

## Cover letter

Genomic selection is a newly-developed selecting elite breeding stocks in animal or plant breeding field using dense genetic markers. The current genomic selection software face defect as low prediction accuracy or low computational efficiency or inability to handle large-scale sample data. With the advent of big data breeding, breeders urgently need an all-powerful genome selection soft.

In our study, A fast genomic prediction software named FCF-MixP with four zero-mean normal distributions as the prior distribution was developed to optimize the prediction accuracy and computing efficiency. The variance of the prior distribution in our model is precisely determined by an F2 population with 374 phenotypes, and GEBV can be obtained accurately and quickly in combination with an iterative conditional expectation algorithm. Our study has demonstrated that FCF-MixP has the advantage on computational efficiency and prediction accuracy compare with some other popular softwares as GBLUP, SSgbup, BayesR, BayesA and BayesB. Most importantly, FCF-MixP may handle large-scale sample data, which will meet the need of large breeding companies or combined breeding schedule. Our FCF-MixP software can be freely accessed at <https://github.com/xuwenwu24/FCF-MixP>.

We are prepared to submit our manuscript to the BMC genomics and guarantee that our manuscript has not been presented or published anywhere else.