

Statistical model for background mutation rate in cancer genomes

Lin Hou

Tsinghua University
E-mail: houl@tsinghua.edu.cn

Abstract: The identification of driver genes is an important problem in cancer genome analysis. Driver genes are identified via hypothesis testing procedures, which contrasts observed counts with the background mutation rate. In this work, we introduce a statistical model to estimate the background mutation rate in cancer genomes. We are able to identify driver genes of relatively low prevalence with high precision. The proposed method is evaluated in simulation settings and in real data.