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Biotechnology and  
Biological Sciences  
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# Spatial modelling improves genetic evaluation of Tanzanian smallholder crossbred dairy cattle

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# Large collaboration

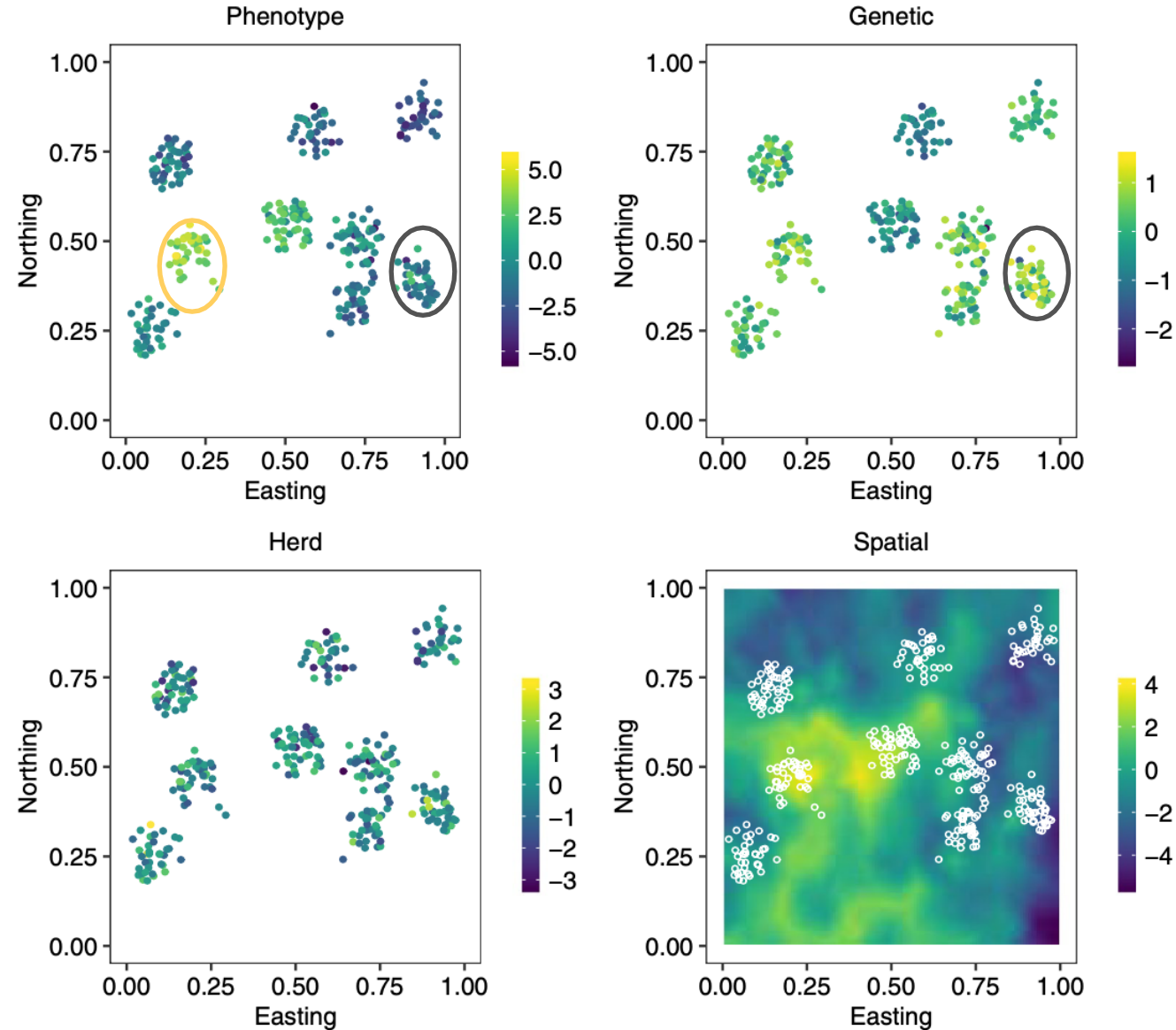


# African Smallholder breeding programmes

“Phenotype and genotype some cows and you can do genomic selection”

