HapShared - a software for pedigree reconstruction

A Python script for performing complex pedigree analysis with high sensitivity.

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Applications

- Pedigree reconstruction for breeding, genetic studies, germplasm characterization, etc.

Key Benefits & Differentiators

- Supports complex pedigree reconstruction
- High sensitivity
- Applicable for unphased or phased genotypic data
- Useful for establishing previously unknown genetic relationships

Overview

Pedigrees are used to analyze the pattern of inheritance of a particular trait throughout a family. Pedigrees show the presence or absence of a trait as it relates to the relationship among parents, offspring, and siblings. Detailed pedigree information is useful in breeding, genetic studies, germplasm characterization, and for resolving questions regarding cultivar histories. So far, most researchers have used unlinked single nucleotide polymorphisms (SNPs) or microsatellite markers to perform complex pedigree reconstruction. However, the lack of linkage information in these methods makes it highly challenging to find deeper relationships (such as grandparent-grandchild relationships), especially due to asexual propogation and extensive inbreeding.

Researchers at the University of Minnesota have developed a software, named HapShared, based on a novel method that supports complex pedigree reconstruction in plants via efficient calculation of total summed potential lengths of shared haplotypes (SPLoSH). Development and validation of this method was enabled by large genome-wide SNP array datasets, integrated genetic maps, and previously identified pedigree relationships. Researchers have demonstrated that this pedigree reconstruction method is proven to be highly sensitive and is applicable for both unphased and phased genotypic data as well as null-alleles.

Software Specifications and System Requirements

Language: Python

Phase of Development

TRL: 8-9
Software is tested and validated and is available for download.

Desired Partnerships

This technology is now available for licensing. Interested non-profit organizations may download and use the software free of charge by executing the license agreement provided on the right panel. Please contact us for commercial needs and learn more.

Researchers

- **[Kevin Silverstein, PhD](#)** Scientific Lead, Minnesota Supercomputing Institute
- **[James Luby, PhD](#)** Professor, Horticultural Science
- **Nicholas Howard, PhD**
- **Ana Poets, PhD**

References

Nicholas P. Howard, Cameron Peace, Kevin A. T. Silverstein, Ana Poets, James J. Luby, Stijn Vanderzande, Charles-Eric Durel, Hélène Muranty, Caroline Denancé & Eric van de Weg, https://doi.org/10.1038/s41438-021-00637-5, Horticulture Research volume 8, Article number: 202 (2021)

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