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Developing a Logical Model of Yeast Metabolism

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Abstract: *With the completion of the sequencing of genomes of an increasing number of organisms, the focus of biology is moving to determining the role of these genes (functional genomics). To this end it is useful to view the cell as a biochemical machine: it consumes simple molecules to manufacture more complex ones by chaining together biochemical reactions into long sequences referred to as metabolic pathways. Such metabolic pathways are not linear but often intersect to form a complex network. Genes play a fundamental role in this network by synthesising the enzymes that catalyse biochemical reactions. Although developing a complete model of metabolism is of fundamental importance to biology and medicine, the size and complexity of the network has proven beyond the capacity of human reasoning. This paper presents intermediate results in the Robot Scientist research programme that aims to discover the function of genes in the metabolism of the yeast *Saccharomyces cerevisiae*. Results include: (1) the first logical model of metabolism; (2) a method to predict phenotype by deductive inference; and (3) a method to infer reactions and gene function by abductive inference. We describe the *in vivo* experimental set-up which will allow these *in silico* inferences to be automatically tested by a laboratory robot.*

Publication and review history

This work was first presented at the Machine Intelligence 18 Workshop, held on September 19-21, 2001 at the University of York, UK. Attendance at this workshop was based on invitations. Speakers at the workshop were invited to submit their articles for consideration in the forthcoming workshop volume. The subsequent publication and review history for the present article was as follows.

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5. Revised version appears in Electronic Transactions on Artificial Intelligence, Volume 5 (2001), section B, pages 223–244. The section and the annual volume are made permanently available at <http://www.ep.liu.se/ej/etai/>
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