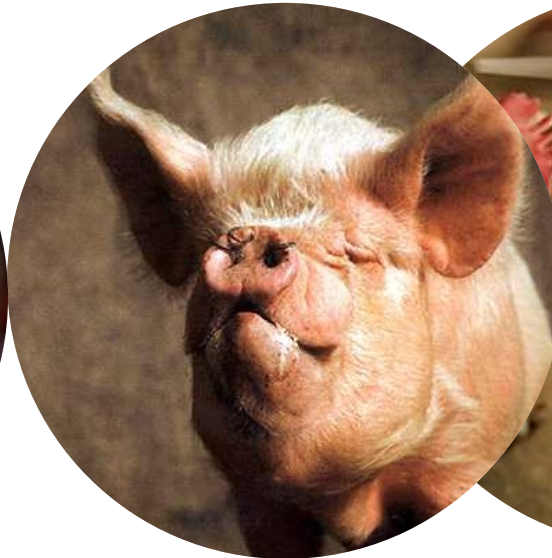


# Using pooled data to estimate genetic parameters for social interaction traits

Katrijn Peeters, Esther Ellen and Piter Bijma



# Pooling phenotypic data



Collecting individual data  
in group housing systems

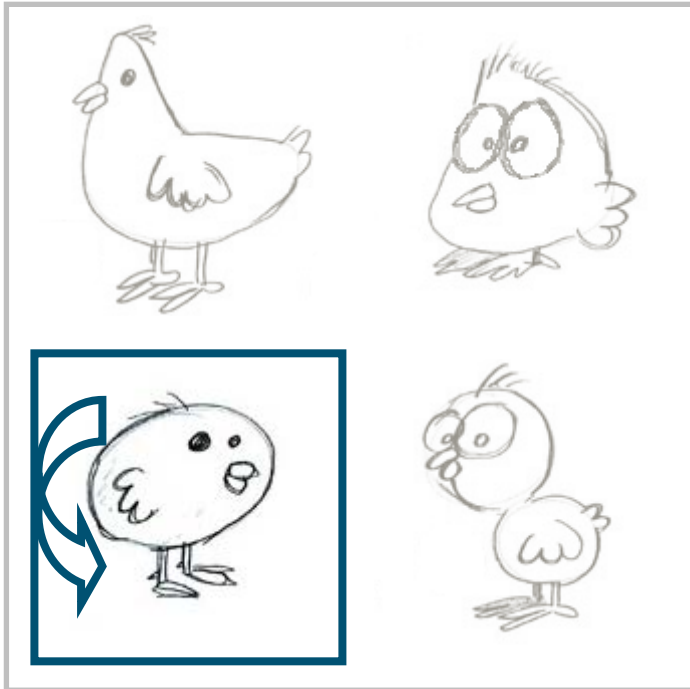
*Expensive*

*Difficult*



