

## **Analysis of tumour progression using fish copy number**

FISH – Fluorescence in situ hybridization is a technique to find the tumour progression in case of cancer. The results using FISH has been as emerging as on tests with the actual tumour samples and the progression using conventional methods. Fishtree data sets are compared with the rectilinear Steiner minimum trees and the uncertainty was balanced using the fish tree datasets on par with practical datasets. Fish tree led to order matters and inference score. Inference score is the definition of Steiner count of the node in the current tree and the inference score of potential Steiner nodes to be added.

RMST was shown to be a good model for phylogenic analysis by using FISH cell count pattern data. FISH cell count pattern data, but it need efficient heuristics because it is a NP-hard problem. The iFiSHtree heuristic method was used here to approximate the RMST based on medium idea. The proposed method runs relatively faster speed than earlier method and is supposed to be better with increasing number of gene markers. The proposed method also tried to produce the solution with minimum number of Steiner nodes. Our method can be extended to apply on other data type such as copy number variation (CNV) data.