

# Estimation of variance components using the pedigree, G or APY\_G

- **Michael Aldridge**, Jeremie Vandenplas & Mario Calus



# Acknowledgements



# How should we make variance estimates?

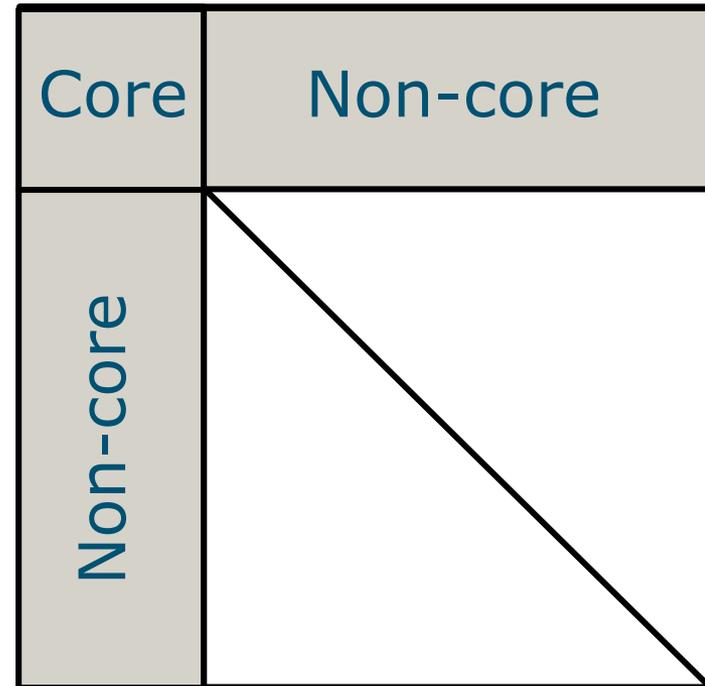
- Increasing amount of **Genotyped data**.
- **Computer limitations** are being reached.
- Algorithm for Proven and Young animals (**APY**).

# Algorithm for Proven and Young animals (APY)

$$G \longrightarrow G^{-1}$$



$$\text{APY } G \longrightarrow \text{APY } G^{-1}$$



# Objective

Compare **variance** estimates  
between **APY  $G^{-1}$** , **pedigree  $A^{-1}$** , and  
single step using the **full  $G^{-1}$** .

# Methods - Data

Core	Non-core
Non-core	



- ~5,000 **non-core** animals.
- ~5,000 **core** animals (PCA).

# Methods - Data

- $A^{-1}$ ,  $G^{-1}$  and  $APY_G^{-1}$  are constructed with the **same base**
- $G^{-1}$  is constructed with the **current** allele frequencies but the **base is adjusted** to be compatible with A
- We expect **variance estimates** to be **the same**

# Methods – overview

- Average litter birth weight
- Fixed effects
  - Parity
  - Line group at farrowing
  - Herd\*Year\*Season
  - Total number born
- Random effects
  - Residual
  - Permanent environmental
  - Animal
- Estimates made using REMLF90.

# Results – Variance estimates

---

Method	$A^{-1}$	$G^{-1}$
Genetic	13,535 (688)	14,284 (647)
Permanent Environment	3,552 (361)	4,247 (210)
Residual	14,172 (129)	14,281 (130)

