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Network Visualisation and Analysis of Complex Biological Data

In recent years enormous amounts of data pertaining to the activity of genes and proteins and their interactions in the cell, have been generated by a number of high throughput techniques, including yeast two-hybrid assays, mass spectrometry, RNA interference and microarray gene expression analysis. In order to understand the data generated by these functional genomics and proteomics approaches, there has been increasing need to develop new mathematical and computational analytical methods. Network-based analyses are playing an increasing role in this respect primarily because the interaction or distance between biological components can be either measured experimentally or calculated and used as a basis to draw network graphs. I will discuss some the work we have been carrying in this area, in particular with respect to our studies on inflammation and infection and the development of the program BioLayout Express3D (www.biolayout.org). I will also discuss how Fios Genomics (<http://www.fiosgenomics.com/>) a new company set up by us, is using these and more convention approaches to provide genomics data analysis services.