CanVis: Towards a Web Platform for Cancer Progression Tree Analysis

Authors: Michael Aupetit, Mahmoud Al-ismail, Khaled Mohamed

Abstract : Cancer is a major public health problem all over the world. Breast cancer has the highest incidence rate over all cancers for women in Qatar making its study a top priority of the country. Human cancer is a dynamic disease that develops over an extended period through the accumulation of a series of genetic alterations. A Darwinian process drives the tumor cells toward higher malignancy growing the branches of a progression tree in the space of genes expression. Although it is not possible to track these genetic alterations dynamically for one patient, it is possible to reconstruct the progression tree from the aggregation of thousands of tumor cells' genetic profiles from thousands of different patients at different stages of the disease. Analyzing the progression tree is a way to detect pivotal molecular events that drive the malignant evolution and to provide a guide for the development of cancer diagnostics, prognostics and targeted therapeutics. In this work we present the development of a Visual Analytic web platform CanVis enabling users to upload gene-expression data and analyze their progression tree. The server computes the progression tree based on state-of-the-art techniques and allows an interactive visual exploration of this tree and the gene-expression data along its branching structure helping to discover potential driver genes.

Keywords: breast cancer, progression tree, visual analytics, web platform

Conference Title: ICCB 2016: International Conference on Computational Biology

Conference Location : Paris, France **Conference Dates :** February 22-23, 2016