

## **Confidence Regions for the Location of Putative Trait Genes**

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Abstract:

Preliminary genome screens are usually succeeded by fine mapping analyses focusing on the regions that signal linkage. It is advantageous to reduce the size of the regions where follow-up studies are performed, since this will help better tackle, among other things, the multiplicity adjustment issue associated with them. I will describe an approach that uses a confidence set inference procedure as a tool for intermediate mapping (between preliminary genome screening and fine mapping) to further localize disease loci. Apart from the usual Hardy-Weiberg and linkage equilibrium assumptions, the only other assumption of the proposed approach is that each region of interest houses at most one of the disease contributing loci.