Abstract Submitted
for the MAR09 Meeting of
The American Physical Society

A Network Model For Sea Urchin Development[1] XINWEI GONG, Department of Physics, Duke University, XIANRUI CHENG, Computational Biology and Bioinformatics Program, Duke University, JOSHUA SOCOLAR, Department of Physics, Duke University — The sea urchin embryo developmental gene regulatory network has been a subject of experimental study for decades. While current knowledge of the network is incomplete, boolean network models with autonomous updating can reveal dynamical features of the known network. Our analysis of such a model based on the network provided by Davidson et al [http://sugp.caltech.edu/endomes/index.html] shows that, with the suggested initial inputs and certain sets of logic functions that are consistent with the known regulatory relations, a 3-cell system settles into an attractor that corresponds to the 3 different cell fates expected for the organism. The attractor is not sensitive to modest variations in the time delay parameters.

[1] This research is supported by NSF and NIH through Grant No.s PHY-0417372 and 1P50-GM081883.

Xinwei Gong
Department of Physics, Duke University

Date submitted: 19 Nov 2008

Electronic form version 1.4