PLANTCOM meeting, Dijon

Quantitative genetics of plant–plant interactions: case of crop mixtures

Jemay Salomon

UMR GQE Le Moulon
Université Paris–Saclay, INRAE, CNRS, AgroParisTech

Outline

Context and motivation

Case of crop mixtures
    Material and methods
    Results
    Conclusions and perspectives

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Gaps of knowledge:

▶ Which experimental designs?
▶ Which magnitude of genetic (co)variances?
▶ Which genetic architectures?

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Genetic model

Social intra-genotypic value: $SIGV := SBV^{SC} + (DBV \times SBV)^{SC}$

Genetic model

Intercrop of i (species s_1) and j (species s_2):

$$Y_{i(j)} = \mu^{s_1,IC} + DBV_i + SBV_j^{IC} + (DBV \times SBV)_{ij}^{IC}$$
$$Y_{j(i)} = \mu^{s_2,IC} + DBV_j + SBV_i^{IC} + (DBV \times SBV)_{ji}^{IC}$$

Sole crop of i and sole crop of j:

▶ $Y_i = \mu^{s_1,SC} + DBV_i + SIGV_i$

▶ $Y_j = \mu^{s_2,SC} + DBV_j + SIGV_j$

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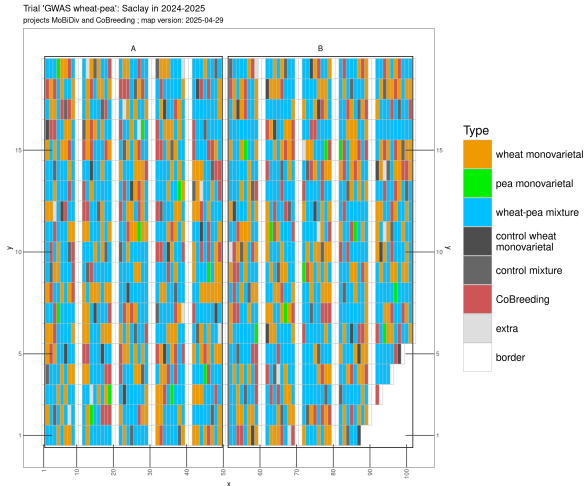
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▶ Software implementation: `plantmix` (R package)

Panel and field trial

- 200 wheat varieties
  - 395k SNPs

- 2 pea varieties (testers)

- All sole and intercrops in 2 complete blocks

- Traits per species: grain yield, TKW, final height, SLA, soil cover

Trial 'GWAS wheat-pea': Saclay in 2024-2025
projects MoBiDiv and CoBreeding ; map version: 2025-04-29

Type
- wheat monovarietal
- pea monovarietal
- wheat-pea mixture
- control wheat monovarietal
- control mixture
- CoBreeding
- extra
- border