Pooling data

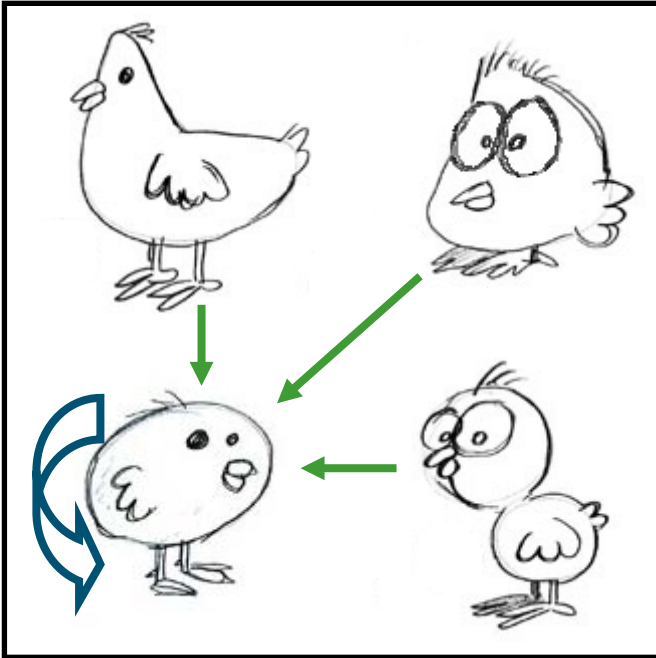
# Social interaction theory



Direct

$$P_i = A_{D_i} + E_{D_i}$$

# Social interactions theory

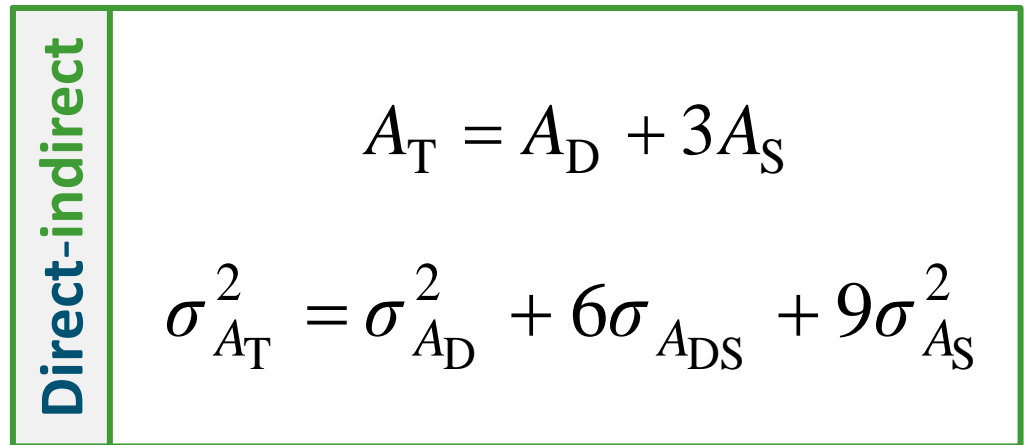
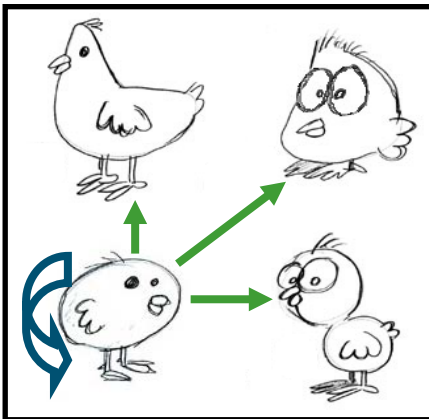
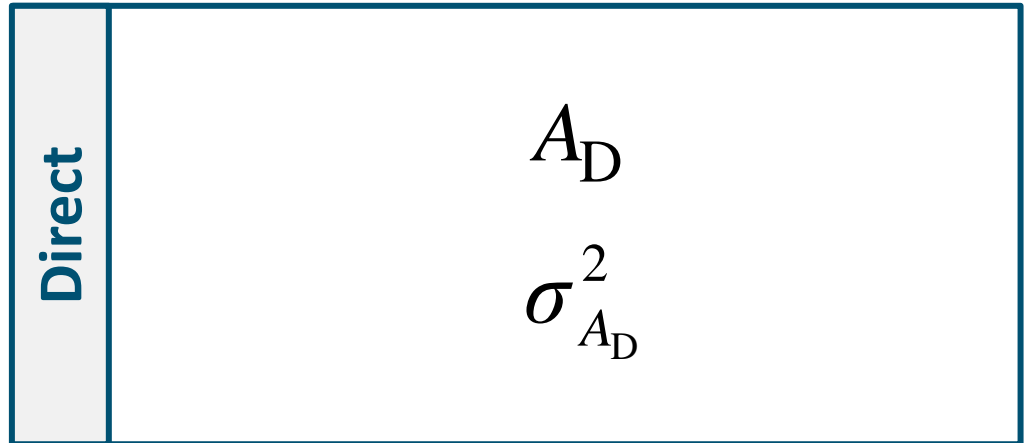
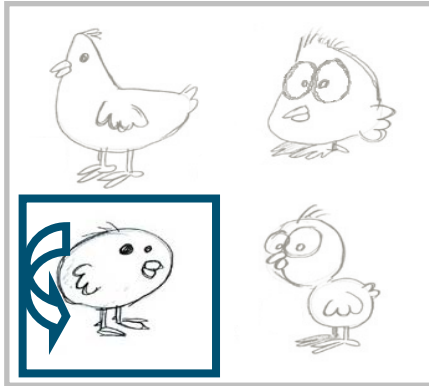


