

Pseudocode marker assisted selection

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1 Summary

Marker Assisted selection code for Soybean breeding program. Pseudo code description of steps that we will follow in `c++`.

2 Pseudocode

2.1 Steps

1. Read SNP names from genotype data,
2. Read SNP names from MAS targeted traits.
3. Compare SNP names as vector intersection of strings
4. Generate index for SNP names from genotype data
5. Save index
6. Load index
7. Load SNP marker dataset
8. subset SNP marker dataset based on index values
9. look on each column for the genotype score
10. subset rows - lines - based on genotype score
11. save genotype index -name-