

A User-Friendly Java-Based Statistical Tool to Analyse the Segregation Data of Crosses in Genetics and Breeding

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Genetic and breeding studies are characterised by making crosses between selected parental organisms and establishing segregating populations such as F₂, back crosses, test crosses, pseudo test crosses and recombinant inbred lines followed by detailed observations and statistical analyses of phenotypic data for traits of interest. The phenotypic data are often considered as ratios (e.g. 26 short: 37 tall in plants) for both major gene and poly gene controlled traits. In genetics, there are standard ratios for genetic segregations and using standard ratios as expected ratios. A goodness of fit test for observed phenotypic ratios is also conducted. When a geneticist or a breeder comes up with a ratio for observed phenotypic data, multiple comparisons could be made against many standard genetic segregation ratios to select the highest significant match for biological interpretation and practical uses. The multiple comparisons under different probability levels are time consuming and demand considerable expertise in non-parametric statistics. Therefore, an attempt was made to design a user-friendly Java-based statistical tool to analyse segregation data from crosses in genetics and breeding. This statistical tool can be used by geneticists and breeders with limited statistical knowledge to get most approximate ratios for observed phenotypic crosses. A statistical tool was developed by using Java programming language in NetBeans IDE 6.8. The population size in number of individuals, standard ratio and observed ratio for phenotypic data have to be entered and highest matching ratio and goodness of fit for other possible standard ratios can be obtained as the output. The tool was tested and validated by using already published data from genetic crosses.

The developed statistical tool is user-friendly and quick in finding the significant standard ratios in genetic and breeding studies. This is useful for purposes of genetic research, breeding, and teaching genetics to undergraduate, postgraduate and Advanced Level Biology students.