Hierarchy of Gene Expression as a Biomarker for Breast Cancer Prognosis MAN CHEN, Rice University — Cancer is a dedifferentiation of healthy cellular and genetic processes. At the same time, specific oncological pathways are activated in the cancer state [1]. Cancer metastasis exposes cancer cells to a variety of microenvironments, in which physics of evolution suggests modularity is a relevant order parameter [2]. We were thus motivated to examine the structure in gene and tissue networks of breast cancer patients. We studied the relation between metastasis and breast cancer network structure. We found that hierarchy of cancer networks distinguishes non-metastatic from metastatic patient populations. We also found that for cancer-associated genes, likelihood of metastasis is correlated with increased network hierarchy. Conversely for tissue networks using all gene data, reduced network structure is correlated with likelihood of metastasis. We suggest hierarchy of gene expression may be useful as a biomarker for breast cancer breast cancer metastasis and recurrence. For those patients with reduced structure, which is at least 5% of the patient population, this biomarker provides a strong signal for likelihood of cancer metastasis.

[1] Paul Davis, Physical Biology vol (2011) page
[2] Jun Sun Phys. Rev. Lett vol (2007) page

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Date submitted: 29 Nov 2012   Electronic form version 1.4