RJaCGH, a package for analyisis of CGH arrays with Reversible Jump MCMC

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Abstract

Frequently, changes in the number of DNA copies are associated to cancer activity. Gains are related to oncogene activation, and losses to tumor suppressor inactivation. Comparative Genome Hybridization (CGH) is a technique that allows to detect such changes.

RJaCGH is a package that performs analysis of CGH arrays through a non-homogeneous hidden Markov model. It assumes that the true number of DNA copies follows a Markov chain whose transition matrix is dependent of the distance to the next gene. But, due to the fact that what is measured in the array are fluorescent intensities, the states can't be directly observed. Instead, the emissions are modelled through independent gaussian distribution conditional to the hidden states. One of the main problems with this kind of models is the selection of the number of hidden states. Here, we address that issue through a bayesian analysis and the use of Reversible Jump Markov Chain Monte Carlo (RJMCM) techniques. This method allows us to answer several important biological questions, such as estimating the probability of no changes in DNA copy number in a given chromosome, or the probability that a particular gene is gained or lost.

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