Panel and field trial

Le Moulon, Saclay, 2025

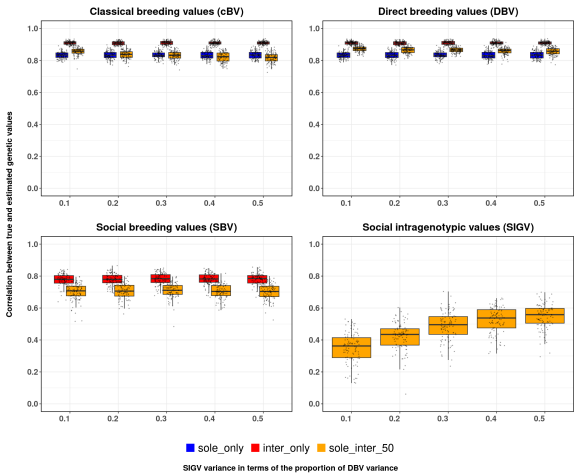# Outline

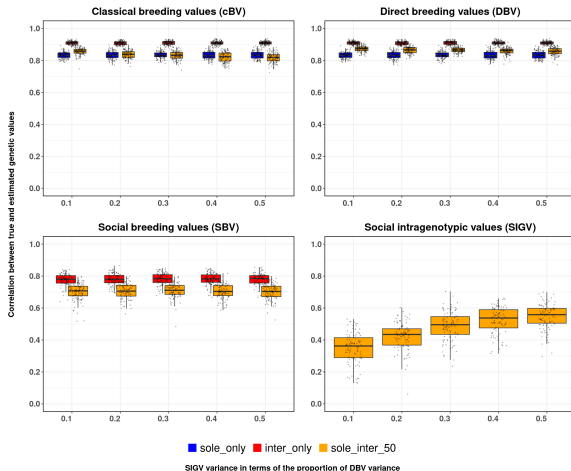# Accuracy of parameter estimation
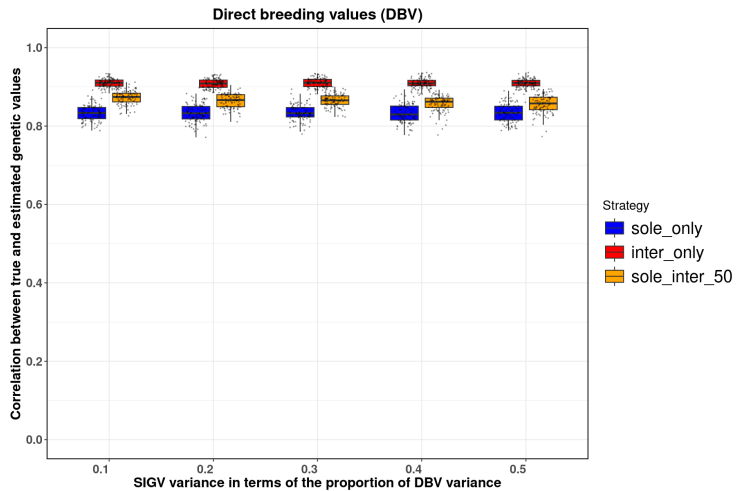
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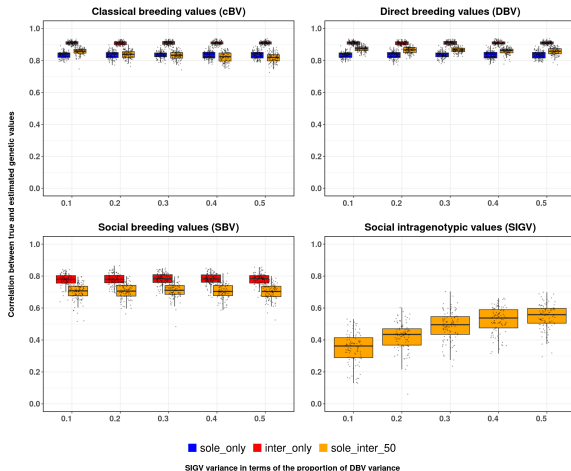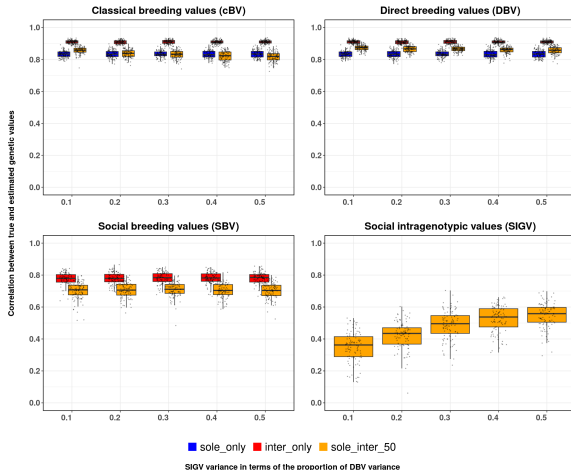- **Inter_only provides the most accurate estimates**.

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- **Experimental design**, **genetic effects**, and the ratio $\sigma^2_{SIGV}/\sigma^2_{DBV}$ influence **accuracy**.

- **Inter_only provides the most accurate estimates**.

- **Sole_inter_50 helps decoupling SIGV and DBV**, improving their estimation.

Variance estimates for grain yield

σ^2_{DBV}	σ^2_{SBV}	σ^2_{SIGV}	$\sigma^2_{DBVxSBV}$	$\sigma^2_{e\text{-}pur(w)}$	$\Sigma^2_{e\text{-}mix(w)}$	$\Sigma^2_{e\text{-}mix(p)}$
10.1	**1.25**	**2.49**	**2.19**	**16.6**	**12.78**	**18.53**
[8.01, 11.39]	[0.17, 247]	[0, 5.23]	[0.14, 5.76]	[12.00, 20.00]	[10.61, 13.98]	[15.56, 21.30]

Values are shown as the estimate (first line), followed by the 95% confidence interval in brackets (second line), calculated across 500 replicates using bootstrapping.
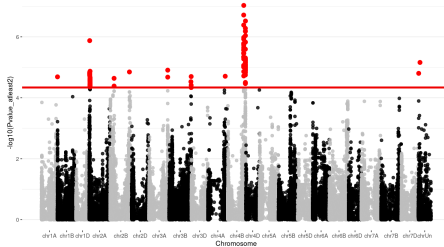
▶ Social genetic variances < variance of direct breeding values

Correlation estimates for grain yield

$\rho_{\text{DBV-SBV}}$	$\rho_{\epsilon\text{-mix}}$
0.24	-0.19
[0.01, 1]	[-0.29, -0.07]

▶ Unexpected positive correlation observed between DBV and SBV
  $\Rightarrow$ favorable wheat–pea interactions

Meta-GWAS on grain yield
[DBV, SBV, SIGV]

H0 rejected when a SNP is associated with
at least two traits (FDR controlled at 5%)

▶ **9 pleiotropic regions detected**

- Not detected in single-trait GWAS.

- Further analyses underway for validation.

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- Analyze the other traits, notably those from drone imaging (PhD V. Freitas).

Acknowledgments

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- **BIOGER**: T. Vidal, M. Delrieu

- **IGEPP**: N. Moutier, R. Perronne

- **AGAP**: A. Baranger

Supp 1: meta-GWAS on grain yield [DBV, SBV, SIGV]
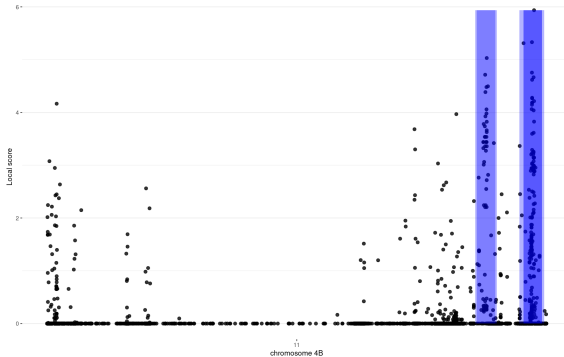
Local scores along chromosome 4B. The boxes represent the significant zones identified. The threshold was set to $\xi = 2$, and the nominal FDR level is fixed at 0.05.