- Small-holder farms are small & very variable
- Limited use of assisted reproduction (AI, MOET, ...)  
→ hard to separate genetic and environmental effects
- A solution?
  - borrow information from neighbours (spatial model)

# Spatial context



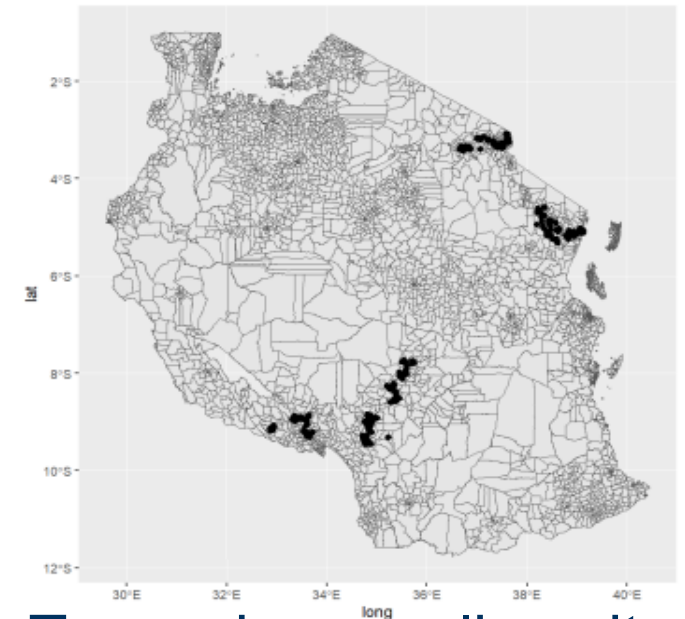
Selle et al.. 2020 (<https://doi.org/10.1186/s12711-020-00588-w> )

# Data

- 1911 crossbred cows  
(4 classes of exotic genes)
- Genotyped with 664,822 SNPs
- 1386 herds (1-9 cows/herd; 75% < 3 cows)
- 72 wards
- 19,375 test-day milk yields
- Average ( $\pm$  SD) milk yield (Kg)  $8.31 \pm 4.31$



