

Resource allocation for maximizing prediction accuracy and genetic gain of genomic selection in plant breeding: A simulation experiment

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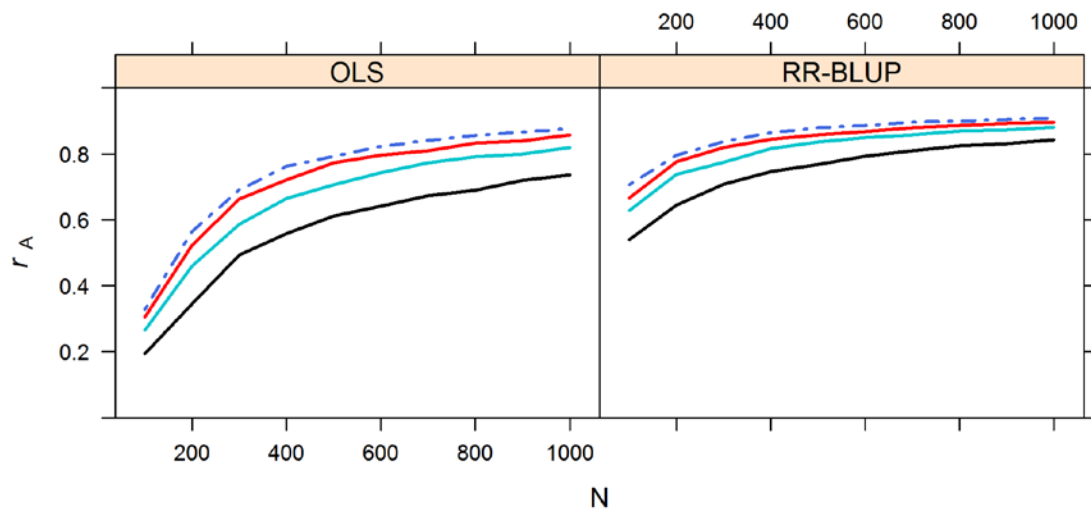


Figure S1 Prediction accuracy (r_A) as a function of replication number and population size for each of two statistical models. Black = 1 rep, Teal = 2 reps, Red = 3 reps, Dashed blue = 4 reps.

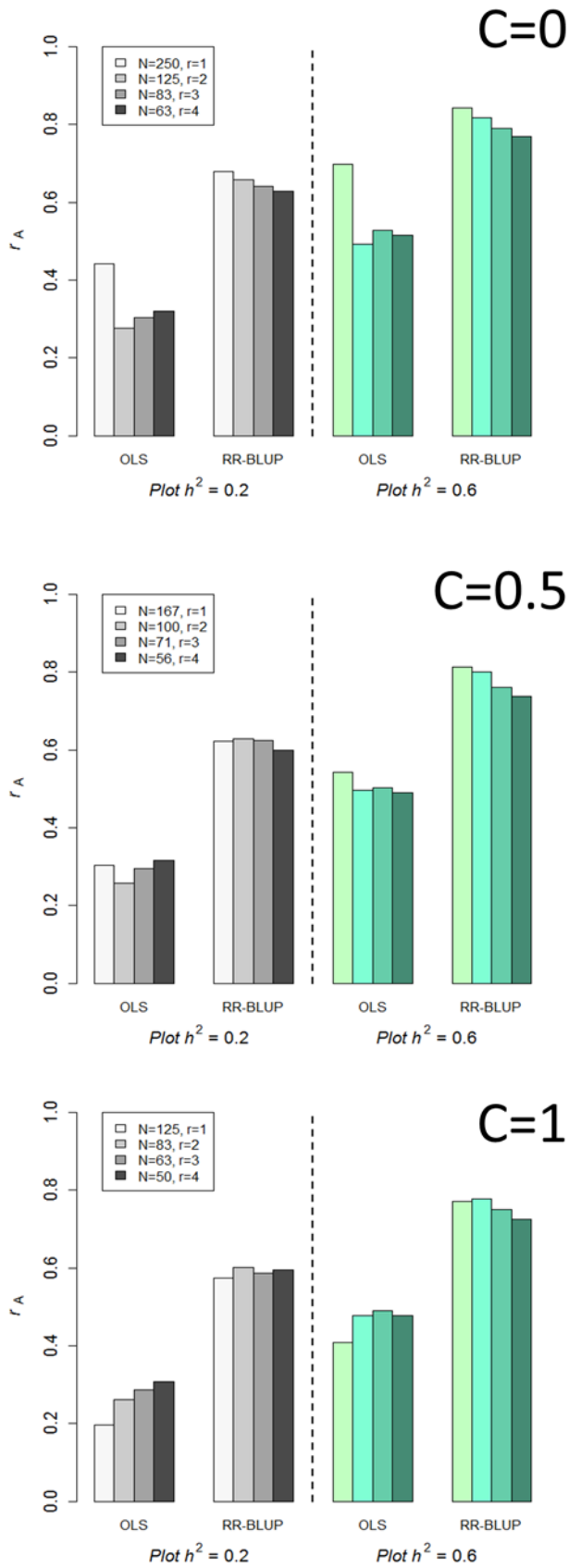


Figure S2 Prediction accuracy (r_A) for two statistical models as affected by tradeoffs between replication (r) and population size (n) for various levels of relative genotyping costs (C) expressed in field plot equivalents. Total budget is set to 250 field plot equivalents.

