

Poster presentation

Time-series Explorer: An Animated Information Visualisation for Microarray Time-course Data

Paul Craig*, Jessie Kennedy and Andrew Cumming

Address: School of Computing, Napier University, Edinburgh, UK.

Email: Paul Craig* - p.craig@napier.ac.uk

* Corresponding author

from BioSysBio: Bioinformatics and Systems Biology Conference
Edinburgh, UK, 14–15 July 2005

Published: 21 September 2005

BMC Bioinformatics 2005, **6**(Suppl 3):P8

Microarray technologies are a relatively new development that allow biologists to monitor the activity of thousands of genes (normally around 8,000) in parallel across multiple stages of a biological process. While this new perspective on biological functioning is recognised as having the potential to have a significant impact on the diagnosis, treatment, and prevention of diseases, it is only through effective analysis of the data produced that biologists can begin to unlock this potential. A significant obstacle to achieving effective analysis of microarray time-course is the combined scale and complexity of the data. This inevitably makes it difficult to reveal certain significant patterns in the data. In particular it is less dominant patterns and, specifically, patterns that occur over smaller intervals of an experiment's overall time-frame that are more difficult to find. While existing techniques are capable of finding either unexpected patterns of activity over the majority of an experiment's time frame or expected patterns of activity over smaller intervals of the time frame, there are no techniques, or combination of techniques, that are suitable for finding unsuspected patterns of activity over smaller intervals. In order to overcome this limitation we have developed the Time-series Explorer, which specifically supports biologists in their attempts to reveal these types of pattern by allowing them to visualise their data controlling an animated interval scatter-plot linked to two complementary graph views. An evaluation, involving biologists working with real data, tested the extent of the tools desired functionality and assessed the technique's practical utility within the wider context of microarray time-course analysis. This proved the technique not only capable of revealing previously unsuspected temporal patterns but also, in certain cases, more appropriate for find-

ing previously suspected patterns and patterns that occurred over the majority of the time-frame.