---

# Results – Variance estimates

---

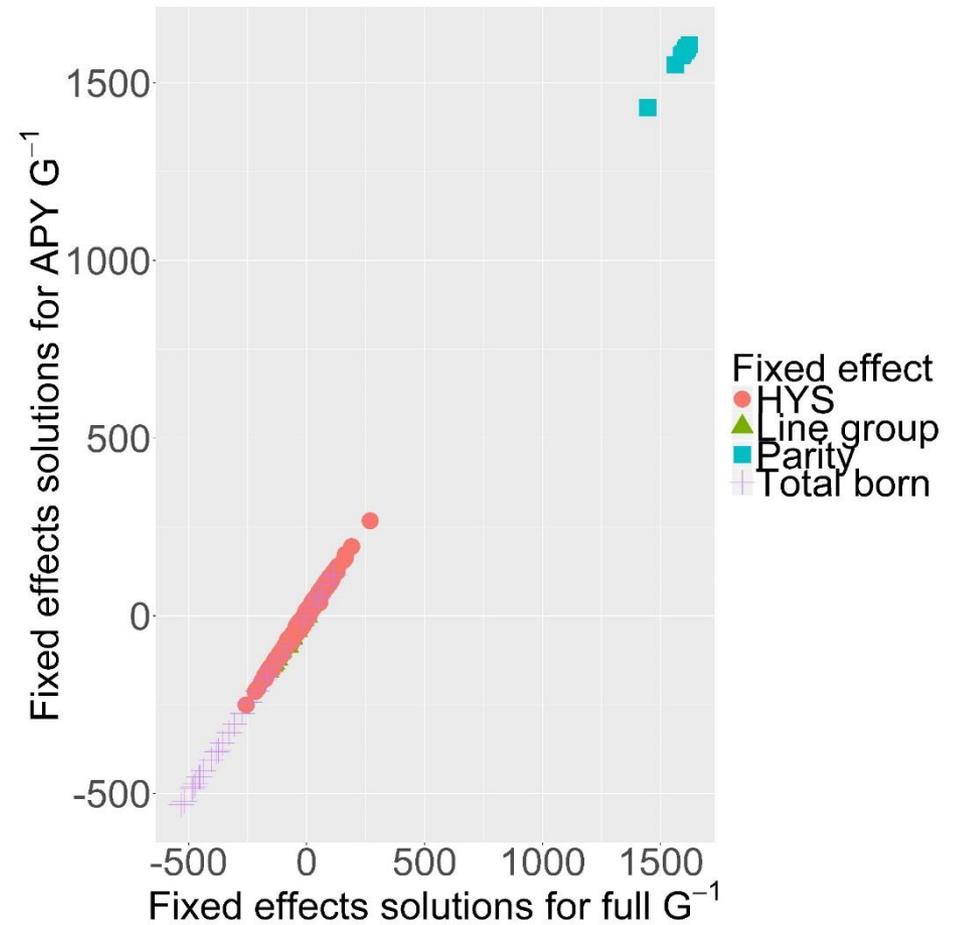
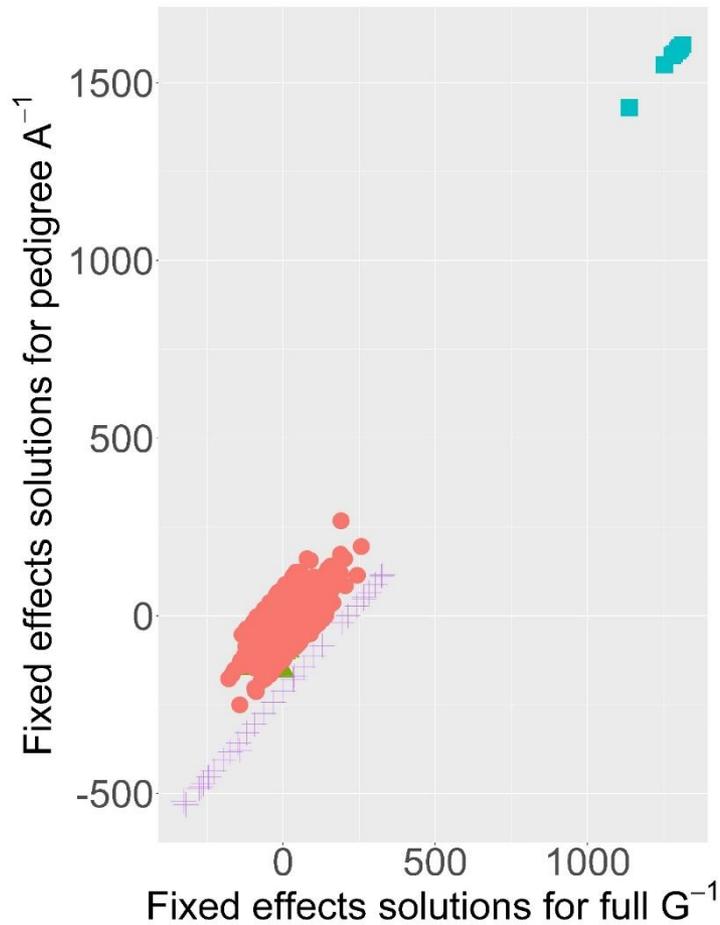
Method	$A^{-1}$	$G^{-1}$	$APY_G^{-1}$
Genetic	13,535 (688)	14,284 (647)	14,140 (695)
Permanent Environment	3,552 (361)	4,247 (210)	5,195 (199)
Residual	14,172 (129)	14,281 (130)	14,287 (130)

