

Figure 2. Number of dynamics vs. dynamical robustness for activation/inhibition networks.

3. Results and Discussion

Figure 2 demonstrates that most networks do not share their steady state dynamics with others, while a few networks are highly robust. Precisely, different steady state dynamics versus the robustness seems to follow a power law with exponent 2.5. This result is surprising, since according to the theory of random graphs, network characteristics should follow Poisson distributions. We hypothesize that power law behavior observed in biological networks is a consequence of dynamic robustness.

To test this hypothesis we analyzed the dynamics of three activation inhibition networks: transcriptional regulation network for E-coli [1], and two Yeast gene regulatory networks ([7], and a network inferred from microarray data [8]). In all networks, we found that the number of subgraphs (modules) with up to five nodes increased with dynamical robustness. We also found that dynamical robustness increased with node degree. These results can be explained by considering that biological networks are composed of modules connected together [9], and that networks composed of modules can be constructed with power law degree distribution, $P(k)$, if the modules have a power law, $\rho(r)$. Precisely, Caldarelli et al. have shown that networks of N modules can be constructed with the following distribution of node degrees $r_M^2 / (N \langle r \rangle) \rho[r_M^2 / (N \langle r \rangle) k]$, where $\langle r \rangle$ and r_M^2 are averaged and maximum robustness of the modules, respectively. It follows that $P(k)$ follows a power law as long as $\rho(r)$ follows a power law. The growth of such networks is simply carried out by inserting modules, one with robustness r and the other with robustness s , with probability rs/r_M^2 . Figure 3 was compiled for a network of 150,000 modules generated using the above probability and following the robustness

distribution of Figure 2. Clearly both figures show the same power law distribution. Thus, we conclude that the distribution of module robustness can be used to predict the node degree distribution found in gene regulatory networks.

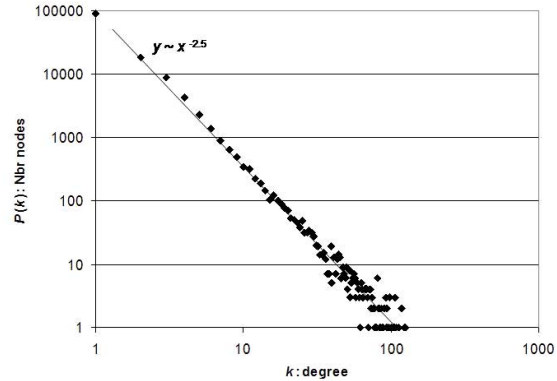


Figure 3. Degree distribution for networks generated using $\rho(r) \sim r^{-2.5}$ and edge probability rs/r_M^2 .

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