Direct

Social

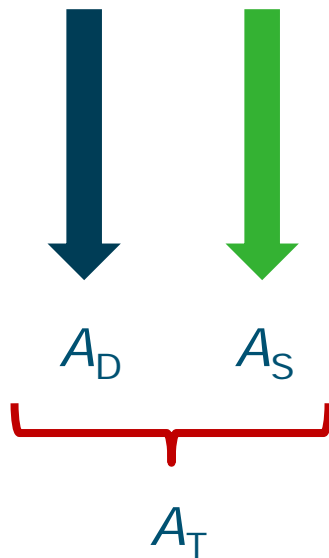
$$P_i = A_{D_i} + E_{D_i} + \sum_{i \neq j}^{n-1} A_{S_j} + \sum_{i \neq j}^{n-1} E_{S_j}$$

# Direct model ↔ Direct-Social model

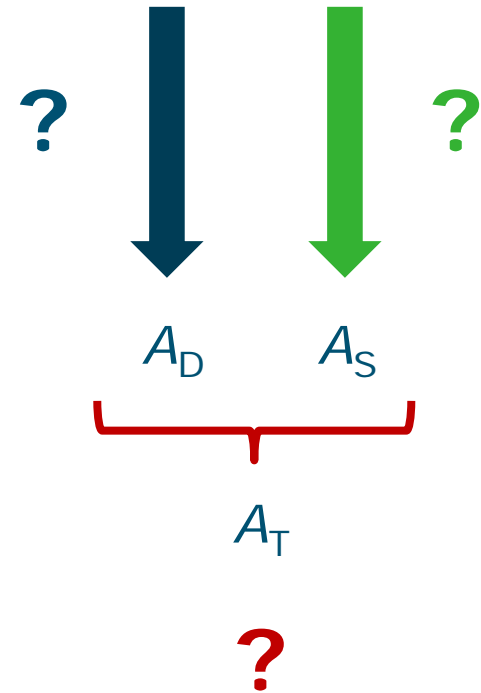


# Aim: what can we estimate?

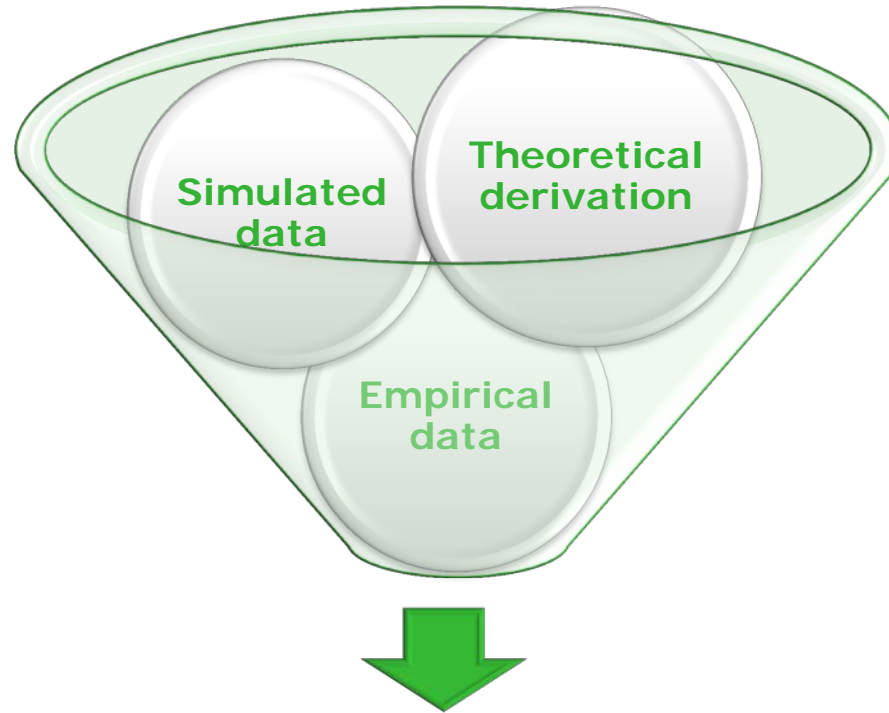
Individual data



Pooled data

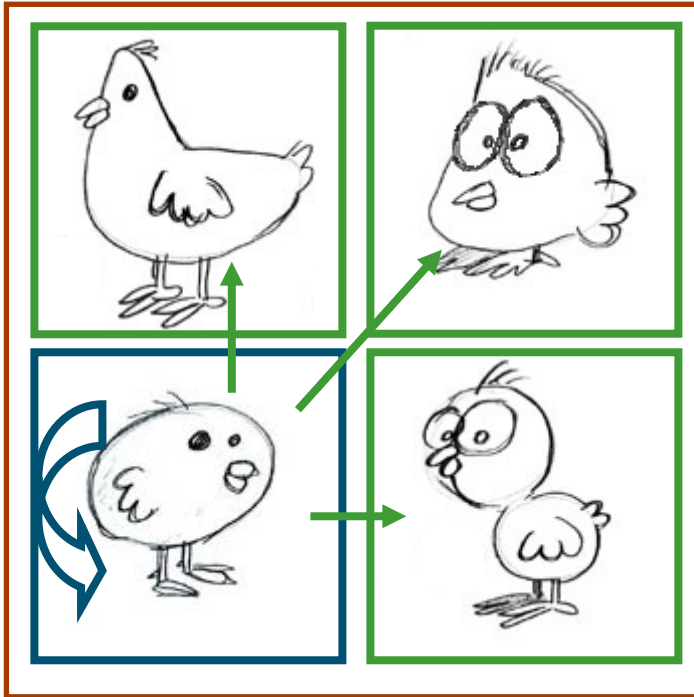


# Three Methods



Can we estimate  
direct and social genetic parameters  
from pooled data?

# 1. Theoretical derivation: Individual data



$$P_1 = \mathbf{A}_{D1} + A_{S2} + A_{S3} + A_{S4} + E$$

