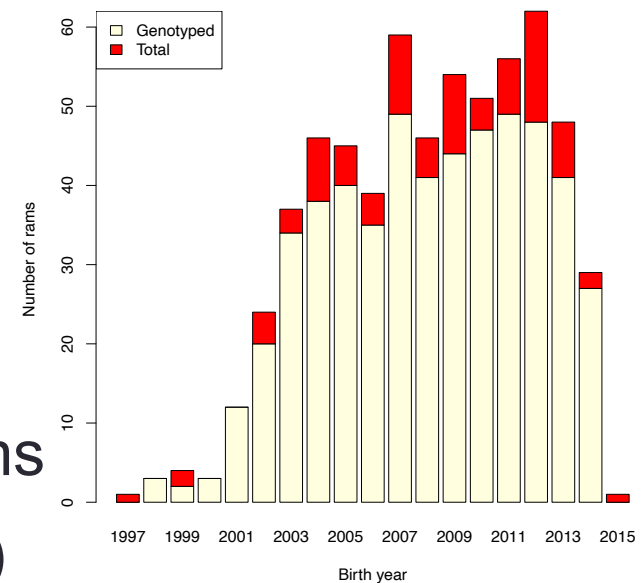


Objective & data

- To compare different methods to estimate inbreeding depression in semen traits

Trait	Mean (SD)
Sperm volume (ml)	1.41 (0.63)
Sperm concentration (10^6 /ml)	3.23 (0.64)
Motility score	4.61 (0.54)

- 16,196 phenotypic records for 620 rams
- 533 of them genotyped (36,464 SNPs)
- 8,266 animals in pedigree (rams + ancestors)



Inbreeding depression analysis

Multiple-trait analysis

Volume
Concentration
Motility

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{F}b + \mathbf{Z}_u\mathbf{u} + \mathbf{Z}_{pe}\mathbf{pe} + \mathbf{e}$$

Inbreeding coefficients:

$$\mathbf{F}_{PED}$$

Wright, 1992

$$\mathbf{F}_{PED_{non-zero}}$$

VanRaden, 1992

$$\mathbf{F}_{PED_{MF}}$$

$$\mathbf{A}^{(\Gamma)}$$

$$\mathbf{F}_{H_{MF}}$$

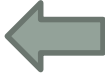
$$\mathbf{H}^{(\Gamma)} = \begin{pmatrix} \mathbf{A}_{11}^{(\Gamma)} + \mathbf{A}_{12}^{(\Gamma)}\mathbf{A}_{22}^{(\Gamma)-1}(\mathbf{G}_{05} - \mathbf{A}_{22}^{(\Gamma)})\mathbf{A}_{22}^{(\Gamma)-1}\mathbf{A}_{21}^{(\Gamma)} & \mathbf{A}_{12}^{(\Gamma)}\mathbf{A}_{22}^{(\Gamma)-1}\mathbf{G}_{05} \\ \mathbf{G}_{05}\mathbf{A}_{22}^{(\Gamma)-1}\mathbf{A}_{21}^{(\Gamma)} & \mathbf{G}_{05} \end{pmatrix}$$

$$\mathbf{F}_{ROH}^*$$

McQuillan et al., 2008

* For the subset of 533 genotyped rams

Estimated inbreeding depression

Models	Semen traits ¹			Estimate (s.e.)
	Volume	Concentration	Motility	
PED	-0.096 (0.880)	1.104 (0.978)	-1.241 (0.681)	
PED _{non-zero}	-0.290 (0.996)	1.056 (1.108)	-1.259 (0.771)	
PED _{MF}	-0.979 (1.006)	1.617 (1.103)	-1.676 (0.768)	
H _{MF}	-0.248 (0.703)	0.545 (0.807)	-1.115 (0.557)	
ROH	-0.931 (0.609)	-0.247 (0.684)	-0.905 (0.413)	

A 10% increase in inbreeding resulted in a reduction in motility of around 0.1 points in the scale (from 1 to 5) and a small deterioration in male fertility

Conclusions

- Metafounders help with missing pedigree information
- Inbreeding depression estimation was more accurate using metafounders
- Analyses with ROH confirm these results
- Motility was unfavorably impacted by the increase of inbreeding in Basco-Béarnaise breed

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Thanks for your attention!