

# **5<sup>th</sup> Annual Joint Bioinformatics Workshop**

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## ***Genetic Network Inference Based on Time Series Gene Expression Profiles***

### ***ABSTRACT***

Motivation: Time series expression profiles provide dynamic information for inferring gene regulatory relationships. Identifying feedback cycles and telling direct interactions from indirect interactions are among major challenges of genetic network inference. In this work, we proposed to use time correlation to estimate the time delay and edge direction, and combine with partial correlation and d-separation theory to tell the direct and indirect interactions and identify feedback cycles.

Results: The proposed algorithm was evaluated using simulated data and real yeast cell cycle data. The simulation evaluated the performance of the algorithm under different parameter settings and compared with other algorithms. Using the yeast cell cycle data, the algorithm successfully identified the yeast cell cycle development stages, cell cycle loop and negative feedback loops. The inferred network was also evaluated with the cell cycle transcriptional factors and their binding location data and provided hypothesis for further biological studies.