

# **Fine-Scale Mapping of Disease Genes via Spatial Clustering Techniques with Applications**

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## **Abstract:**

We present a method to perform fine mapping by placing haplotypes into clusters based upon risk. Each cluster has a haplotype "center". Cluster allocation is defined according to haplotype centers, with each haplotype assigned to the cluster with the "closest" center. The closeness of two haplotypes is determined by a similarity metric that measures the length of the shared segment around the location of a putative functional mutation for the particular cluster. This method allows for missing marker information while still estimating risks of complete haplotypes without resorting to a marker-at-a-time analysis. The dimensionality issues that can occur in haplotype analyses are removed by sampling over the haplotype space, allowing for estimation of haplotype risks without explicitly assigning a parameter to each haplotype to be estimated. As such, we are able to handle haplotypes of arbitrary size. Various extensions of this method will also be presented along with applications where the method has been applied to real datasets.