$$P_2 = A_{D2} + \mathbf{A}_{S1} + A_{S3} + A_{S4} + E$$

$$P_3 = A_{D3} + \mathbf{A}_{S1} + A_{S2} + A_{S4} + E$$

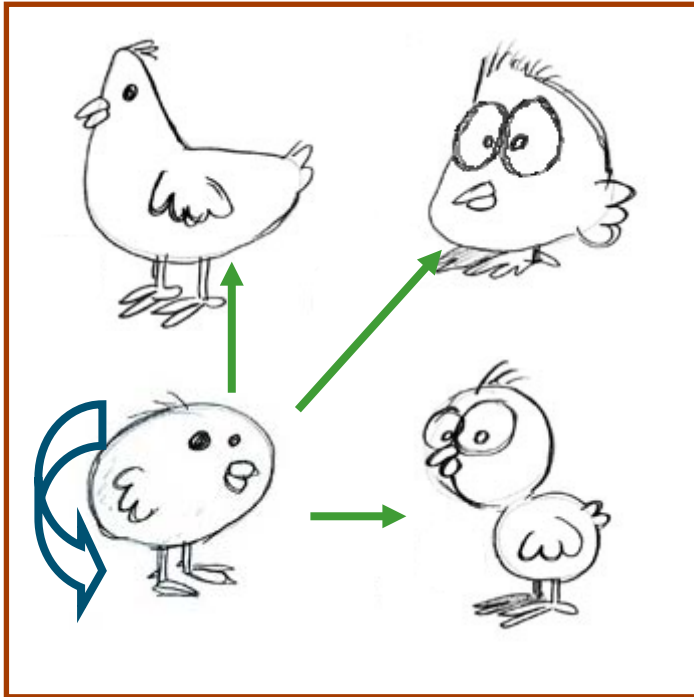
$$P_4 = A_{D4} + \mathbf{A}_{S1} + A_{S2} + A_{S3} + E$$

Information on  $A_D$  and  $A_S$  is obtained from different phenotypes ( $P_1 \neq P_{2/3/4}$ )

Both  $A_D$  and  $A_S$  are estimable



# 1. Theoretical derivation: Pooled data ( $P^*$ )



$$P^* = A_{D1} + A_{D2} + A_{D3} + A_{D4} + 3(A_{S1} + A_{S2} + A_{S3} + A_{S4}) + E$$

An individual's  $A_D$  and its full  $A_S$  is always lumped into a single record ( $P^*$ )