---

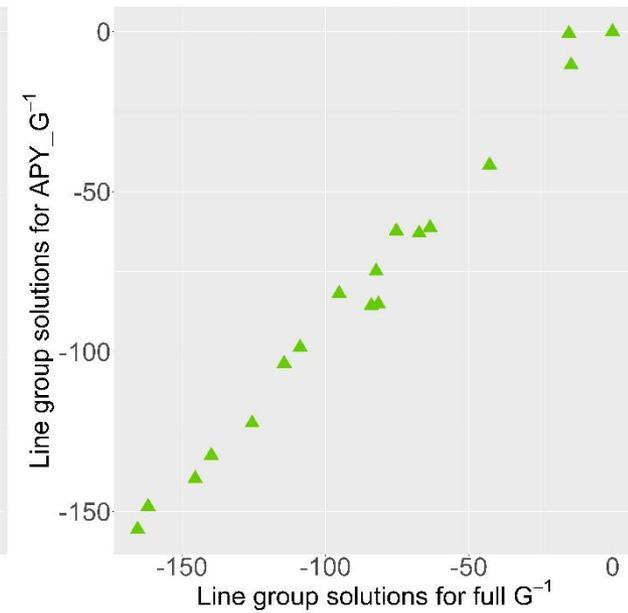
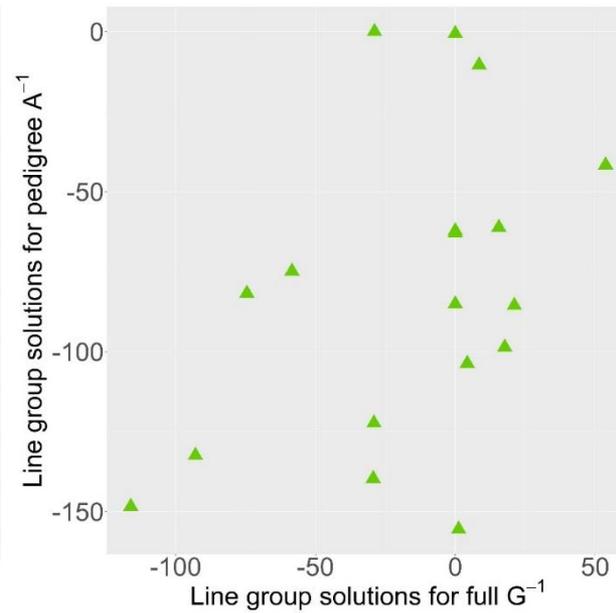
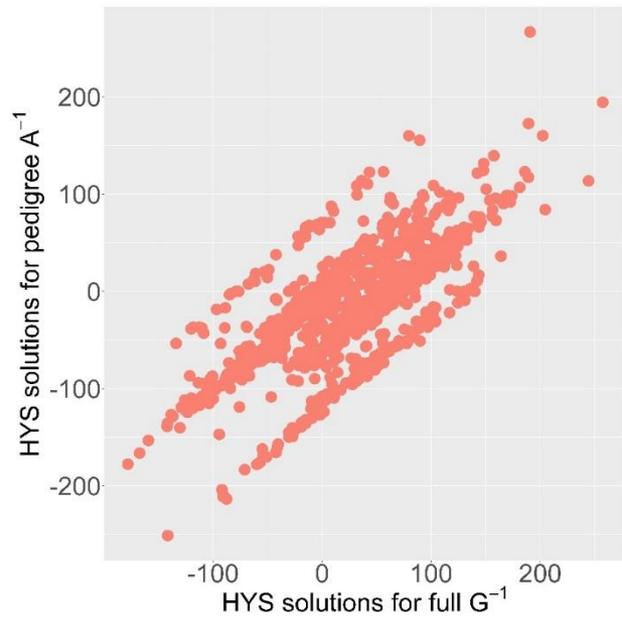
# Results – Variance estimates

