From Tassel to Joinmap part 1

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First step: Tassel was executed and produced a VCF file. χ^2 scores and P_values were computed at each locus. These values along with marker information and genotypic data were included into a new file. This step can take one or more input files (eg. because data were treated in parallel or to save memory space). For each input file, a genotypic file and a marker info file are created.

Preliminary

Information on the dataset

Data curation for the set of 240+2 individuals from plates 1 to 6. data are in D://Mes donnees/sequencage/2017/article sequence/Tassel_to_J/data/

Additional comments

procedure

execution

The first test consisted in retaining only those markers whose distribution is not too far from 50-50.

This step ended with the status ok. Data with p.values below -1 were filtered out. A negative value means no filtering.

- The number of markers was reduced from 17,548 to 17,548. 100 % of loci were conserved.
- The number of scaffolds reduced from 3,017 to 3,017. 100 % of scaffolds were conserved.

Data were in file(s)
first_round.tab

in folder
data/set1

Created files

genot_first_round.txt

markid_first_round.txt

in folder

data/set1/step1