→  $A_D$  and  $A_S$  are fully confounded

$$P^* = A_{T1} + A_{T2} + A_{T3} + A_{T4} + E$$

→  $A_T$  can be estimated

→  $y = Xb + \Sigma Za + e$  will estimate  $A_T$

---

## 2. Simulated data

- 500 Sires, 500 Dams, 12 offspring per mating
- 12,000 individuals
- Direct and Social effects
- 3,000 groups of 4 individuals each
- Record = pooled phenotype per group



## 2. Simulated data

- Input

$$\sigma_{A_D}^2 = 1; \sigma_{A_S}^2 = 1; \sigma_{A_{DS}} = 0.5$$

$$\sigma_{E_D}^2 = 2; \sigma_{E_S}^2 = 2; \sigma_{E_{DS}} = 0$$

- Pooled data model (ASReml)

$$\mathbf{y} = \mathbf{Xb} + \mathbf{\Sigma Za} + \mathbf{e}$$

$$y \sim \mu \text{ FIXED } !r \ A_1 \text{ and}(A_2) \text{ and}(A_3) \text{ and}(A_4)$$

- Expected values  $\Leftrightarrow$  obtained values (100 replicates)

$$\sigma_{A_T}^2 = \sigma_{A_D}^2 + 6 \sigma_{A_{DS}} + 9 \sigma_{A_S}^2 = 13 \quad \Leftrightarrow \hat{\sigma}_A^2 = 13.05 (\pm 2.12)$$

$$\sigma_{E^*}^2 = 4(\sigma_{E_D}^2 + 6 \sigma_{E_{DS}} + 9 \sigma_{E_S}^2) = 80 \quad \Leftrightarrow \hat{\sigma}_E^2 = 80.32 (\pm 7.30)$$

Note:  $\hat{\sigma}_A^2 \neq \hat{\sigma}_{A_D}^2$  but  $\hat{\sigma}_A^2 = \hat{\sigma}_{A_T}^2$

### 3. Empirical data: cannibalistic laying hens



- 12,944 Laying hens  $\begin{cases} \rightarrow 6,092 \text{ W1} \\ \rightarrow 6,852 \text{ WB} \end{cases}$

- Individual survival time:

$$y \sim \mu \text{ FIXED } | r \ A_{D1} \ A_{I2} \ \text{and} \ (A_{I3}) \ \text{and} \ (A_{I4}) \ \text{Cage}$$

- Group survival time (pooled per cage):

$$y \sim \mu \text{ FIXED } | r \ A_{T1} \ \text{and} \ (A_{T2}) \ \text{and} \ (A_{T3}) \ \text{and} \ (A_{T4})$$

### 3. Empirical data

Individual data

Pooled data

	W1	WB
$\sigma_{AD}^2$	705 ( $\pm 171$ )	1,404 ( $\pm 301$ )
$\sigma_{ADS}$	59 ( $\pm 61$ )	-162 ( $\pm 105$ )
$\sigma_{AS}^2$	104 ( $\pm 41$ )	292 ( $\pm 72$ )
$\sigma_{Cage}^2$	799 ( $\pm 166$ )	1,191 ( $\pm 238$ )
$\sigma_E^2$	7,980 ( $\pm 210$ )	12,675 ( $\pm 365$ )

