

**Implementation of different relationship estimate methodologies in Breeding Value prediction in kiwiberry
(*Actinidia arguta*)**

Molecular Breeding

Daniel Mertten*, Samantha Baldwin, Canhong H. Cheng, John McCallum, Susan Thomson, David T. Ashton,
Catherine McKenzie, Michael Lenhard, Paul M. Datson

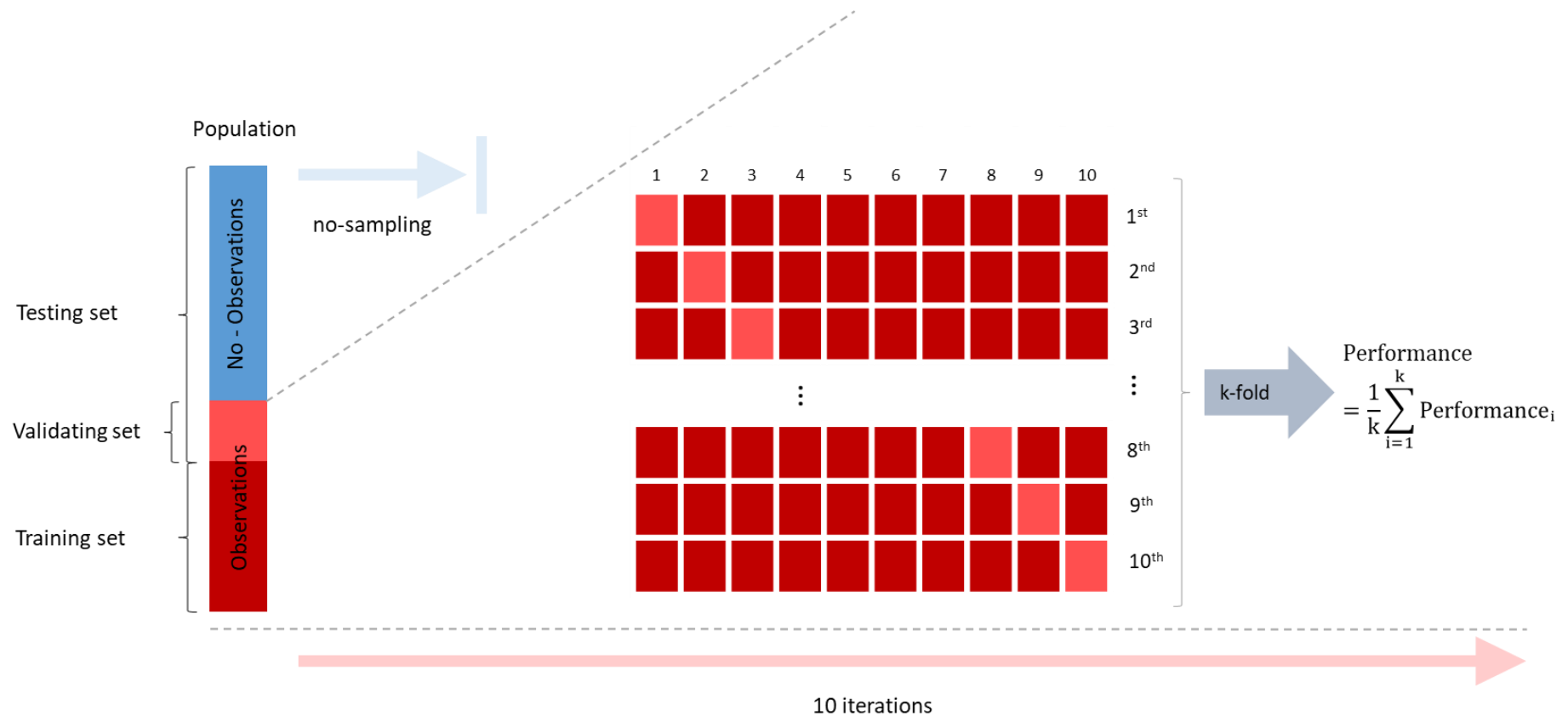
***Corresponding author:**

Daniel Mertten

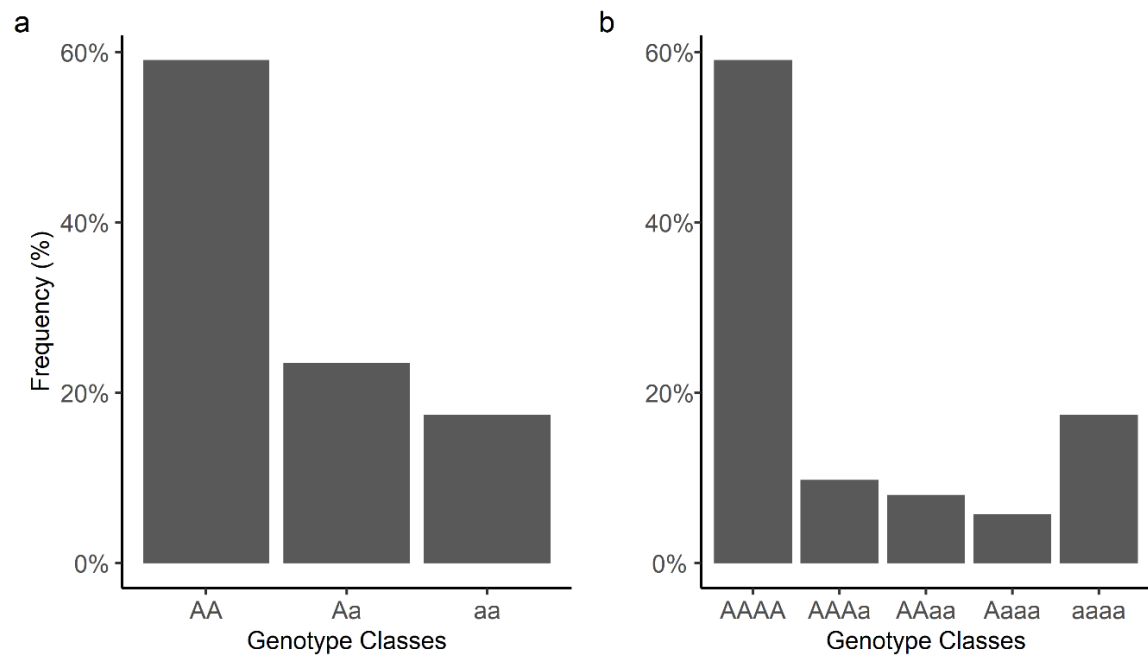
The New Zealand Institute for Plant and Food Research Ltd (PFR)

Auckland 1142, New Zealand

Email: Daniel.Mertten@plantandfood.co.nz



Supplementary Fig. 1 10-fold cross-validation methodology. The base population contained *Actinidia arguta* female progeny with observations (red), parental individuals as well as distant ancestors and male progeny without records (blue). Female progeny with observed records were divided randomly into training and validation sets using a 10-fold cross-validation approach. In the validation set, the observations were masked. Progeny with observations were randomly grouped into 10 groups; each was used once as a validation set (light red), whereas nine groups were used to train the model (training set, dark red). Individuals with no phenotypic information were explored using the full model



Supplementary Fig. 2 Heterozygosity, distribution of *Actinidia arguta* kiwiberry allele dosage classes shown under re-classification for pseudo-diploid (a) and tetraploid dosage classification (b)