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and **Xin Dang, Yixin Chen** and **Dawn Wilkins**. *Graph ranking on gene network*.

Microarray technology has made it possible to simultaneously monitor the expression levels of thousands of genes in a single experiment. However, the large number of genes greatly increases the challenges of analyzing, comprehending and interpreting the resulting mass of data. Selecting a subset of important genes is inevitable to address the challenge. Gene selection has been investigated extensively over the last decade. Most selection procedures, however, are not sufficient for accurate inference of underlying biology, because biological significance does not necessarily have to be statistically significant. Additional biological knowledge needs to be integrated into the gene selection procedure. (Received September 16, 2009)