A crossbred cow

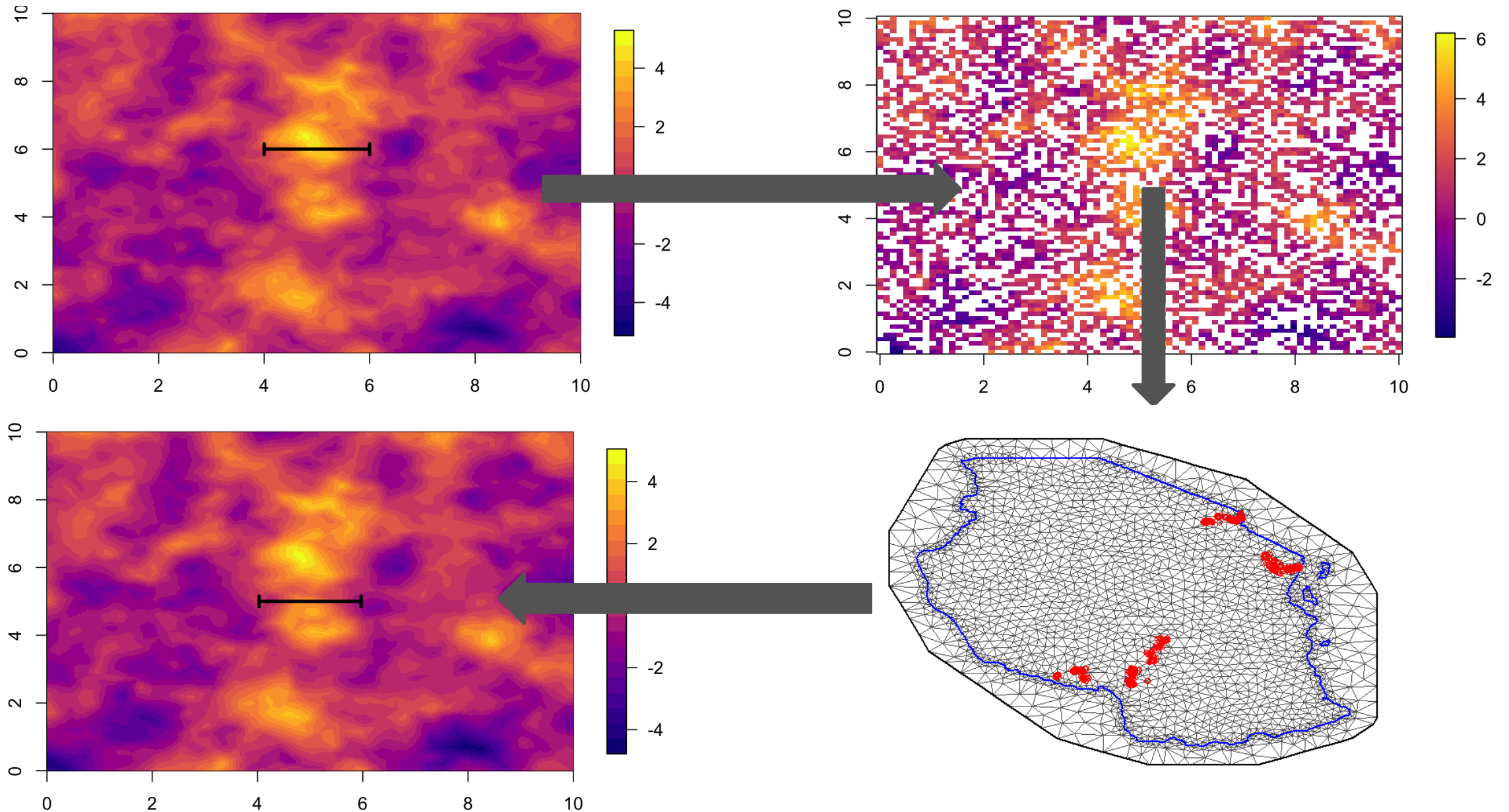


Tanzania sampling sites

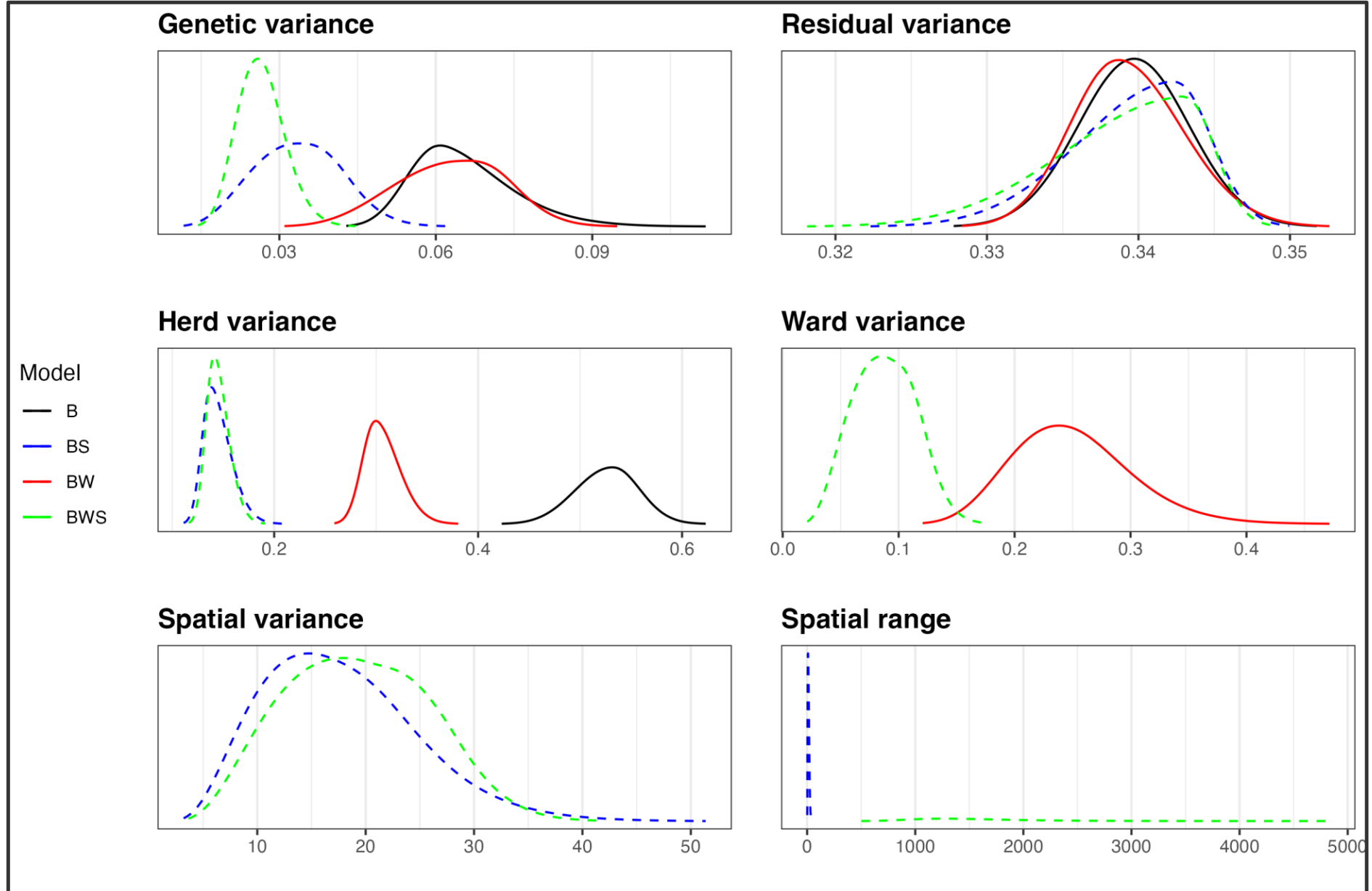
# Modelling

- Baseline model (B):
  - Phenotype = Fixed + Herd + Perm + Genetics + Noise
  - Herd  $\mathbf{h} \sim N(0, \mathbf{I} \sigma^2_h)$
  - Perm  $\mathbf{p} \sim N(0, \mathbf{I} \sigma^2_p)$
  - Genetics  $\mathbf{a} \sim N(\mathbf{0}, \mathbf{G} \sigma^2_g)$
  - Noise  $\mathbf{e} \sim N(0, \mathbf{I} \sigma^2_e)$
- Alternative models
  - BW = B + Wards  $\mathbf{w} \sim N(0, \mathbf{I} \sigma^2_w)$
  - BS = B + Location (spatial)  $\mathbf{L} \sim N(0, \text{Matern}(\mathbf{E}, \text{Kappa}, \sigma^2_L))$
  - BWS = BW + Spatial effects
- All models fitted with R-INLA

