







stationary biological time series. we design a lag determine mechanism by considering TLMI between genes. By using  $l_1$  variable selection to identify each variable's Markov blanket, we efficiently reduce the model optimizing space, capture the dynamic interactions between genes based on their time series of expression values. Given the rapid advances in data collection technologies for biological systems, we expect that complex, high-dimensional, and feature rich data from complex dynamic biological processes, such as cancer progression, immune responses, and developmental processes, will continue to grow. Thus, we believe our new method is a timely contribution that can narrow the gap between imminent methodological needs and the available data and offer deeper understanding of the mechanisms and processes underlying biological networks.

## 5. References

- [1] M. Hecker, S. Lambeck, S. Toepfer, E.V. Someren, R. Guthke, "Gene regulatory network inference: Data integration in dynamic models—A review," *BioSystems*, 96(1): 86-103, 2009.
- [2] M. Grzegorzcy, et al., "Modelling non-stationary gene regulatory processes with a non-homogeneous Bayesian network and the allocation sampler," *Bioinformatics*, 24:2071-2078, 2008.
- [3] S. Lebre, J. Becq, F. Devaux, M.P. Stumpf, and G. Lelandais: "Statistical inference of the time-varying structure of gene-regulation networks," *BMC Systems Biology*, 4:130, 2010.
- [4] A. Ahmed, and E. Xing, "Recovering time-varying networks of dependencies in social and biological studies," *Proceedings of the National Academy of Sciences*, 106(29):118, 2009.
- [5] L. Song, M. Kolar, and E. Xing, "KELLER: estimating time-varying interactions between genes," *Bioinformatics*, 25(12), i128-i136, 2009.
- [6] M. Zou, S.D. Conzen, "A new dynamic Bayesian network (DBN) approach for identifying gene regulatory networks from time course microarray data," *Bioinformatics*, 21:71-79, 2004.
- [7] Z. Xing, D. Wu, "Modeling Multiple Time Units Delayed Gene Regulatory Network Using Dynamic Bayesian Network," *IEEE International Conference on Data Mining Workshops*, pp. 190-195, 2006.
- [8] V. Chaitankar, P.Ghosh, J.P. Edward, Ping Gong, Chaoyang Zhang, "Time lagged information theoretic approaches to the reverse engineering of gene regulatory networks," *BMC Bioinformatics*, 11(Suppl 6):S19, 2010.
- [9] J. Besag, "Statistical analysis of non-lattice data," *Proceedings of the Twenty-First National Conference on Artificial Intelligence (AAAI-06)*, pp: 179-195, 1975.
- [10] P. Spellman et al., "Comprehensive identification of cell cycle-regulated genes of the yeast *saccharomyces cerevisiae* by microarray hybridization," *Molecular Biology of the Cell*, 9(12): 3273-3297, 1998.
- [11] A. Bernard and A.J. Hartemink, "Informative structure priors: Joint learning of dynamic regulatory networks from multiple types of data," *Pacific Symposium on Bio-computing 2005 (PSB05)*, 2005.
- [12] <http://www.yeastgenome.org>