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**Coping with uncertainty in temporal gene expressions using symbolic representations.** (English) [Zbl 1202.68126](#)

Hüllermeier, Eyke (ed.) et al., Information processing and management of uncertainty in knowledge-based systems. Applications. 13th international conference, IPMU 2010, Dortmund, Germany, June 28–July 2, 2010. Proceedings. Part II. Berlin: Springer (ISBN 978-3-642-14057-0/pbk; 978-3-642-14058-7/ebook). Communications in Computer and Information Science 81, 11-20 (2010).

Summary: DNA microarrays can provide information about the expression levels of thousands of genes, however these measurements are affected by errors and noise; moreover biological processes develop in very different time scales. A way to cope with these uncertain data is to represent expression level signals in a symbolic way and to adapt sub-string matching algorithms (such as the Longest Common Subsequence) for reconstructing the underlying regulatory network. In this work a first simple task of deciding the regulation direction given a set of correlated genes is studied. As a validation test, the approach is applied to four biological datasets composed of Yeast cell-cycle regulated genes under different synchronization methods.

For the entire collection see [\[Zbl 1200.68011\]](#).

**MSC:**

[68P10](#) Searching and sorting

[92D10](#) Genetics and epigenetics

**Keywords:**

[DNA microarrays](#); [sub-string matching algorithms](#)

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