

1014-92-725

Philipp Kuegler* (philipp.kuegler@jku.at), Altenbergerstrasse 69, RICAM, 4040 Linz, Austria. *Inferring gene regulatory networks as nonlinear inverse problem with sparsity constraints.*

In the search for a better understanding of the functionality of organisms, molecular biologists put significant research efforts on the reconstruction of gene regulatory networks from time course gene expression data. In this talk we discuss a nonlinear operator approach to solve this inverse problem. The biologically known sparsity of the network is taken into account by using the " l_p -norm" with $0 < p \leq 1$ as penalty term. We present numerical results for real data and give a comparison to existing methods. (Received September 23, 2005)