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HaploMAGIC: phasing and accurately detecting recombination in multi-parental populations with genotyping errors

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Background:

Allopolyploidisation followed by strong artificial selection reduced genetic diversity of oilseed rape material available for breeding. Meiotic recombination has a key role in restoring genetic diversity by creating new combinations of alleles. However, recombination is not uniform across the genome and understanding the genome-wide recombination patterns can help optimize its use for breeding.

In this context, multi-parental populations (MPP) constitute an excellent platform for precise genotype phasing, identification of genome-wide crossovers, estimation of recombination frequencies and construction of recombination maps. While some available tools such as duoHMM or LINKPHASE can apply pedigree information to phase haplotypes and detect crossovers in related individuals, they may not be applicable or optimal for MPPs.

Methods:

Here, we introduce haploMAGIC, a pipeline to detect crossovers in MPPs with SNP data by exploiting the pedigree relationships for accurate genotype phasing and inference of grandparental haplotypes. HaploMAGIC presents functionalities that can be adjusted to the genotyping error rate to prevent the emergence of false positive crossovers. For example, users can specify the minimum number of informative alleles required to retain haploblocks or decide whether the parental genotypes should be used to impute alleles that could not be phased.

Results:

A performance analysis with alphaSimR simulations revealed that haploMAGIC consistently outperforms duoHMM and LINKPHASE at crossover detection in terms of recall and precision, especially over increasing genotyping error rates. Furthermore, we constructed recombination maps on two large rapeseed multi-parental populations using haploMAGIC and observed good correlation in recombination frequency compared with the other two programs.

Conclusions:

haploMAGIC is a new tool which can be used to detect crossovers in multi-parental populations with available pedigrees and corresponding genotyping data. Moreover, we will release the code as open source to enable users to customize and manipulate output to suit specific requirements and to collaborate in the software's development.

References:

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