

Assessment proposed by the supervisor: Successful defense

Assessment proposed by the reviewer: Successful defense

Course of the defence:

Questions:

1. Where is the centromere located on the chromosome 25 of cattle?
2. Why does the lowest SNP density region (LDR) have less informative recombination rates? What can you do to check whether it is because it does not have SNPs or because there is no recombination happening?
3. Can you please explain the degrees of relationship for the inbreeding coefficients of 0.125 and 0.0625? What is the meaning of these numbers?
4. Do you see a development in the recombination rates considering the level of inbreeding?
5. Does Fleckvieh have a better training dataset? Is the average inbreeding fraction different?
6. Can the difference in the number of hotspots be explained by the number of individuals that are being removed from each category? Is this due to the dataset or biological phenomenon?
7. Why did not you choose a higher inbreeding coefficient for the estimation of recombination rates?
8. Would you get the same recombination map if you choose a higher inbreeding?
9. Would the SNP count change with decreasing inbreeding coefficient?
10. What is the average SNP count per segment in the highest SNP count region?
11. How does the SNP count affect the recombination rate?
12. Do you see a difference in recombination maps if a SNP occurs frequently or not?
13. How did you count the SNPs in the highest and lowest SNP-count regions?
14. How is the data structured in VCF files?

Score:

Assessment:Excellent.....

Date of defence: 20.11.2020

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committee chairman