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A population based confidence set inference method for SNPs that regulate quantitative phenotypes. (English) [Zbl 1351.92031](#)

Choudhary, Pankaj K. (ed.) et al., Ordered data analysis, modeling and health research methods. In honor of H. N. Nagaraja's 60th birthday. Selected papers based on the presentations at the international conference, Austin, TX, USA, March 7–9, 2014. Cham: Springer (ISBN 978-3-319-25431-9/hbk; 978-3-319-25433-3/ebook). Springer Proceedings in Mathematics & Statistics 149, 235-244 (2015).

Summary: The increased use of genome-wide association studies based on genetic maps consisting of hundreds of thousands of SNPs has prompted the need for methods that can be used in preliminary analyses to limit the number of SNPs investigated in follow-up studies. I introduce a Confidence Set Inference method for independent individuals that can be used as a first step in association studies to derive a set of SNPs that contribute at least a specific percentage to the total variance of a quantitative trait. The main advantage of the method is that it allows control over the confidence level with which one can identify genes with specific effects on the genetic variance of the trait of interest. Developed in the framework of linear models, the method can efficiently incorporate information on pertinent covariates. I investigate the properties of the method through an extensive simulation study under various simple inheritance models and compare its performance to that of a standard association approach as it is implemented in the software package Merlin.

For the entire collection see [\[Zbl 1337.92005\]](#).

MSC:

[92D10](#) Genetics and epigenetics
[92B15](#) General biostatistics

Keywords:

GWAS; association studies; confidence sets; fine mapping; CSI

Software:

SimPed; MERLIN

Full Text: [DOI](#)

References:

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