$$\sigma_{AD}^2 + 6 \sigma_{ADS} + 9 \sigma_{AS}^2 = \sigma_{AT}^2$$

$$16 \sigma_{Cage}^2 + 4 \sigma_E^2 = \sigma_{E^*}^2$$



### 3. Empirical data

Individual data

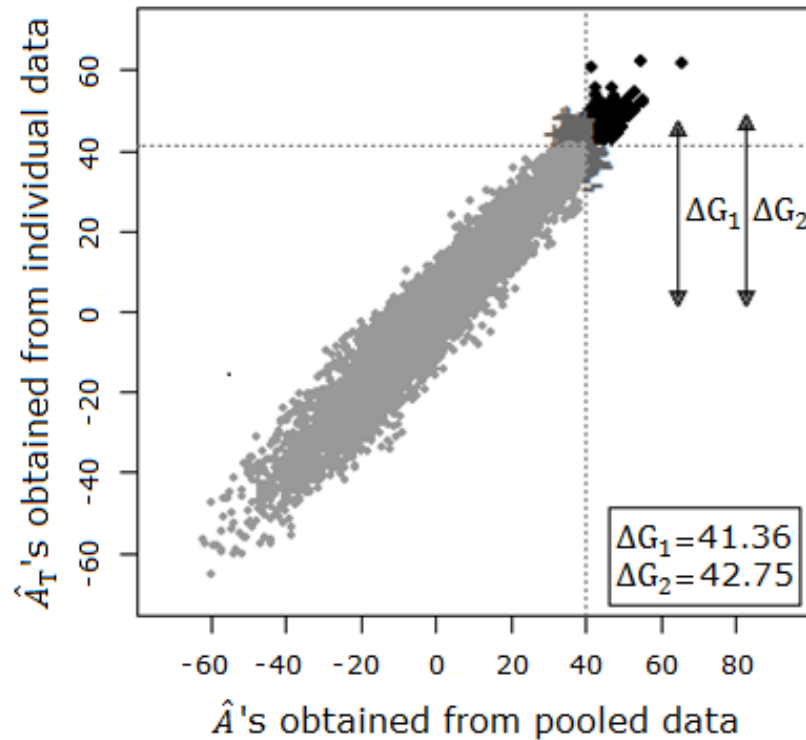
Pooled data

	W1	WB		W1	WB
$\sigma_{A_T}^2$	1,996 ( $\pm 640$ )	2,521 ( $\pm 842$ )	$\sigma_{A_T}^2$	1,979 ( $\pm 643$ )	2,521 ( $\pm 845$ )
$\sigma_{E^*}^2$	44,700 ( $\pm 2,526$ )	69,752 ( $\pm 3,513$ )	$\sigma_{E^*}^2$	44,750 ( $\pm 2,538$ )	69,750 ( $\pm 3,519$ )

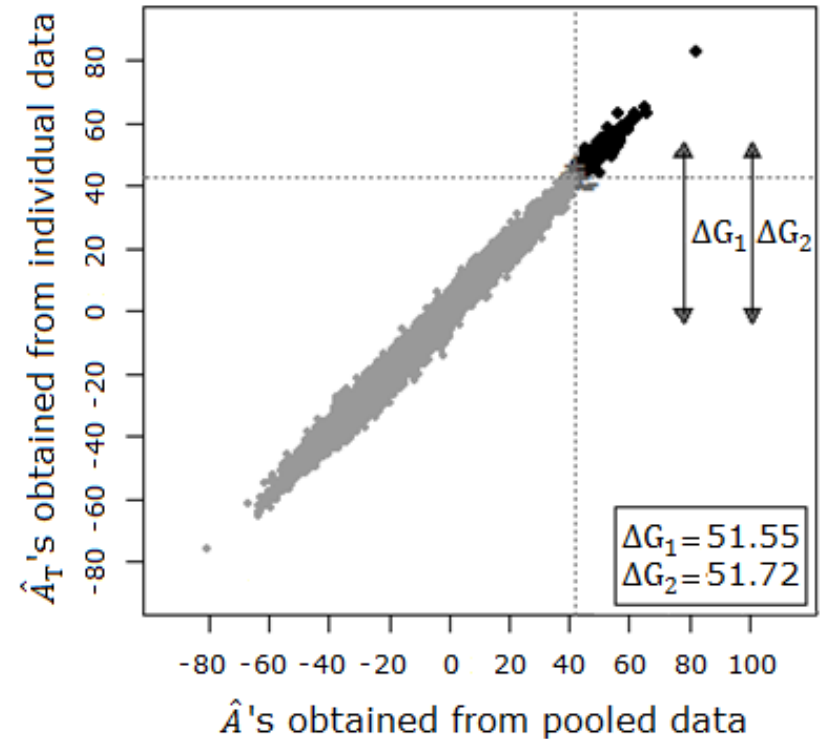
Indeed: analysis of pooled records yields  $\hat{\sigma}_{A_T}^2$  rather than  $\hat{\sigma}_{A_D}^2$