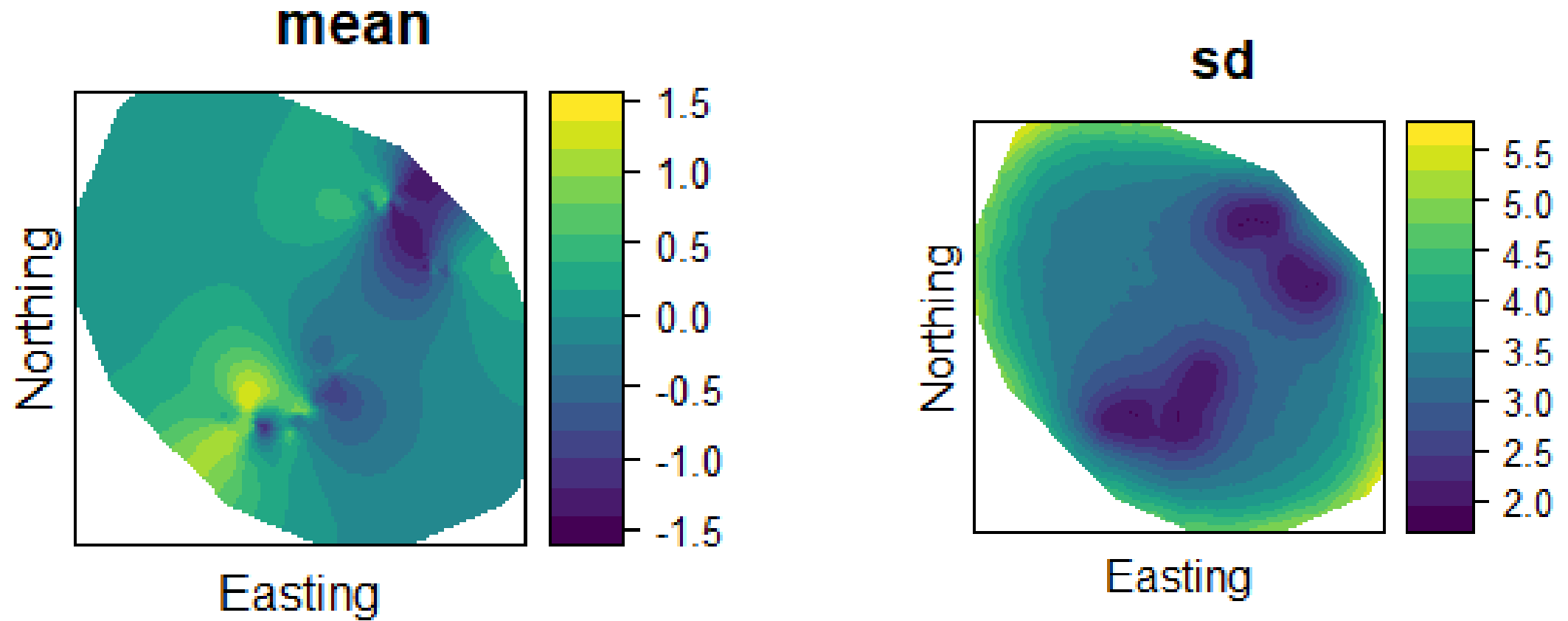
# Spatial modelling with R-INLA



# Variance components (posterior distribution)

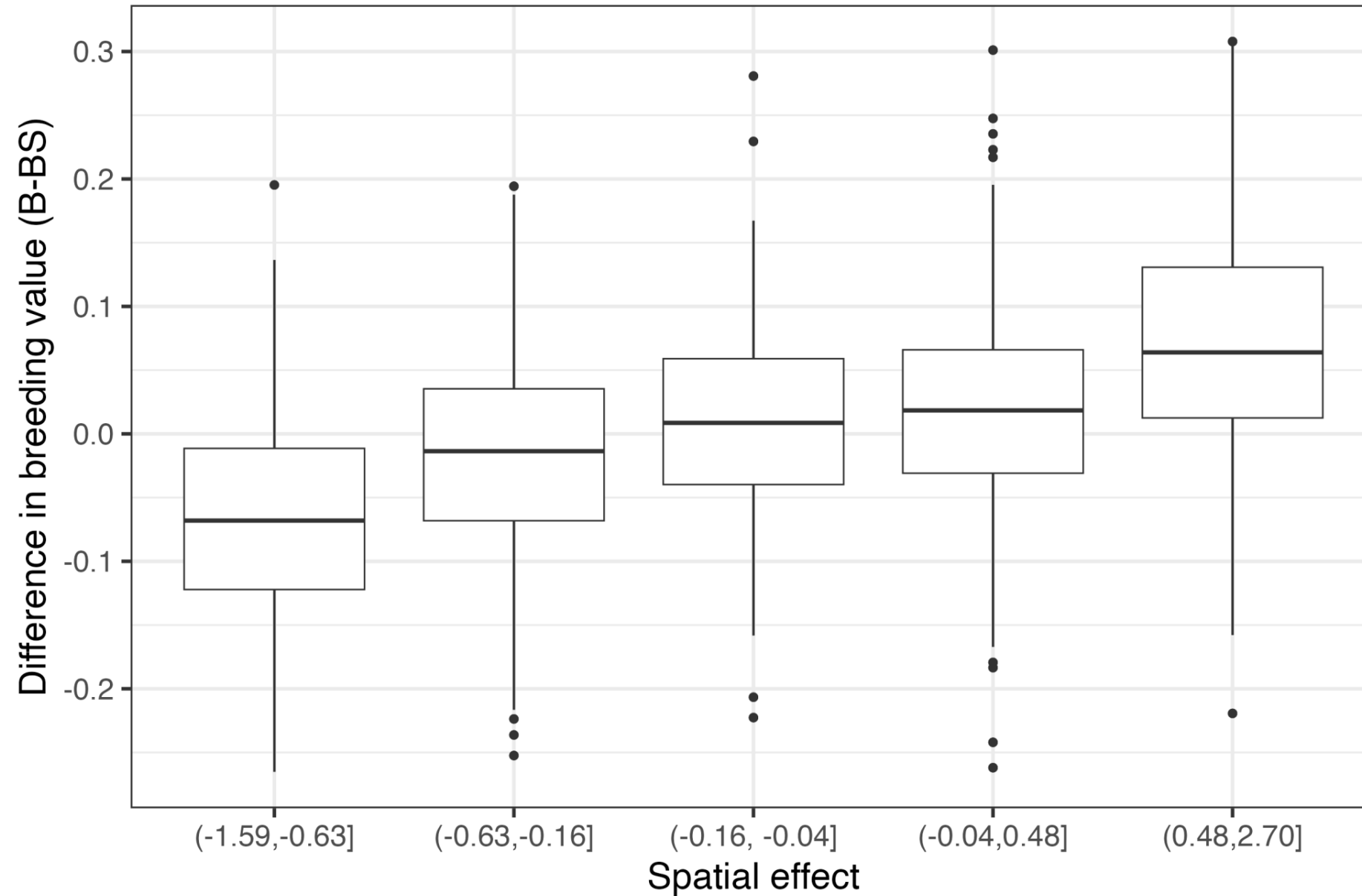


# Spatial effects



**Fig:** Posterior mean and standard deviation of estimated spatial effect from model BWS

# Does it matter? Yes!



# Phenotype predictive accuracy of models

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## Proportion of exotic genes (cross validation)

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**<0.36      0.36-0.6      0.61-0.875      >0.875**

| <b>Models</b> | <b>(n=84)</b> | <b>(n=309)</b> | <b>(n=770)</b> | <b>(n=731)</b> | <b>Average</b> | <b>Forward validation<br/>(n=146 )</b> |
|---------------|---------------|----------------|----------------|----------------|----------------|----------------------------------------|
|---------------|---------------|----------------|----------------|----------------|----------------|----------------------------------------|

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**B**

**BW**

**BS**

**BWS**

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# Phenotype predictive accuracy of models

Proportion of exotic genes (cross validation)

| Models | <0.36<br>(n=84) | 0.36-0.6<br>(n=309) | 0.61-0.875<br>(n=770) | >0.875<br>(n=731) | Average | Forward validation<br>(n=146 ) |
|--------|-----------------|---------------------|-----------------------|-------------------|---------|--------------------------------|
| B      | -0.05           | 0.28                | 0.34                  | 0.24              | 0.20    | 0.40                           |
| BW     |                 |                     |                       |                   |         |                                |
| BS     |                 |                     |                       |                   |         |                                |
| BWS    |                 |                     |                       |                   |         |                                |

# Phenotype predictive accuracy of models

Proportion of exotic genes (cross validation)

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|        | (n=84) | (n=309)  | (n=770)    | (n=731) |         |                                |
| B      | -0.05  | 0.28     | 0.34       | 0.24    | 0.20    | 0.40                           |
| BW     | 0.22   | 0.39     | 0.51       | 0.42    | 0.39    | 0.59                           |
| BS     |        |          |            |         |         |                                |
| BWS    |        |          |            |         |         |                                |

