Physics of reliable genetic information processing

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Information processing in networks of dynamical units is a favorite theme in statistical physics, as motivated by the stochastic information processing present in nervous systems. Today, as massive data on the dynamics among regulatory genes in the cell nucleus becomes available, we can draw upon our experience with modeling neural nets when thinking about models for gene networks. However, the requirements of gene networks in living cells are different from nervous systems and our intuition from modeling neural networks utterly fails in some points. I here review some aspects of modeling and understanding gene networks where classical models fail.
One astonishing aspect, for example, is the extreme reproducibility performed by the information processing by a gene network. Obviously, biological survival depends on a highly reproducible dynamical output of the regulatory processes in the cells of an organism. However, gene networks rely on switching elements (regulatory genes) which are intrinsically noisy, yet truly autonomous (i.e. not synchronized by a central clock as in electronic computers). In large networks of these elements this should cause severe stability problems to system behavior, desynchronizing system dynamics (e.g. via fluctuating transmission times or response times of the elements). We sketch how this problem can be solved and can explain structural properties of real biological gene networks as well.

[1] K. Klemm and S. Bornholdt, *q-bio/0309013* (2003)

[2] K. Klemm and S. Bornholdt, *q-bio/0409022* (2004)

[3] K. Klemm and S. Bornholdt, *cond-mat/0411102* (2004)