### 3. Empirical data: The cost of pooling

W1



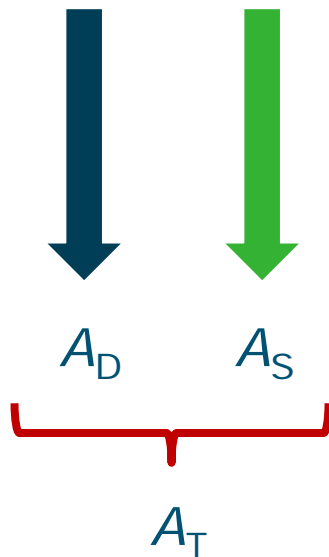
WB



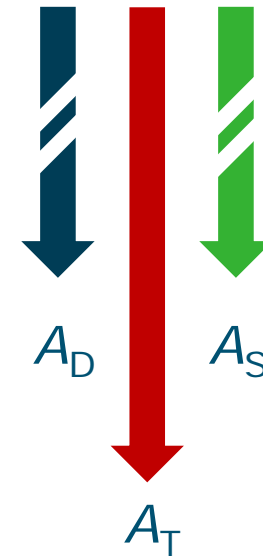
Pooling causes surprisingly little reduction in response to selection for socially-affected traits.

# Conclusion

Individual data



Pooled data



With social interactions,  
estimated  $\text{Var}(A)$  from pooled data will differ from ordinary  $\text{Var}(A)$ .

$$\text{Var}(A)_{\text{pooled}} = \text{Var}(A_T)$$



# Social interactions

Peeters *et al.*, Genetics Selection Evolution **45**:27

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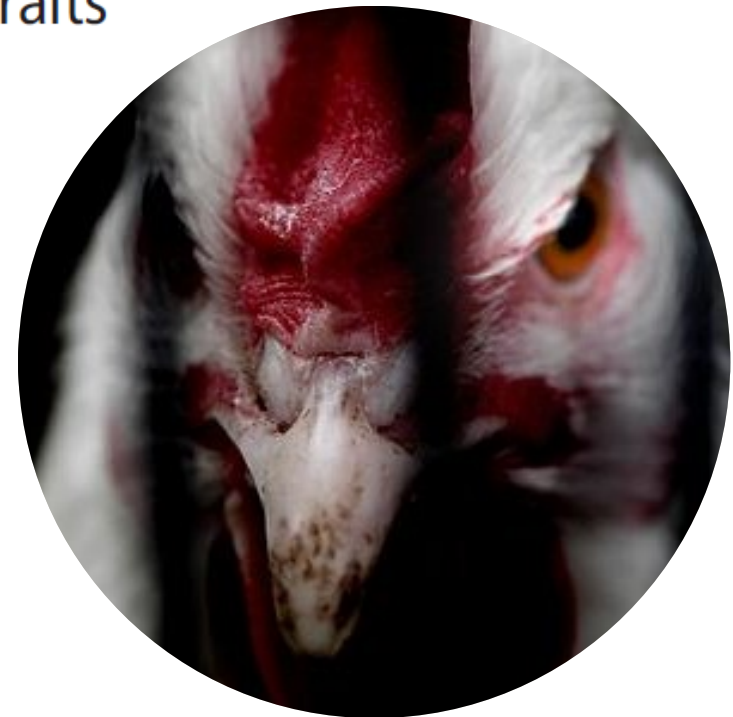


**RESEARCH**

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## Using pooled data to estimate variance components and breeding values for traits affected by social interactions

