

Modeling for Ambiguous SNP Calls in Allotetraploid Peanut

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Cultivated peanut is an allotetraploid crop with highly similar A and B sub-genomes, and a relatively large genome size of around 2.7 Gbps. Accurate genotype of allotetraploid peanut is challenging due to alignment ambiguities caused by homology leading to an excess of heterozygous calls. In this study we propose an allotetraploid specific method that carefully assesses the strength of A and B alignments to estimate the genotype of a sequenced individual at a single locus in a homoeologous region. The proposed method does not require evidence of haplotypes, in contrast to other methods which have been developed earlier. This method was validated on WGS re-sequenced data and simulated amplicon sequences. In providing this tool, we hope to benefit plant breeding programs by genotyping allotetraploids with greater accuracy and thereby better revealing the true variations among genotypes.