Abstract

The majority of human diseases are related with the dynamic interaction of many genes and their products as well as environmental constraints. Cancer (and breast cancer in particular) is a paradigmatic example of such complex behavior. Since gene regulation is a non-equilibrium process, the inference and analysis of such phenomena could be done following the tenets of non-equilibrium physics. The traditional programme in statistical mechanics consists in inferring the joint probability distribution for either microscopic states (equilibrium) or mesoscopic-states (non-equilibrium), given a model for the particle interactions (e.g. the potentials). An inverse problem in statistical mechanics, in the other hand, is based on considering a realization of the probability distribution of micro- or meso-states and used it to infer the interaction potentials between particles. This is the approach taken in what follows. We analyzed 261 whole-genome gene expression experiments in breast cancer patients, and by means of an information-theoretical analysis, we deconvolute the associated set of transcriptional interactions, i.e. we discover a set of fundamental biochemical reactions related to this pathology. By doing this, we showed how to apply the tools of non-linear statistical physics to generate hypothesis to be tested on clinical and biochemical settings in relation to cancer phenomenology.

Keywords

Cancer genomics, information theory, molecular networks.