

Sections 5.3.3.1 and 5.3.3.2 to simplify the network to contain 267 nodes and 751 arcs.

Saadatpour *et al.* [18] further investigated the T-LGL network and found that 14 nodes of the network have high importance in the sense that blocking any of these nodes disrupts (almost) all signaling paths from the complementary node to apoptosis, thus providing these nodes as possible candidate therapeutic targets. All of these nodes are also found to be essential for the T-LGL survival state according to a dynamic model, *i.e.*, reversing their states causes apoptosis to be the *only possible* outcome of the system. Moreover, experimental verification of the importance of these nodes exists for 10 of the 14 nodes [18].

REFERENCES

1. R. Albert, B. DasGupta, R. Dondi, S. Kachalo, E. Sontag, A. Zelikovsky and K. Westbrooks. A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence, *Journal of Computational Biology*, 14 (7), 927-949, 2007.
2. R. Albert, B. DasGupta, A. Gitter, G. Gürsoy, R. Hegde, P. Pal, G. S. Sivanathan and E. Sontag. A New Computationally Efficient Measure of Topological Redundancy of Biological and Social Networks, *Physical Review E*, 84 (3), 036117, 2011
3. R. Albert, B. DasGupta and E. Sontag. Inference of signal transduction networks from double causal evidence, in *Methods in Molecular Biology: Topics in Computational Biology*, D. Fenyo (ed.), 673, Chapter 16, Springer, 2010.
4. R. Albert and H. Othmer. The topology of the regulatory interactions predicts the expression pattern of the segment polarity genes in *Drosophila melanogaster*, *Journal of Theoretical Biology*, 223, 1-18, 2003.
5. D. Angeli and E.D. Sontag. Monotone control systems, *IEEE Transactions on Automatic Control*, 48, 1684-1698, 2003.
6. M. R. Blatt and A. Grabov. Signal redundancy, gates and integration in the control of ion channels for stomatal movement, *Journal of Experimental Botany*, 48, 529-537, 1997.
7. B. DasGupta, G. A. Enciso, E. Sontag and Y. Zhang. Algorithmic and complexity results for decompositions of biological networks into monotone subsystems, *Biosystems*, 90 (1), 161-178, 2007.
8. G. von Dassow, E. Meir, E. M. Munro, and G. M. Odell. The segment polarity network is a robust developmental module, *Nature*, 406, 188-192, 2000.
9. J. Duch and A. Arenas. Community identification using extremal optimization, *Physical Review E*, 72, 027104, 2005.
10. L. M. Fan, Z. Zhao and S. M. Assmann. Guard cells: A dynamic signaling model, *Current Opinions in Plant Biology*, 7, 537-546, 2004.
11. A. M. Hetherington and F. I. Woodward. The role of stomata in sensing and driving environmental change, *Nature*, 424, 901-908, 2003.
12. N. T. Ingolia. Topology and robustness in the *Drosophila* segment polarity network, *PLoS Biology*, 2 (6), e123, 2004.
13. H. Jeong, B. Tombor, R. Albert, Z. N. Oltvai and A.-L. Barabasi. The large-scale organization of metabolic networks, *Nature*, 407, 651-654, 2000.

14. S. Kachalo, R. Zhang, E. Sontag, R. Albert and B. DasGupta. NET-SYNTHESIS: A software for synthesis, inference and simplification of signal transduction networks, *Bioinformatics*, 24 (2), 293-295, 2008.
15. S. Li, S. M. Assmann and R. Albert. Predicting Essential Components of Signal Transduction Networks: A Dynamic Model of Guard Cell Abscisic Acid Signaling, *PLoS Biology*, 4(10), e312, 2006.
16. E. A. MacRobbie. Signal transduction and ion channels in guard cells, *Philosophical Transactions of the Royal Society B: Biological Sciences*, 353, 1475-1488, 1998.
17. K. Oda, Y. Matsuoka, A. Funahashi and H. Kitano. A comprehensive pathway map of epidermal growth factor receptor signaling, *Molecular Systems Biology*, 1 (1), 2005.
18. A. Saadatpour, R. S. Wang, A. Liao, X. Liu, T. P. Loughran, I. Albert and R. Albert R. Dynamical and Structural Analysis of a T Cell Survival Network Identifies Novel Candidate Therapeutic Targets for Large Granular Lymphocyte Leukemia, *PLoS Computational Biology*, 7, e1002267, 2011.
19. A. I. Volpert, V. A. Volpert and V. A. Volpert. Traveling Wave Solutions of Parabolic Systems, volume 140 of *Translations of Mathematical Monographs*, American Mathematical Society, 2000.

EXERCISES

7.1 The purpose of this exercise is to get the reader familiar with the algorithmic framework shown in Fig. 5.4 and the NET-SYNTHESIS software in [14] that uses this algorithmic framework. Consider the following small subset of the interactions reported in [15]:

ABA \neg NO
 ABA \rightarrow PLD
 ABA \rightarrow GPA1
 ABA \rightarrow PLC
 GPA1 \rightarrow PLD
 PLD \rightarrow PA
 NO \neg KOUT
 KOUT \rightarrow Closure
 PA \rightarrow Closure
 PLC \rightarrow (ABA \rightarrow KOUT)

For each of the following tasks, report the network generated and verify that it is correct.

- a) Generate the network using only the direct interactions and perform transitive reduction on the graph (*e.g.*, in NET-SYNTHESIS software, select “Reduction (slower)” from the Action menu).
- b) Add double-causal inferences to the network (*e.g.*, in NET-SYNTHESIS software, select “Add pseudonodes” from the Action menu).