Method	$A^{-1}$	$G^{-1}$	APY_ $G^{-1}$
Genetic	13,535	14,284	14,140
Permanent Environment	3,552	4,247	5,195
Residual	14,172	14,281	14,287
Phenotypic	31,259	32,799	33,622
$h^2$	0.43	0.44	0.42
$r$	0.55	0.57	0.58

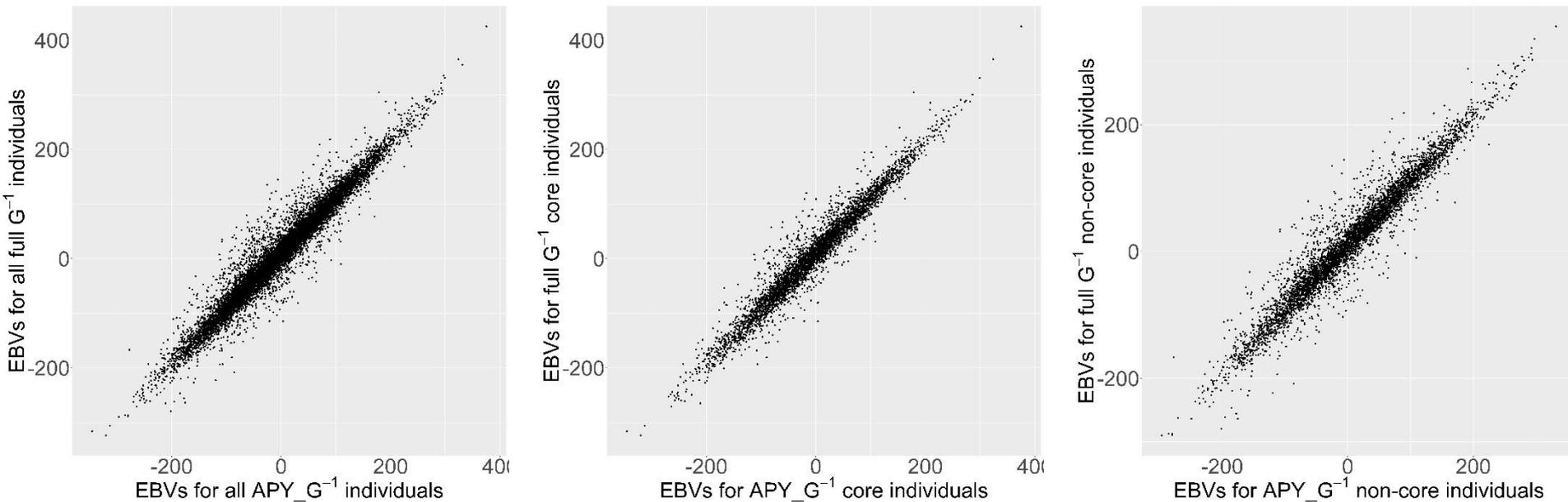
# Results – Fixed effects



# Results – Fixed effects

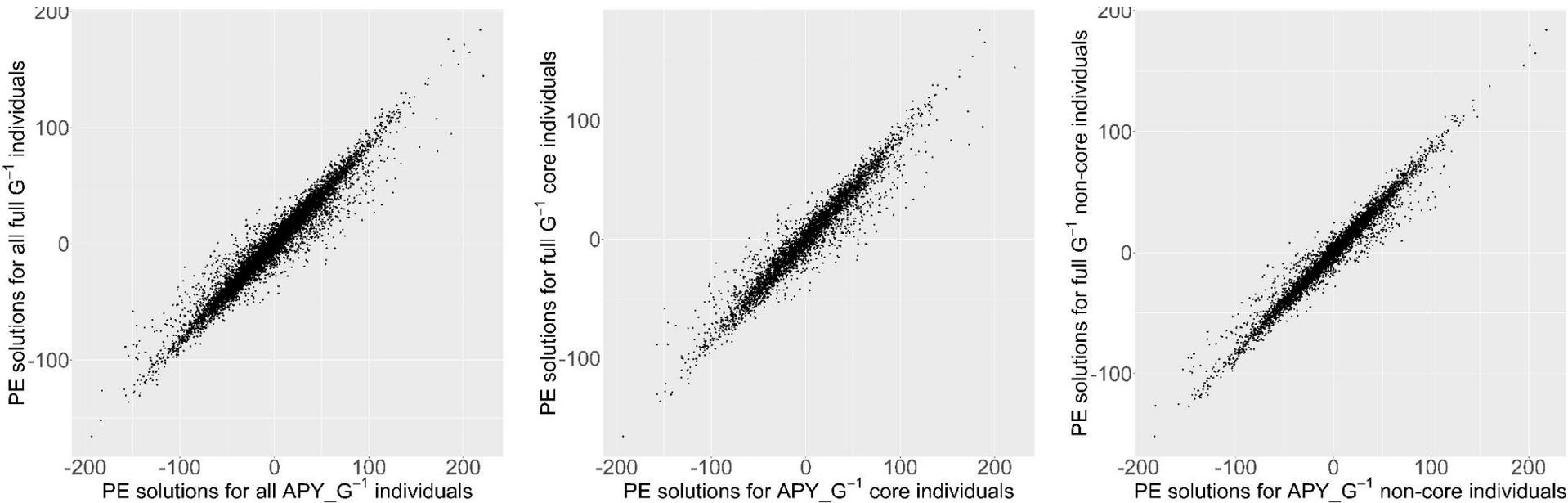


# Results – EBVs



<b>EBV Variance</b>	<b>All individuals</b>	<b>Core individuals</b>	<b>Non-core individuals</b>
$G^{-1}$	5,822	8,710	8,565
APY_ $G^{-1}$	5,458	8,135	8,018

# Results – Permanent environment solutions



<b>PE Variance</b>	<b>All individuals</b>	<b>Core individuals</b>	<b>Non-core individuals</b>
$G^{-1}$	764	1,531	1,231
APY_ $G^{-1}$	1,146	2,274	1,863

# Discussion

- PE variances appears **overestimated** with **APY**.
- Differences were **not significant**.
- Suggestions for application
  - Continue with **current practice**
  - Model **consistency** should be maintained

# Conclusions

- The amount of genotyped data is increasing.
- How we make variance estimates should consider that.
- Differences in estimates suggest to use G or APY\_G for VCE; but continuing VCE based on A probably won't affect EBV.

# Estimation of variance components using the pedigree, G or APY\_G

- **Michael Aldridge**, Jeremie Vandenplas & Mario Calus



# Results – Variance estimates with SE

Method	$A^{-1}$	$G^{-1}$	$APY\_G^{-1}$
Genetic	13,535 (688)	14,284 (647)	14,140 (695)
Permanent Environment	3,552 (361)	4,247 (210)	5,195 (199)
Residual	14,172 (129)	14,281 (130)	14,287 (130)