Reviewer Report

Title: Developing best practices for genotyping-by-sequencing analysis in the construction of linkage maps

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Reviewer Comments to Author:

The paper titled "Developing best practices for genotyping-by-sequencing analysis using linkage maps as benchmarks" aims to present an end to end workflow uses GBS genotyping datasets to generate genetic linkage maps. This is a valuable tool for geneticists intending to generate a high confidence linkage map from a mapping population with GBS data as input.I got confused on reading the MS though, is this a workflow paper or is this a review of the component software for each step of genetic mapping and how parameter/use differences affect the output ? If it's a review, then the choice of software reviewed are not comprehensive enough, esp on SNP calling, and linkage mapping.There is no clear justification why each component software was used,example the use of GATK and freebayes for SNP calling I am familiar with using TASSEL GBS and STACKS for SNP calling using GBS data, why weren't they included in the SNP calling software. The MS would benefit greatly from including these SNP calling software in their benchmarking.Onemap and gusmap seems also pre-selected for linkage mapping, without reason for use, or maybe the reason(s) were not highlighted in the text. I've had experience in the venerable MAPMAKER and MSTMap, and would like to see more comparisons of the chosen genetic linkage mapping software with others, if this is the intent of the MS.The MS also clearly focuses on genetic linkage mapping using GBS, which should be more explicitly stated in the title. GBS is also extensively used in diversity collections and there is scant mention of this in the MS, and whether the workflow could be adapted to such populations.Versions of sofware used in the workflow are also not explicitly stated within the MS.The shiny app is also not demonstrated well in the MS, it could be presented better with screenshots of the interface , with one or two sample use cases.

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