

TOWARDS CELLULAR FUNCTION THROUGH METABOLITE SCREENING

Ms Priti Talwar, Thomas Lengauer¹, Vidya Mangadu², Christoph Wittmann², Elmar Heinzle²

¹ Max-Planck-Institut für Informatik, Stuhlsatzenhausweg 85, Saarbruecken 66123, Germany

² Technical Biochemie, Saarland University, Saarbruecken 66123, Germany

We are approaching the problem of protein function prediction via combination of

1. Identification of "Metabolic fingerprints"
2. Analysis of ¹³C labeling data

Gene disruption is a fundamental technique in function prediction of genes and facilitates determination of loss of function cellular state. Here we use mass spectrometric techniques

to identify the metabolic fingerprints reflected by the change in pattern of carbon assimilation by the organism.

Basis: Pattern of carbon assimilation is reflective of the abrupt changes in the genetic material and the interdependencies present in various key metabolites.

We study selected set of *Saccharomyces cerevisiae* knock out strains grown in minimal media under aerobic conditions. Mass Isotopomer Distribution (MID) of a set of mutants is analyzed for identification of underlying principal components, which represent the functional differences among different genes.

Contact: Tel: +49 0681 9325328 Fax: +49 0681 9325399 Email: ptalwar@mpi-sb.mpg.de