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*Classifying Cancer Types for Treat-ability Using PPI Network Structure*

The existence of a correlation between cancer protein-protein interaction (PPI) network degree-entropy and cancer 5-year survival probability has been shown (Breitkreutz *et al.*, PNAS, 2012). We investigate the correlation between epidemiological survival data and the molecular details of specific cancers further through higher levels of degree-connectedness and through the evolution of cancer network connections compared to a random graph evolution. By comparing the cancer networks to random graphs of the same size, we create a new metric that correlates with 5-year survival and may act as a classifier. The correlative relationship suggests that our method is able to surpass individual variabilities such as cancer site, disease stage, and structural features of the PPI network, through the use of proxy measurements: 5-year survival data and our entropy-based metrics. Our findings suggest that the underlying structure of cancer protein-protein interaction networks may be used to classify cancer types into two groups: those that are more treatable for various reasons and those that are not. Furthermore, using spectral analysis techniques we present a new method to identify potential drug targets, and discuss their effects on residual network structure.

This is joint work with Dr. M La Croix and Dr. P Hahnfeldt