Bogotá, March 20th, 2020

Dear Editorial Board,

We would like to submit our manuscript for your consideration for publication in Bioinformatics. The manuscript title is *MultiGWAS: A tool for GWAS analysis on tetraploid organisms by integrating results of four GWAS software*.

GWAS allows analyzing genomics data to identify the set of variants across different individuals of a species that are associated with a specific trait. Due to the advances in the next-gen sequencing technology, currently, the GWAS analysis is extended to non-model tetraploid crops important for agriculture. Currently, the GWAS software to analyze tetraploid species is limited.

One of the main challenges in the GWAS analysis is to identify real associations. A reliable method to validate the results is by replicating the study using different software. To solve this problem, we developed the MultiGWAS tool that performs GWAS analyses for tetraploid species using four software in parallel. The tool deals with preprocessing data, running four GWAS tools in parallel, and create reports to help the user decide more intuitively the possible true or false associations.

MultiGWAS summarize the results in tables, Venn diagrams, SNP profiles, and Manhattan plots. We consider these tool and output reports are helpful for the user.

We are confident that our work will be of interest to your journal.

Thank you in advance for your consideration, Best regards.

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