

Abstract Submitted
for the MAR06 Meeting of
The American Physical Society

Network growth models and genetic regulatory networks¹

JOSHUA SOCOLAR, DAVID FOSTER, Duke University, Durham, NC, STUART KAUFFMAN, Institute for Biocomplexity and Informatics, University of Calgary — We study a class of growth algorithms for directed graphs that are candidate models for the evolution of genetic regulatory networks. The algorithms involve partial duplication of nodes and their links, together with innovation of new links, allowing for the possibility that input and output links from a newly created node may have different probabilities of survival. We find some counterintuitive trends as parameters are varied, including the broadening of indegree distribution when the probability for retaining input links is decreased. We also find that both the scaling of transcription factors with genome size and the measured degree distributions for genes in yeast can be reproduced by the growth algorithm if and only if a special seed is used to initiate the process.

¹Supported by NSF Grant No. PHY-0417372.

Joshua Socolar
Duke University

Date submitted: 30 Nov 2005

Electronic form version 1.4