

Profiling Time Course Expression of Virus Genes

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Time course expression of virus genes are studied, based on microarray data, in a hierarchical Bayesian shape restricted regression model. The prior is introduced through Bernstein polynomials so as to take into consideration the geometry of the regression functions, which are assumed to be zero initially, increasing after a while and staying positive later on. One advantage of this method is that it offers an assessment of the strength of the evidence provided by the data in favor of hypothesis on the shape of the regression function; for example, the hypothesis that it is unimodal. Another advantage of this approach is that estimates of many salient features of the profile like onset time, inflection point, maximum value, time to maximum value, etc. can be obtained immediately.

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