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**Using mutual information to infer gene-gene interactions from microarray expression series** THOMAS FINK, Bioinformatics, Institut Curie, SEBASTIAN AHNERT, University of Cambridge, FRANCOIS RADVANYI, Institut Curie, NICOLAS STRANSKY, Institut Curie, KAREN WILLBRAND, Ecole des Mines de Paris — Identifying network structure from microarray data rests crucially on what is meant by 'similarity' between two gene expression patterns. We introduce a method of inferring gene-gene interactions without making assumptions about what kind of expression correlations to look for. Our approach is to bound the mutual algorithmic information, measured in bits, between sets of measurements for two genes; a higher level of mutual information corresponds to a greater confidence of interaction. We have applied our method to yeast cell cycle and bladder cancer.

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