Construction of Potential Landscape Uncovers Robust Dynamical Structure in Prostate Carcinogenesis

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Short Abstract —We explored endogenous molecular-cellular network hypothesis for prostate cancer by constructing relevant endogenous interaction network model and analyzing its dynamical properties. Molecular regulations involved in cell proliferation, apoptosis, differentiation and metabolism are included in a hierarchical mathematical modeling scheme. This dynamical network organizes into multiple robust functional states, including physiological and pathological ones. Some states have characteristics of cancer: elevated metabolic and immune activities, high concentration of growth factors and different proliferating, apoptotic and adhesion behaviors. The molecular profiling of calculated cancer state agrees with existing experiments. We developed a novel numerical method of constructing potential landscape for large scale interacting biological network. Robust topological structures such as invariant surface in the phase space are revealed by the potential landscape obtained.

Keywords - Prostate Cancer, Endogenous Molecular-cellular Network, Dynamical System, Potential Landscape, Attractors.

I. BACKGROUND

MANY ideas have been put forward for carcinogenesis. At the two ends of the spectrum are accumulation of mutations in somatic cells and endogenous molecular-cellular network hypotheses [1-5]. The former focuses on a few accidental hits due to environmental insult. The later blames the whole biological structure formed by evolution: The molecular-cellular interactions which enable organisms to cope with different living conditions also lay down "traps", robust pathological states, in the endogenous molecular-cellular interaction network. While events leading to the pathological states vary, these disease causing states are well defined and therefore, having common features among individuals, according to the hypothesis.

II. METHOD

We explored endogenous molecular-cellular network hypothesis for prostate cancer by constructing relevant endogenous interaction network model and analyzing its dynamical properties. We developed a new numerical method of calculating potential landscape for large-scale endogenous network.

III. RESULTS

This dynamical network organizes into multiple robust functional states, including physiological and pathological ones. Some states have characteristics of cancer: elevated metabolic and immune activities, high concentration of growth factors and different proliferating, apoptotic and adhesion behaviors. The potential landscape constructed even suggested the existence of more complex topological structure beyond stable states, such as invariant surface in the phase space.

IV. CONCLUSION

We developed a hierarchical mathematical model of endogenous molecular-cellular interactions for prostate cancer. By utilizing a new numerical method of calculating potential landscape, we effectively and intuitively demonstrate the dynamical behavior of the endogenous network, and even find out more robust topological structure hidden inside the complex biological interactions.

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