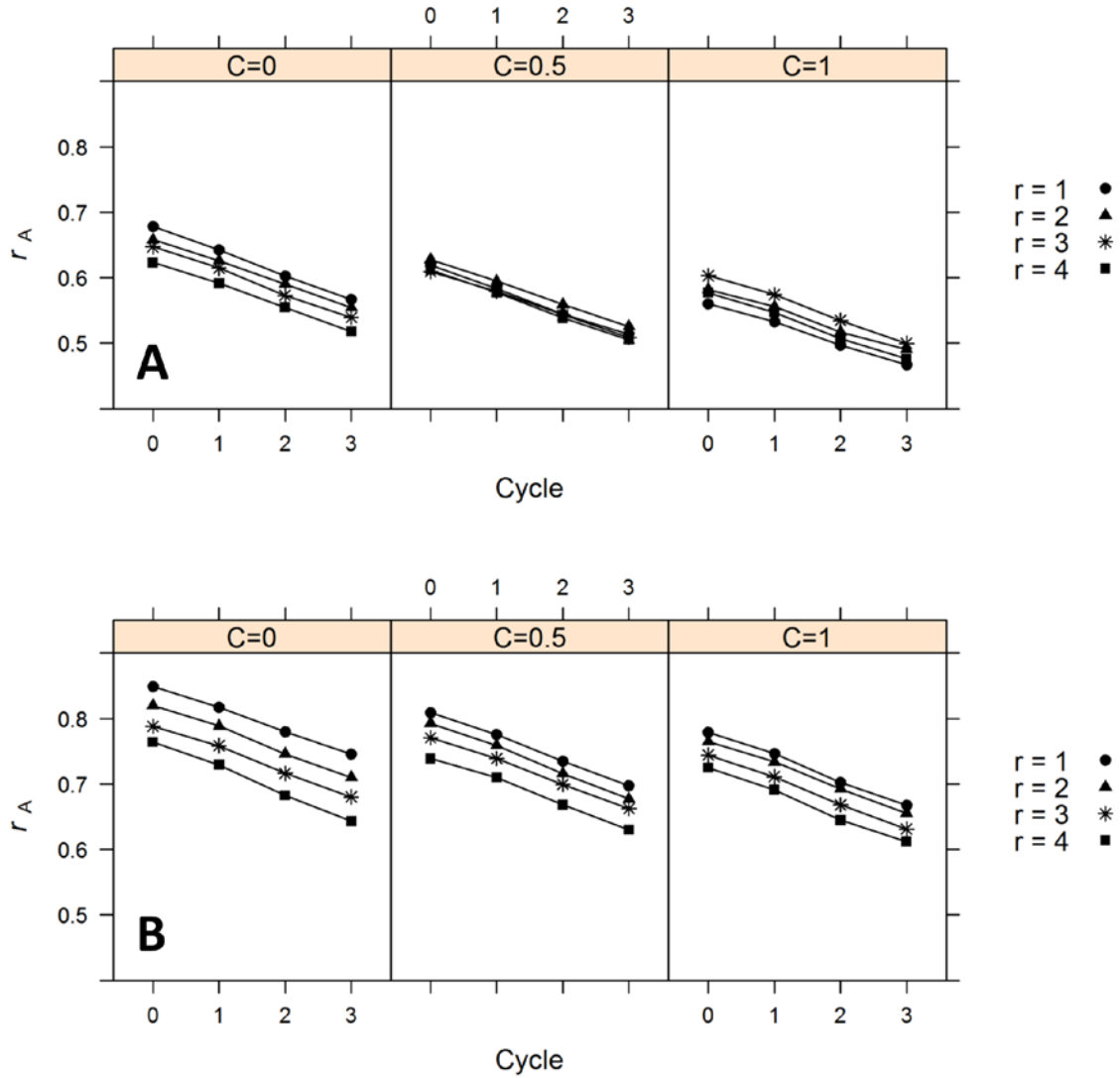


Figure S3 Prediction accuracy (r_A) for each relative genotyping cost and resource allocation strategy across generations of random mating (Cycle). Population sizes corresponding to each level of r can be observed in Figure 2. Total budget was set to 250 field plot equivalents. Panel A: Heritability of single plot measurements set to 0.20. Panel B: Heritability of single plot measurements set to 0.60. Average standard error of prediction accuracies was 0.006 and ranged from 0.003 to 0.008.

Files S1-S2

File S1: R script containing functions used in the simulation

File S2: User script executing the functions

Files S1-S2 are available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.112.004911/-/DC1>.