

BAYESIAN PENALIZED COX MODEL FOR MICROARRAY DATA

Giulia Tonini, Michela Baccini, Annibale Biggeri

University of Florence, Italy and CSPO, Florence, Italy

In Microarray experiments interest can be on estimating the predictive value of gene expressions on patients survival. Penalized Cox Regression model can be used to analyze the simultaneous effect of many genes, eventually adjusting for other prognostic variables. The penalty term constrains the genes coefficients estimates so that they are shrunken toward zero. In this way the model helps detecting genes which are most related to survival. It can be shown that different penalty terms take differently into account for the correlation between genes.

Several Bayesian variable selection approaches have been proposed to identify relevant markers by jointly assessing sets of genes.

In our work we consider a Bayesian mixed model approach. We assume that the coefficients are a sample from the same distribution with zero mean and a given variance. This condition acts as a constrain on the coefficients. Large values of the variance correspond to low amount of smoothing, while small variance acts as a strong penalty on the coefficients.

Specifying a prior distribution on the variance parameter, the uncertainty on the amount of shrinkage is taken into account. Alternative specifications of coefficients distribution and of variance prior distribution are considered.

We present applications on published cancer data.