

Pattern Discovery and Exploration with an Application
to Time Course Microarray Data

Susan R Wilson and Yvonne E Pittelkow

*Centre for Bioinformation Science, Mathematical Sciences Institute, The Australian National
University, Canberra ACT 0200, Australia*

Finding genes with similar profiles in microarray studies is a challenge of increasing importance, and many techniques have been proposed. Visualization of gene expression profiles can aid this process, potentially contributing to the identification of co-regulated genes and gene function as well as network development.

To display gene expression profiles, we introduce the h-Profile plot. Thumbnail versions of plots of gene expression profiles are plotted at coordinates such that profiles of similar shape are located in the same sector, with decreasing variance towards the origin. Negatively correlated profiles can easily be identified. A new method for selecting genes with fixed periodicity, but different phase and amplitude has been developed and will be used to demonstrate the use of the plots on cell cycle data.

Visualization tools for gene expression data are important and h-profile plots provide a timely contribution to the field. They allow the simultaneous visualization of many gene expression profiles and can be used for the identification of genes with similar or reversed profiles, the foundation step in many analyses.