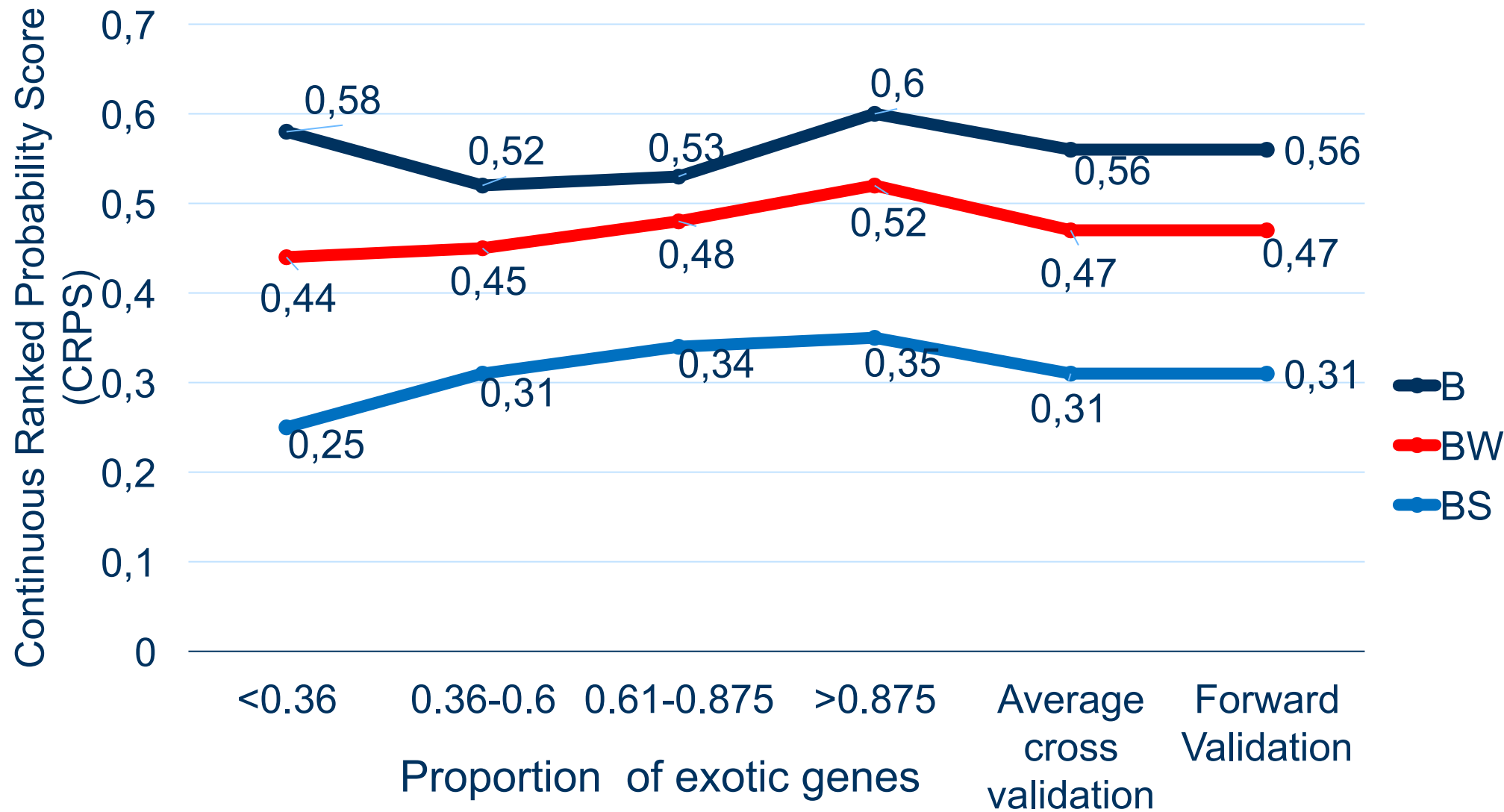
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| BS     | 0.75                                          | 0.78     | 0.82       | 0.81    | 0.79    | 0.86                           |
| BWS    |                                               |          |            |         |         |                                |

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| BWS    | 0.75                                          | 0.78     | 0.82       | 0.81    | 0.79    | 0.86                           |

# Continuous Ranked Probability Score (CRPS)



# Conclusion

- Spatial modelling has a significant effect on estimated variance components
- Estimated breeding values change when we account for location (likely fixes over/under-estimation)
- Doubles phenotype prediction accuracy
- Future: Work with environmental covariates and  $G \times E$



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