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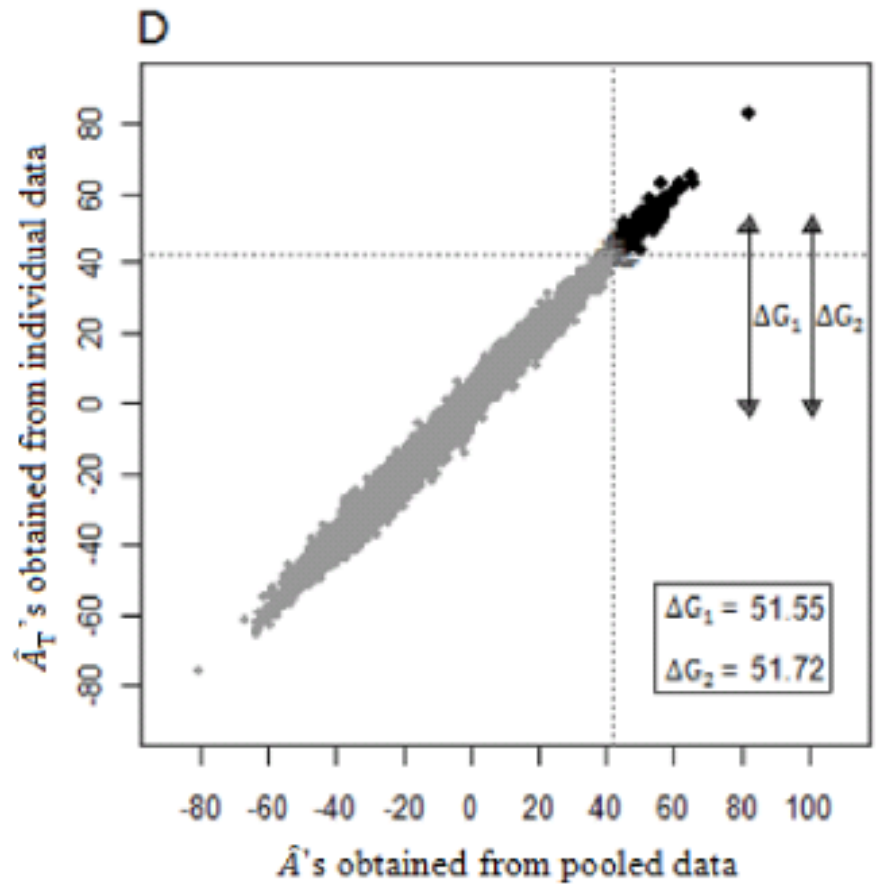
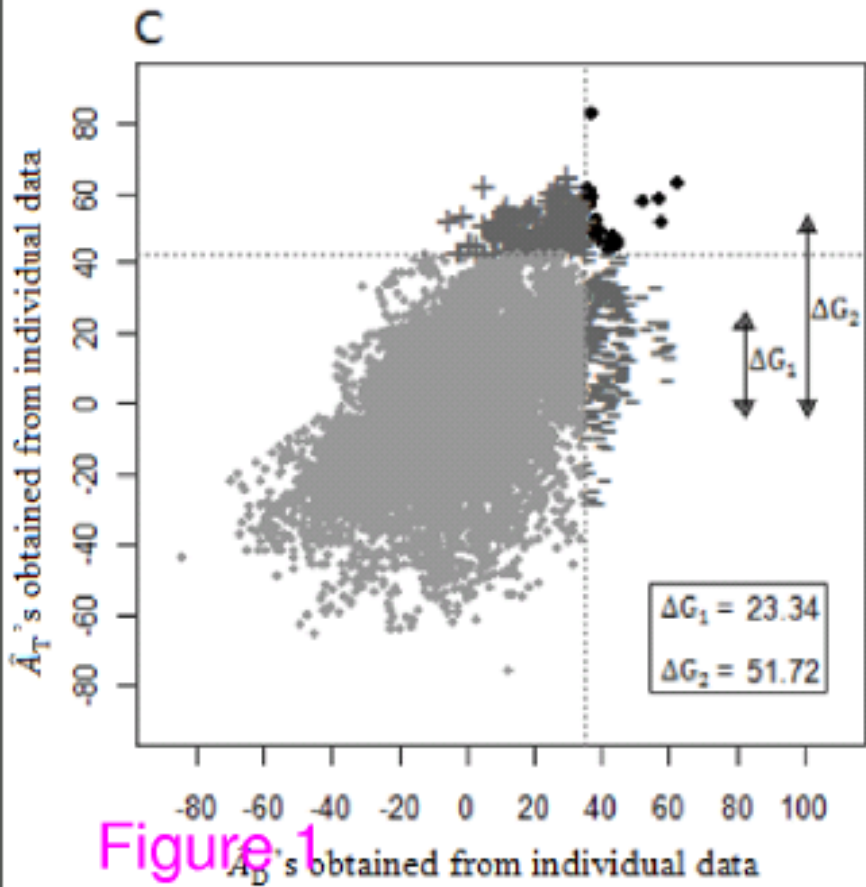


Figure 1