

ΔΙΑΛΕΞΗ



Mixture Modeling of DNA Copy Number Aberrations



Dr. Jaakko Hollmen
Chief Research Scientist,
Dept. of Information & Computer Science
Aalto University School of Science and Technology

Περίληψη

DNA copy number aberrations, i.e. copy number amplifications and copy number deletions, are hallmarks of nearly all advanced tumors. We present the data collection of genome-wide DNA copy number amplification data consisting of data of over 4500 cases of human neoplasms. The data set has been gathered from scientific journal articles covering a period of ten years and is naturally represented as 0-1 data. We motivate the use of mixture models in probabilistic clustering of amplification data and present a mixture model of multivariate Bernoulli distributions to yield patterns that are relevant to all cancer types. Appropriate complexity for the mixture model for each chromosome is selected with a model selection procedure. A methodology to create a naming scheme for the identified patterns is also presented. The names are based on the extracted maximal frequent item sets from the clustered data. Results are interpreted and the diagnostic value of the findings is further investigated in the light of background risk factors.

Σύντομο Βιογραφικό

Jaakko Hollmen received the degrees of M.Sc.(Tech.) in 1996, Lic.Sc.(Tech.) in 1999 and D.Sc.(Tech.) in 2000, all at the Department of Computer Science and Engineering at the Helsinki University of Technology. He has worked at the Department of Information and Computer Science (formerly Laboratory of Computer and Information Science) at the Helsinki University of Technology (TKK) since the year 2000. Before joining TKK, he worked at the Siemens Corporate Technology in Munich, Germany. Currently, he is a Chief Research Scientist at Aalto University, School of Science and Technology (former TKK). His research interests include theory and practice of machine learning and data mining, especially their applications in bioinformatics and environmental informatics. Jaakko Hollmen is a senior member of IEEE.

Πληροφορίες: Ιωάννης Φούντος

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