Pseudo-Likelihood: Theory and Applications to Population-Based genetic
Association Studies

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This talk is divided into two parts. In Part I, we review the motivation behind and
theoretical developments of the pseudo-likelihood method, which was originally
advocated by Gong and Samaniego (1981, annals of Statistics). A series of examples
drawn from the biomedical studies (Liang and Self, 1996, JRSSB) are presented
illustrating the wealth of its applications. We then turn the attention in Part II to its
application to population-based genetic association studies. One concern about
conducting population-based association studies is on population stratification (PS), i.e.,
the positive association observed between risk of disease and genetic markers is due to
heterogeneity in ethnic makeup between cases and controls. One approach to alleviate
this concern is to use the so called genomic controls to detect and correct PS. We
propose a pseudo-likelihood approach, which eases several concerns of the conventional
likelihood approach including, among others, computational burden and tangling between
parameters of interest and nuisance parameters. This approach is illustrated through a
population-based case-control study on asthma.