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PhD Dissertation Proposal Presentation

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A Poisson Point Process Model with Its Applications and Network Analysis of Genome-wide Association Study

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Abstract 1:

Although Bayes's theorem demands a prior that is a probability distribution on the parameter space, the calculus associated with Bayes's theorem sometimes generates sensible procedures from improper priors. However, improper priors may also lead to Bayes procedures that are paradoxical or otherwise unsatisfactory prompting some authors to insist that all priors be proper. Our model begins with the observation that an improper measure on the parameter space satisfying Kingman's countability condition is in fact a probability distribution on the power set. We show how to extend a model in such a way that the extended parameter space is the power set. Under an additional finiteness condition, which is needed for the existence of a sampling region, the conditions for Bayes's theorem are satisfied by the extension. Lack of interference ensures that the posterior distribution in the extended space is compatible with the original parameter space. Provided that the key finiteness condition is satisfied, this probabilistic analysis of the extended model may be interpreted as a vindication of improper Bayes procedures derived from the original model. An explanation of the so-called Marginalization Paradox also follows.

Abstract 2:

The GWAS (genome-wide association studies) approach have identified a number of very compelling statistical association between particular single nucleotide polymorphisms (SNPs) and many common, complex diseases. However, most of the published GWAS results tend to focus on single marker (genotyped or untyped), and markers with modest effects that do not exceed the stringent threshold are generally neglected. One alternative under development is to incorporate network information from independent study to help the genes with modest effects from different.

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