

PREDICTION ERRORS IN DISEASE MAPPING

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Disease mapping can be considered as a small area problem because the standardized mortality ratio (SMR), a common direct index of disease incidence and mortality in a particular region, can be very unprecise in small areas or counties with sparse population and few or no observed cases. Then, the use of models that borrow information from related regions smoothing the crude mortality or incidence risks is inevitable. However, as sampling is not involved, this problem has been approached from a different perspective than in classical small area estimation literature, where the target quantity is usually a mean or a total. In disease mapping applications, the interest is twofold, to make predictions of the relative risks, and to assess the mean squared error (prediction error) to build confidence intervals for the relative risks, allowing to decide whether the regions exhibit extreme risks.

In this work, mixed Poisson models are used to derive relative risk predictors because of their flexibility to incorporate the spatial variation of the risks, and the focus is on the estimation of the mean squared error. In particular, we compare mean square error estimators used in Empirical Bayes disease mapping with alternative proposals from the small area estimation literature to check if second order approximations are necessary in this framework. We also assess empirically the performance of a double bootstrap mean square error estimator recently proposed by Hall and Maiti (2006). The well known Scottish lip cancer data will be used for illustrative purposes.